

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Dumas Milne Edwards, J., et al.
Application. No. : To be assigned
Filed : Herewith
For : **FULL-LENGTH HUMAN cDNAs ENCODING
POTENTIALLY SECRETED PROTEINS**

1c406 U.S. PTO
09/731872
12/07/00

SEQUENCE SUBMISSION STATEMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

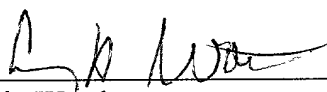
Dear Sir:

A copy of the Sequence Listing in computer readable form as required by 37 C.F.R.
§ 1.821(e) is submitted herewith.

As required by 37 C.F.R. § 1.821(f), the data on the enclosed disk is identical to the
Sequence Listing in the application filed herewith.

Respectfully submitted,

Dated: 12/7/00

By: 
Craig Worthem
Patent/Legal Assistant
Genset Corporation
875 Prospect Street
Suite #206
La Jolla, CA 92037
(858) 551-3031

SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean Baptiste
Bougueleret, Lydie
Jobert, Severin

<120> FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

<130> 78.US3.REG

<150> US 60/169,629
<151> 1999-12-08

<150> US 60/187,470
<151> 2000-03-06

<160> 482

<170> Patent.pm

<210> 1
<211> 2201
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 169..1692

<220>
<221> sig_peptide
<222> 169..249
<223> Von Heijne matrix
score 7.15265901862021
seq VLLLLLLERGMFS/SP

<400> 1
agatgtgaat agctccacta taccagcctc gtcttccttc cgggggacaa cgtgggtcag 60
ggcacagaga gatatttaat gtcaccctct tggggctttc atgggactcc ctctgccaca 120
ttttttggag gttgggaaag ttgctagagg cttcagaact ccagccta atg gat ccc 177
Met Asp Pro
-25
aaa ctc ggg aga atg gct gcg tcc ctg ctg gct gtg ctg ctg ctg ctg 225
Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu Leu Leu Leu
-20 -15 -10
ctg ctg gag cgc ggc atg ttc tcc tca ccc tcc ccg ccc ccg gcg ctg 273
Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro Pro Ala Leu
-5 1 5
tta gag aaa gtc ttc cag tac att gac ctc cat cag gat gaa ttt gtg 321
Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp Glu Phe Val
10 15 20
cag acg ctg aag gag tgg gtg gcc atc gag agc gac tct gtc cag cct 369
Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser Val Gln Pro
25 30 35 40
gtg cct cgc ttc aga caa gag ctc ttc aga atg atg gcc gtg gct gcg 417
Val Pro Arg Phe Arg Gln Glu Leu Phe Arg Met Met Ala Val Ala Ala
45 50 55
gac acg ctg cag cgc ctg ggg gcc cgt gtg gcc tcg gtg gac atg ggt 465

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| Asp | Thr | Leu | Gln | Arg | Leu | Gly | Ala | Arg | Val | Ala | Ser | Val | Asp | Met | Gly | | |
| | | | 60 | | | | | 65 | | | | | 70 | | | | |
| cct | cag | cag | ctg | ccc | gat | ggt | cag | agt | ctt | cca | ata | cct | ccc | gtc | atc | | 513 |
| Pro | Gln | Gln | Leu | Pro | Asp | Gly | Gln | Ser | Leu | Pro | Ile | Pro | Pro | Val | Ile | | |
| | | | 75 | | | | | 80 | | | | | 85 | | | | |
| ctg | gcc | gaa | ctg | ggg | agc | gat | ccc | acg | aaa | ggc | acc | gtg | tgc | ttc | tac | | 561 |
| Leu | Ala | Glu | Leu | Gly | Ser | Asp | Pro | Thr | Lys | Gly | Thr | Val | Cys | Phe | Tyr | | |
| | | | 90 | | | | 95 | | | | | 100 | | | | | |
| ggc | cac | ttg | gac | gtg | cag | cct | gct | gac | cgg | ggc | gat | ggg | tgg | ctc | acg | | 609 |
| Gly | His | Leu | Asp | Val | Gln | Pro | Ala | Asp | Arg | Gly | Asp | Gly | Trp | Leu | Thr | | |
| | | | | | 110 | | | | | 115 | | | | | 120 | | |
| gac | ccc | tat | gtg | ctg | acg | gag | gta | gac | ggg | aaa | ctt | tat | gga | cga | gga | | 657 |
| Asp | Pro | Tyr | Val | Leu | Thr | Glu | Val | Asp | Gly | Lys | Leu | Tyr | Gly | Arg | Gly | | |
| | | | | | 125 | | | | | 130 | | | | | 135 | | |
| gcg | acc | gac | aac | aaa | ggc | cct | gtc | ttg | gct | tgg | atc | aat | gct | gtg | agc | | 705 |
| Ala | Thr | Asp | Asn | Lys | Gly | Pro | Val | Leu | Ala | Trp | Ile | Asn | Ala | Val | Ser | | |
| | | | | | 140 | | | | | 145 | | | | | 150 | | |
| gcc | ttc | aga | gcc | ctg | gag | caa | gat | ctt | cct | gtg | aat | atc | aaa | ttc | atc | | 753 |
| Ala | Phe | Arg | Ala | Leu | Glu | Gln | Asp | Leu | Pro | Val | Asn | Ile | Lys | Phe | Ile | | |
| | | | | | 155 | | | | | 160 | | | | | 165 | | |
| att | gag | ggg | atg | gaa | gag | gct | ggc | tct | gtt | gcc | ctg | gag | gaa | ctt | gtg | | 801 |
| Ile | Glu | Gly | Met | Glu | Glu | Ala | Gly | Ser | Val | Ala | Leu | Glu | Glu | Leu | Val | | |
| | | | | | | 175 | | | | | 180 | | | | | | |
| gaa | aaa | gaa | aag | gac | cga | ttc | ttc | tct | ggt | gtg | gac | tac | att | gta | att | | 849 |
| Glu | Lys | Glu | Lys | Asp | Arg | Phe | Phe | Ser | Gly | Val | Asp | Tyr | Ile | Val | Ile | | |
| | | | | | | 190 | | | | 195 | | | | | 200 | | |
| tca | gat | aac | ctg | tgg | atc | agc | caa | agg | aag | cca | gca | atc | act | tat | gga | | 897 |
| Ser | Asp | Asn | Leu | Trp | Ile | Ser | Gln | Arg | Lys | Pro | Ala | Ile | Thr | Tyr | Gly | | |
| | | | | | 205 | | | | | 210 | | | | | 215 | | |
| acc | cgg | ggg | aac | agc | tac | ttc | atg | gtg | gag | gtg | aaa | tgc | aga | gac | cag | | 945 |
| Thr | Arg | Gly | Asn | Ser | Tyr | Phe | Met | Val | Glu | Val | Lys | Cys | Arg | Asp | Gln | | |
| | | | | | 220 | | | | 225 | | | | | | 230 | | |
| gat | ttt | cac | tca | gga | acc | ttt | ggt | ggc | atc | ctt | cat | gaa | cca | atg | gct | | 993 |
| Asp | Phe | His | Ser | Gly | Thr | Phe | Gly | Gly | Ile | Leu | His | Glu | Pro | Met | Ala | | |
| | | | | | 235 | | | | 240 | | | | | | 245 | | |
| gat | ctg | gtt | gct | ctt | ctc | ggt | agc | ctg | gta | gac | tgc | tct | ggt | cat | atc | | 1041 |
| Asp | Leu | Val | Ala | Leu | Leu | Gly | Ser | Leu | Val | Asp | Ser | Ser | Gly | His | Ile | | |
| | | | | | | 250 | | | | 255 | | | | | 260 | | |
| ctg | gtc | cct | gga | atc | tat | gat | gaa | gtg | gtt | cct | ctt | aca | gaa | gag | gaa | | 1089 |
| Leu | Val | Pro | Gly | Ile | Tyr | Asp | Glu | Val | Val | Pro | Leu | Thr | Glu | Glu | Glu | | |
| | | | | | | 270 | | | | 275 | | | | | 280 | | |
| ata | aat | aca | tac | aaa | gcc | atc | cat | cta | gac | cta | gaa | gaa | tac | cgg | aat | | 1137 |
| Ile | Asn | Thr | Tyr | Lys | Ala | Ile | His | Leu | Asp | Leu | Glu | Glu | Tyr | Arg | Asn | | |
| | | | | | 285 | | | | | 290 | | | | | 295 | | |
| agc | agc | cgg | gtt | gag | aaa | ttt | ctg | ttc | gat | act | aag | gag | gag | att | cta | | 1185 |
| Ser | Ser | Arg | Val | Glu | Lys | Phe | Leu | Phe | Asp | Thr | Lys | Glu | Glu | Ile | Leu | | |
| | | | | | 300 | | | | 305 | | | | | | 310 | | |
| atg | cac | ctc | tgg | agg | tac | cca | tct | ctt | tct | att | cat | ggg | atc | gag | ggc | | 1233 |
| Met | His | Leu | Trp | Arg | Tyr | Pro | Ser | Leu | Ser | Ile | His | Gly | Ile | Glu | Gly | | |
| | | | | | 315 | | | | 320 | | | | | | 325 | | |
| gcg | ttt | gat | gag | cct | gga | act | aaa | aca | gtc | ata | cct | ggc | cga | gtt | ata | | 1281 |
| Ala | Phe | Asp | Glu | Pro | Gly | Thr | Lys | Thr | Val | Ile | Pro | Gly | Arg | Val | Ile | | |
| | | | | | | 330 | | | | 335 | | | | | 340 | | |
| gga | aaa | ttt | tca | atc | cgt | cta | gtc | cct | cac | atg | aat | gtg | tct | gcg | gtg | | 1329 |
| Gly | Lys | Phe | Ser | Ile | Arg | Leu | Val | Pro | His | Met | Asn | Val | Ser | Ala | Val | | |
| | | | | | | 345 | | | | 350 | | | | | 355 | | |
| gaa | aaa | cag | gtg | aca | cga | cat | ctt | gaa | gat | gtg | ttc | tcc | aaa | aga | aat | | 1377 |
| Glu | Lys | Gln | Val | Thr | Arg | His | Leu | Glu | Asp | Val | Phe | Ser | Lys | Arg | Asn | | |

```

          365          370          375
agt tcc aac aag atg gtt gtt tcc atg act cta gga cta cac ccg tgg      1425
Ser Ser Asn Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp
          380          385          390
att gca aat att gat gac acc cag tat ctc gca gca aaa aga gcg atc      1473
Ile Ala Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile
          395          400          405
aga aca gtg ttt gga aca gaa cca gat atg atc cgg gat gga tcc acc      1521
Arg Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
          410          415          420
att cca att gcc aaa atg ttc cag gag atc gtc cac aag agc gtg gtg      1569
Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val Val
          425          430          435          440
cta att ccg ctg gga gct gtt gat gat gga gaa cat tcg cag aat gag      1617
Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln Asn Glu
          445          450          455
aaa atc aac agg tgg aac tac ata gag gga acc aaa tta ttt gct gcc      1665
Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu Phe Ala Ala
          460          465          470
ttt ttc tta gag atg gcc cag ctc cat taatcacaag aaccttctag      1712
Phe Phe Leu Glu Met Ala Gln Leu His
          475          480
tctgatctga tccactgaca gattcacctc cccacatcc ctagacaggg atggaatgta      1772
aatatccaga gaatttgggt ctagtatagt acattttccc ttccatttaa aatgtcttgg      1832
gatatctgga tcagtaataa aatatttcaa aggcacagat gttggaaatg gtttaagggtc      1892
ccccactgca caccttctc aagtcatagc tgcttgcagc aacttgattt cccaaggtcc      1952
tgtgcaatag cccaggatt ggattccttc caacctttta gcatatctcc aaccttgcaa      2012
tttgattggc ataatactc cagtttgctt tctaggtcct caagtgtctg tgacacataa      2072
tcattccatc caatgatcgc ctttgcttta ccactctttc cttttatctt attaataaaa      2132
atgttggtct ccaccactga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagaaaaaa      2192
aaaaaaaaa
2201

<210> 2
<211> 1631
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..1140

<220>
<221> sig_peptide
<222> 148..240
<223> Von Heijne matrix
score 10.0910253445132
seq LVLLLVTRSPVNA/CL

<400> 2
gtctgctgcc gccattgtgc ggcgctggtc cctcagagg gttcctgctg ctgccggtgc      60
cttggaacct cccctcgtc tctcgttcta ctgcccagg agcccggcgg gtccgggact      120
cccgccgtg ccggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc      174
Met Trp Leu Trp Glu Asp Gln Gly Gly
-30 -25
ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg      222
Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr
-20 -15 -10
cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta      270

```



```

300
tacagggata tcaaaatacc ctttgtgcta gcccaggccc tggggaatca ggtgactcac 1250
acaaatgcaa tagttggtca ctgcattttt acctgaacca aagctaaacc cggtgttgcc 1310
accatgcacc atggcatgcc agagttcaac actgttgctc ttgaaaatct ggggtctgaa 1370
aaaacgcaca agagccccctg cctgtcccta gctgaggcac acagggagac ccagtgagga 1430
taagcacaga ttgaattgta caatttgcag atgcagatgt aaatgcatgg gacatgcatg 1490
ataactcaga gttgacattt taaaacttgc cacacttatt tcaaatattt gtactcagct 1550
atgttaacat gtactgtaga catcaaactt gtggccatac taataaaatt attaaaagga 1610
gcacaaaaaa aaaaaaaaaa a 1631

```

```

<210> 3
<211> 1245
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 85..906

```

```

<220>
<221> sig_peptide
<222> 85..135
<223> Von Heijne matrix
      score 3.86022363031904
      seq GFVAALVAGGVAG/VS

```

```

<400> 3
aaaacatggc ggcgccccagc gcgcgaggac gtgatccgct tctgctccgg cttggattgt 60
agccttgacg aggtctgagc gacc atg gac cgg ccg ggg ttc gtg gca gcg 111
                               Met Asp Arg Pro Gly Phe Val Ala Ala
                               -15 -10
ctg gtg gct ggt ggg gta gca ggt gtt tct gtt gac ttg ata tta ttt 159
Leu Val Ala Gly Gly Val Ala Gly Val Ser Val Asp Leu Ile Leu Phe
                               -5 1 5
cct ctg gat acc att aaa acc agg ctg cag agt ccc caa gga ttt agt 207
Pro Leu Asp Thr Ile Lys Thr Arg Leu Gln Ser Pro Gln Gly Phe Ser
10 15 20
aag gct ggt ggt ttt cat gga ata tat gct ggc gtt cct tct gct gct 255
Lys Ala Gly Gly Phe His Gly Ile Tyr Ala Gly Val Pro Ser Ala Ala
25 30 35 40
att gga tcc ttt cct aat gct gct gca ttt ttt atc acc tat gaa tat 303
Ile Gly Ser Phe Pro Asn Ala Ala Ala Phe Phe Ile Thr Tyr Glu Tyr
45 50 55
gtg aag tgg ttt ttg cat gct gat tca tct tca tat ttg aca cct atg 351
Val Lys Trp Phe Leu His Ala Asp Ser Ser Ser Tyr Leu Thr Pro Met
60 65 70
aaa cat atg ttg gct gcc tct gct gga gaa gtg gtt gcc tgc ctg att 399
Lys His Met Leu Ala Ala Ser Ala Gly Glu Val Val Ala Cys Leu Ile
75 80 85
cga gtt cca tct gaa gtg gtt aag cag agg gca cag gta tct gct tct 447
Arg Val Pro Ser Glu Val Lys Gln Arg Ala Gln Val Ser Ala Ser
90 95 100
aca aga aca ttt cag att ttc tct aac atc tta tat gaa gag ggt atc 495
Thr Arg Thr Phe Gln Ile Phe Ser Asn Ile Leu Tyr Glu Glu Gly Ile
105 110 115 120
caa ggg ttg tat cga ggc tat aaa agc aca gtt tta aga gag att cct 543
Gln Gly Leu Tyr Arg Gly Tyr Lys Ser Thr Val Leu Arg Glu Ile Pro
125 130 135

```

```

ttt tct ttg gtc cag ttt ccc tta tgg gag tcc tta aaa gcc ctc tgg      591
Phe Ser Leu Val Gln Phe Pro Leu Trp Glu Ser Leu Lys Ala Leu Trp
      140      145      150
tcc tgg agg cag gat cat gtg gtg gat tct tgg cag tca gca gtc tgt      639
Ser Trp Arg Gln Asp His Val Val Asp Ser Trp Gln Ser Ala Val Cys
      155      160      165
gga gct ttt gca ggt gga ttt gcc gct gca gtc acc acc cct cta gac      687
Gly Ala Phe Ala Gly Gly Phe Ala Ala Ala Val Thr Thr Pro Leu Asp
      170      175      180
gtg gca aag aca aga att atg ctg gca aag gct ggc tcc agc act gct      735
Val Ala Lys Thr Arg Ile Met Leu Ala Lys Ala Gly Ser Ser Thr Ala
      185      190      195      200
gat ggg aat gtg ctc tct gtc ctg cat ggg gtc tgg cgg tca cag ggg      783
Asp Gly Asn Val Leu Ser Val Leu His Gly Val Trp Arg Ser Gln Gly
      205      210      215
ctg gca gga tta ttt gca ggt gtc ttc cct cga atg gca gcc atc agt      831
Leu Ala Gly Leu Phe Ala Gly Val Phe Pro Arg Met Ala Ala Ile Ser
      220      225      230
ctg gga ggt ttc atc ttt ctg ggg gct tat gac cga acg cac agc ttg      879
Leu Gly Gly Phe Ile Phe Leu Gly Ala Tyr Asp Arg Thr His Ser Leu
      235      240      245
ctg ttg gaa gtt ggc aga aag agt cct tgaagcagag acaagcctca      926
Leu Leu Glu Val Gly Arg Lys Ser Pro
      250      255
cctccacttc tgtcaagaga ggggcctgca gtgcaaacc tcttccgctg agcagctgtc      986
tgaactatag gccccagtgc tgaagaccag ttgtgctaag ataccggcat ggagattgtg      1046
ccatccgtgg tataggctgg ctggtatgaa gtcattggcc tgtatgccag agagctaaga      1106
gaagaaaacg gggctctgtgg cgggtactctg aacaatttcc tcagaacctc ttaataaata      1166
agtttggtaa tgctgagaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1226
agaaaaaaaa aaaaaaaaaa

```

```

<210> 4
<211> 1623
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 31..1248

```

```

<220>
<221> sig_peptide
<222> 31..135
<223> Von Heijne matrix
      score 6.3770152988307
      seq TLLLFAAPFGLLG/EK

```

```

<400> 4
aacctcttcc gtcggctgaa ttgcggccgt atg cgc ggc tct gtg gag tgc acc      54
      Met Arg Gly Ser Val Glu Cys Thr
      -35      -30
tgg ggt tgg ggg cac tgt gcc ccc agc ccc ctg ctc ctt tgg act cta      102
Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu
      -25      -20      -15
ctt ctg ttt gca gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag      150
Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln
      -10      -5      1      5
gtg tct ctg gag gtc atc cct aac tgg ctg ggc ccc ctg cag aac ctg      198

```

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Val | Ser | Leu | Glu | Val | Ile | Pro | Asn | Trp | Leu | Gly | Pro | Leu | Gln | Asn | Leu | |
| | | | | 10 | | | | | 15 | | | | | 20 | | |
| ctt | cat | ata | cgg | gca | gtg | ggc | acc | aat | tcc | aca | ctg | cac | tat | gtg | tgg | 246 |
| Leu | His | Ile | Arg | Ala | Val | Gly | Thr | Asn | Ser | Thr | Leu | His | Tyr | Val | Trp | |
| | | | 25 | | | | | 30 | | | | | 35 | | | |
| agc | agc | ctg | ggg | cct | ctg | gca | gtg | gta | atg | gtg | gcc | acc | aac | acc | ccc | 294 |
| Ser | Ser | Leu | Gly | Pro | Leu | Ala | Val | Val | Met | Val | Ala | Thr | Asn | Thr | Pro | |
| | | | 40 | | | | 45 | | | | 50 | | | | | |
| cac | agc | acc | ctg | agc | gtc | aac | tgg | agc | ctc | ctg | cta | tcc | cct | gag | ccc | 342 |
| His | Ser | Thr | Leu | Ser | Val | Asn | Trp | Ser | Leu | Leu | Ser | Pro | Glu | Pro | | |
| | | | 55 | | | 60 | | | | | 65 | | | | | |
| gat | ggg | ggc | ctg | atg | gtg | ctc | cct | aag | gac | agc | att | cag | ttt | tct | tct | 390 |
| Asp | Gly | Gly | Leu | Met | Val | Leu | Pro | Lys | Asp | Ser | Ile | Gln | Phe | Ser | Ser | |
| 70 | | | | | 75 | | | | 80 | | | | | | 85 | |
| gcc | ctt | ggt | ttt | acc | agg | ctg | ctt | gag | ttt | gac | agc | acc | aac | gtg | tcc | 438 |
| Ala | Leu | Val | Phe | Thr | Arg | Leu | Leu | Glu | Phe | Asp | Ser | Thr | Asn | Val | Ser | |
| | | | | 90 | | | | 95 | | | | | 100 | | | |
| gat | acg | gca | gca | aag | cct | ttg | gga | aga | cca | tat | cct | cca | tac | tcc | ttg | 486 |
| Asp | Thr | Ala | Ala | Lys | Pro | Leu | Gly | Arg | Pro | Tyr | Pro | Pro | Tyr | Ser | Leu | |
| | | | 105 | | | | 110 | | | | | 115 | | | | |
| gcc | gat | ttc | tct | tgg | aac | aac | atc | act | gat | tca | ttg | gat | cct | gcc | acc | 534 |
| Ala | Asp | Phe | Ser | Trp | Asn | Asn | Ile | Thr | Asp | Ser | Leu | Asp | Pro | Ala | Thr | |
| | | | 120 | | | | 125 | | | | | 130 | | | | |
| ctg | agt | gcc | aca | ttt | caa | ggc | cac | ccc | atg | aac | gac | cct | acc | agg | act | 582 |
| Leu | Ser | Ala | Thr | Phe | Gln | Gly | His | Pro | Met | Asn | Asp | Pro | Thr | Arg | Thr | |
| | | | 135 | | | 140 | | | | | 145 | | | | | |
| ttt | gcc | aat | ggc | agc | ctg | gcc | ttc | agg | gtc | cag | gcc | ttt | tcc | agg | tcc | 630 |
| Phe | Ala | Asn | Gly | Ser | Leu | Ala | Phe | Arg | Val | Gln | Ala | Phe | Ser | Arg | Ser | |
| 150 | | | | | 155 | | | | | 160 | | | | | 165 | |
| agc | cga | cca | gcc | caa | ccc | cct | cgc | ctc | ctg | cac | aca | gca | gac | acc | tgt | 678 |
| Ser | Arg | Pro | Ala | Gln | Pro | Pro | Arg | Leu | Leu | His | Thr | Ala | Asp | Thr | Cys | |
| | | | 170 | | | | | 175 | | | | | 180 | | | |
| cag | cta | gag | gtg | gcc | ctg | att | gga | gcc | tct | ccc | cgg | gga | aac | cgt | tcc | 726 |
| Gln | Leu | Glu | Val | Ala | Leu | Ile | Gly | Ala | Ser | Pro | Arg | Gly | Asn | Arg | Ser | |
| | | | 185 | | | | 190 | | | | | | 195 | | | |
| ctg | ttt | ggg | ctg | gag | gta | gcc | aca | ttg | ggc | cag | ggc | cct | gac | tgc | ccc | 774 |
| Leu | Phe | Gly | Leu | Glu | Val | Ala | Thr | Leu | Gly | Gln | Gly | Pro | Asp | Cys | Pro | |
| | | | 200 | | | | 205 | | | | | 210 | | | | |
| tca | atg | cag | gag | cag | cac | tcc | atc | gac | gat | gaa | tat | gca | ccg | gcc | gtc | 822 |
| Ser | Met | Gln | Glu | Gln | His | Ser | Ile | Asp | Asp | Glu | Tyr | Ala | Pro | Ala | Val | |
| | | | 215 | | | 220 | | | | | 225 | | | | | |
| ttc | cag | ttg | gac | cag | cta | ctg | tgg | ggc | tcc | ctc | cca | tca | ggc | ttt | gca | 870 |
| Phe | Gln | Leu | Asp | Gln | Leu | Trp | Gly | Ser | Leu | Pro | Ser | Gly | Phe | Ala | | |
| 230 | | | | | 235 | | | | 240 | | | | | 245 | | |
| cag | tgg | cga | cca | gtg | gct | tac | tcc | cag | aag | ccg | ggg | ggc | cga | gaa | tca | 918 |
| Gln | Trp | Arg | Pro | Val | Ala | Tyr | Ser | Gln | Lys | Pro | Gly | Gly | Arg | Glu | Ser | |
| | | | 250 | | | | | 255 | | | | | 260 | | | |
| gcc | ctg | ccc | tgc | caa | gct | tcc | cct | ctt | cat | cct | gcc | tta | gca | tac | tct | 966 |
| Ala | Leu | Pro | Cys | Gln | Ala | Ser | Pro | Leu | His | Pro | Ala | Leu | Ala | Tyr | Ser | |
| | | | 265 | | | | 270 | | | | | 275 | | | | |
| ctt | ccc | cag | tca | ccc | att | gtc | cga | gcc | ttc | ttt | ggg | tcc | cag | aat | aac | 1014 |
| Leu | Pro | Gln | Ser | Pro | Ile | Val | Arg | Ala | Phe | Phe | Gly | Ser | Gln | Asn | Asn | |
| | | | 280 | | | | 285 | | | | | 290 | | | | |
| ttc | tgt | gcc | ttc | aat | ctg | acg | ttc | ggg | gct | tcc | aca | ggc | cct | ggc | tat | 1062 |
| Phe | Cys | Ala | Phe | Asn | Leu | Thr | Phe | Gly | Ala | Ser | Thr | Gly | Pro | Gly | Tyr | |
| | | | 295 | | | 300 | | | | | 305 | | | | | |
| tgg | gac | caa | cac | tac | ctc | agc | tgg | tcg | atg | ctc | ctg | ggg | gtg | ggc | ttc | 1110 |
| Trp | Asp | Gln | His | Tyr | Leu | Ser | Trp | Ser | Met | Leu | Leu | Gly | Val | Gly | Phe | |

| | | | | | | | |
|--|-----|-----|-----|-----|-----|-----|------|
| 310 | | 315 | | 320 | | 325 | |
| cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg | | | | | | | 1158 |
| Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val | | | | | | | |
| | 330 | | 335 | | 340 | | |
| gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg | | | | | | | 1206 |
| Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu | | | | | | | |
| | 345 | | 350 | | 355 | | |
| ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat | | | | | | | 1248 |
| Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn | | | | | | | |
| | 360 | | 365 | | 370 | | |
| taaggcccg cctctggagg gaaggacatt actgaacctg tcttgctgtg cctcgaaact | | | | | | | 1308 |
| ctggagggtg gagcatcaag ttccagcccc cttcactccc ccatcttgct tttctgtgga | | | | | | | 1368 |
| acctcagagg ccagcctcga ctctctggag acccccaggt ggggcttcct tcatactttg | | | | | | | 1428 |
| ttggggggact ttggaggcgg gcaggggaca gggctattga taagggtccc ttggtgttgc | | | | | | | 1488 |
| cttcttgcat ctccacacat ttcccttgga tgggacttgc aggcctaaat gagaggcatt | | | | | | | 1548 |
| ctgactgggt ggctgccctg gaaggcaaga aaatagattt attttttttt cacagggcaa | | | | | | | 1608 |
| aaaaaaaaa aaaaa | | | | | | | 1623 |

<210> 5
 <211> 1454
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 72..143

 <220>
 <221> sig_peptide
 <222> 72..119
 <223> Von Heijne matrix
 score 5.68931280801877
 seq LGMLLGLLMAACT/PS

| | |
|--|------|
| <400> 5 | |
| gtgtctgccca ctcggctgcc ggagccgaa ggtccctgac tatggctccc cagagcctgc | 60 |
| cttcatctag g atg gct cct ctg ggc atg ctg ctt ggg ctg ctg atg gcc | 110 |
| Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala | |
| -15 -10 -5 | |
| gcc tgc aca cct tct gcc tca gtc atc aga acc tgaaggagtt tgccctgacc | 163 |
| Ala Cys Thr Pro Ser Ala Ser Val Ile Arg Thr | |
| 1 5 | |
| aaccagaga agcagcac caaagaaacg gagagaaaag aaaccaaagc cgaggaggag | 223 |
| ctggatgccg aagtcctgga ggtgttccac ccgacgcatt agtggcaggc ccttcagcca | 283 |
| gggcaggctg tccctgcagg atcccacgta cggctgaatc ttcagactgg ggaaagagag | 343 |
| gcaaaactcc aatatgagga caagttccga aataatttga aaggcaaaag gctggatatc | 403 |
| aacaccaaca cctacacatc tcaggatctc aagagtgcac tggcaaaatt caaggagggg | 463 |
| gcagagatgg agagttcaaa ggaagacaag gcaaggcagg ctgaggtaaa gcggtctctc | 523 |
| cgccccattg aggaactgaa gaaagacttt gatgagctga atgttgctcat tgagactgac | 583 |
| atgcagatca tgggtacggct gatcaacaag ttcaatagtt ccagctccag tttggaagag | 643 |
| aagattgctg cgctctttga tcttgaatat tatgtccatc agatggacaa tgcgcaggac | 703 |
| ctgctttcct ttggtggtct tcaagtgtgt atcaatgggc tgaacagcac agagcccctc | 763 |
| gtgaaggagt atgctgcgtt tgtgctgggc gctgcctttt ccagcaaccc caaggtccag | 823 |
| gtggaggcca tcgaaggggg agccctgcag aagctgctgg tcatcctggc cacggagcag | 883 |
| ccgctcactg caaagggagg tgctcaccgt gcgcgtgggc aactgctct acgacctggg | 943 |
| cacggagaag atgttcgccg aggaggaggc tgagctgacc caggagatgt ccccagagaa | 1003 |
| gctgcagcag tatcgccagg tacacctcct gccakgcctg tgggaacagg gctggtgcga | 1063 |
| gatcacggcc cacctcctgg cgctgcccga gcatgatgcc ygtgagaagg tgctgcwgac | 1123 |

```

actgggcgtc ctctgacca cctgceggga ccgctaccgt caggaccccc agctcggcag 1183
gacactggcc agcctgcagg ctgagtagca ggtgctggcc agcctggagc tgcaggatgg 1243
tgaggacgag ggctacttcc aggagctgct gggctctgtc aacagcttgc tgaaggagct 1303
gagatgaggc cccacaccag gactggactg ggatgccgct agtgaggctg aggggtgcca 1363
gcgtgggtgg gcttctcagg caggaggaca tcttggcagt gctggcttgg ccattaaatg 1423
gaaacctgaa ggccaaaaaa aaaaaaaaaa a 1454

```

```

<210> 6
<211> 1639
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 111..1154

```

```

<220>
<221> sig_peptide
<222> 111..197
<223> Von Heijne matrix
      score 4.68065944212013
      seq LLGPLMAACFTFC/LS

```

```

<400> 6
agacggtcgc cgccgcgttt gcgcaggggg agctggtcgc cgccgcggcc gcctggaatt 60
gtgggagttg tgtctgccac tcggctgccg gaggccgaag gtccctgact atg gct 116
                                     Met Ala
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt 164
Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu
      -25                               -20                -15
ggg ccg ctg atg gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac 212
Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn
      -10                               -5                1                5
ctg aag gag ttt gcc ctg acc aac cca gag aag agc agc acc aaa gaa 260
Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu
      10                               15                20
aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc 308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val
      25                               30                35
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg 356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly
      40                               45                50
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg 404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly
      55                               60                65
gaa aga gag gca aaa ctc caa tat gag gac aag ttc cga aat aat ttg 452
Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu
      70                               75                80                85
aaa ggc aaa agg ctg gat atc aac acc aac acc tac aca tct cag gat 500
Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp
      90                               95                100
ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt 548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser
      105                               110                115
tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc 596
Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg
      120                               125                130
ccc att gag gaa ctg aag aaa gac ttt gat gag ctg aat gtt gtc att 644

```

| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|-----|-----|-----|------------|------------|-----|-----|-----|-----|------|--|
| Pro | Ile | Glu | Glu | Leu | Lys | Lys | Asp | Phe | Asp | Glu | Leu | Asn | Val | Val | Ile | | |
| 135 | | | | | | 140 | | | | | 145 | | | | | | |
| gag | act | gac | atg | cag | atc | atg | gta | cgg | ctg | atc | aac | aag | ttc | aat | agt | 692 | |
| Glu | Thr | Asp | Met | Gln | Ile | Met | Val | Arg | Leu | Ile | Asn | Lys | Phe | Asn | Ser | | |
| 150 | | | | | 155 | | | | | 160 | | | | | 165 | | |
| tcc | agc | tcc | agt | ttg | gaa | gag | aag | att | gct | gcg | ctc | ttt | gat | ctt | gaa | 740 | |
| Ser | Ser | Ser | Ser | Leu | Glu | Glu | Lys | Ile | Ala | Ala | Leu | Phe | Asp | Leu | Glu | | |
| | | | | 170 | | | | | 175 | | | | | 180 | | | |
| tat | tat | gtc | cat | cag | atg | gac | aat | gcg | cag | gac | ctg | ctt | tcc | ttt | ggg | 788 | |
| Tyr | Tyr | Val | His | Gln | Met | Asp | Asn | Ala | Gln | Asp | Leu | Leu | Ser | Phe | Gly | | |
| | | | 185 | | | | | 190 | | | | | 195 | | | | |
| ggg | ctt | caa | gtg | gtg | atc | aat | ggg | ctg | aac | agc | aca | gag | ccc | ctc | gtg | 836 | |
| Gly | Leu | Gln | Val | Val | Ile | Asn | Gly | Leu | Asn | Ser | Thr | Glu | Pro | Leu | Val | | |
| | 200 | | | | | 205 | | | | | 210 | | | | | | |
| aag | gag | tat | gct | gcg | ttt | gtg | ctg | ggc | gct | gcc | ttt | tcc | agc | aac | ccc | 884 | |
| Lys | Glu | Tyr | Ala | Ala | Phe | Val | Leu | Gly | Ala | Ala | Phe | Ser | Ser | Asn | Pro | | |
| | 215 | | | | 220 | | | | | 225 | | | | | | | |
| aag | gtc | cag | gtg | gag | gcc | atc | gaa | ggg | gga | gcc | ctg | cag | aag | ctg | ctg | 932 | |
| Lys | Val | Gln | Val | Glu | Ala | Ile | Glu | Gly | Gly | Ala | Leu | Gln | Lys | Leu | Leu | | |
| | 230 | | | 235 | | | | 240 | | | | | | 245 | | | |
| gtc | atc | ctg | gcc | acg | gag | cag | ccg | ctc | act | gca | aag | aag | aag | gtc | ctg | 980 | |
| Val | Ile | Leu | Ala | Thr | Glu | Gln | Pro | Leu | Thr | Ala | Lys | Lys | Lys | Val | Leu | | |
| | | | 250 | | | | | 255 | | | | | | 260 | | | |
| ttt | gca | ctg | tgc | tcc | ctg | ctg | cgc | cac | ttc | ccc | tat | gcc | cag | cgg | cag | 1028 | |
| Phe | Ala | Leu | Cys | Ser | Leu | Leu | Arg | His | Phe | Pro | Tyr | Ala | Gln | Arg | Gln | | |
| | | | 265 | | | | 270 | | | | | | 275 | | | | |
| ttc | ctg | aag | ctc | ggg | ggg | ctg | cag | gtc | ctg | agg | acc | ctg | gtg | cag | gag | 1076 | |
| Phe | Leu | Lys | Leu | Gly | Gly | Leu | Gln | Val | Leu | Arg | Thr | Leu | Val | Gln | Glu | | |
| | 280 | | | | | 285 | | | | | 290 | | | | | | |
| aag | ggc | acg | gag | gtg | ctc | gcc | gtg | cgc | gtg | gtc | aca | ctg | ctc | tac | gac | 1124 | |
| Lys | Gly | Thr | Glu | Val | Leu | Ala | Val | Arg | Val | Val | Thr | Leu | Leu | Tyr | Asp | | |
| | 295 | | | | 300 | | | | 305 | | | | | | | | |
| ctg | gtc | acg | gag | aag | atg | ttc | gcc | gag | gag | taggctgagc | tgacccagga | | | | | 1174 | |
| Leu | Val | Thr | Glu | Lys | Met | Phe | Ala | Glu | Glu | | | | | | | | |
| | 310 | | | 315 | | | | | | | | | | | | | |
| gatgtcccca | gagaagctgc | agcagtatcg | ccaggtacac | ctcctgccag | gcctgtggga | | | | | | | | | | | 1234 | |
| acagggctgg | tgcgagatca | cggccacct | cctggcgctg | cccagacatg | atgcccgtga | | | | | | | | | | | 1294 | |
| gaaggtgctg | cagacactgg | gcgtcctcct | gaccacctgc | cgggaccgct | accgtcagga | | | | | | | | | | | 1354 | |
| ccccagctc | ggcaggacac | tggccagcct | gcaggctgag | taccaggtgc | tggccagcct | | | | | | | | | | | 1414 | |
| ggagctgcag | gatggtgagg | acgagggcta | cttccaggag | ctgctgggct | ctgtcaacag | | | | | | | | | | | 1474 | |
| cttgctgaag | gagctgagat | gaggccccac | accaggactg | gactgggatg | ccgctagtga | | | | | | | | | | | 1534 | |
| ggctgagggg | tgccagcgtg | ggtgggcttc | tcaggcagga | ggacatcttg | gcagtgtctgg | | | | | | | | | | | 1594 | |
| cttggccatt | aaatggaac | ctgaaggcaa | aaaaaaaaaa | aaaaa | | | | | | | | | | | | 1639 | |

<210> 7
 <211> 1768
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 66..1256

 <220>
 <221> sig_peptide
 <222> 66..173
 <223> Von Heijne matrix
 score 4.89555877630516

seq LLLRLNDAALRA/LQ

```

<400> 7
agaggagggtg gcggtgggtgg ccctcgcttg tggcccccggt gctgcttgca ctcgaactcg      60
tcgcc atg gag gag ctc cag gag cct ctg aga gga cag ctc cgg ctc tgc      110
    Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys
        -35                -30                -25
    ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac      158
    Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
        -20                -15                -10
    gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg      206
    Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
        -5                1                5                10
    gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct      254
    Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
        15                20                25
    ggt tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag      302
    Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
        30                35                40
    ggc gct ggt ggt agc ttg gac ctt gtg tgc caa cgc ttc ctc agg tct      350
    Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser
        45                50                55
    ggg cct aac agc ctc cac tgc ctg ggc tca ctc agg gag cgc ctc att      398
    Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile
        60                65                70                75
    att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga      446
    Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly
        80                85                90
    cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca      494
    His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr
        95                100                105
    gga ggc tat tct gaa gga gat gca gta tca cag cca cag atg gca cta      542
    Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu
        110                115                120
    gag gag gtg tca gtg tca gat cca ctg gca agc aac caa gga cag tca      590
    Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser
        125                130                135
    ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc      638
    Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser
        140                145                150                155
    cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct      686
    Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser
        160                165                170
    gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act      734
    Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr
        175                180                185
    gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg cca agc      782
    Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser
        190                195                200
    ccc cta caa ggc ctg acc aat cag gat tta caa gag gga gaa gat tgg      830
    Pro Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp
        205                210                215
    gag caa gaa gat gag gac atg gac ccc aga tta gaa cac agt tcc tca      878
    Glu Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser
        220                225                230                235
    gtt caa gaa gat tct gaa tcc cca agt cct gaa gat ata cca gac tac      926
    Val Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr
        240                245                250

```



```

ctc ctg caa tac agg gcc atc cac agt gca gaa cag caa cat gcc tat      974
Leu Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr
      255                                260                                265
gag cag gac ttt gag aca gat tat gct gaa tac cgc atc ctg cat gcc      1022
Glu Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala
      270                                275                                280
cgt gtt ggg act gca agc caa agg ttc ata gag ctg gga gca gag att      1070
Arg Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile
      285                                290                                295
aaa aga gtt cgg cga gga act cca gaa tac aag gtc ctg gaa gac aag      1118
Lys Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys
      300                                305                                310                                315
ata atc cag gaa tat aaa aag ttc agg aag cag tac cca agt tac aga      1166
Ile Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg
      320                                325                                330
gaa gaa aag cgt cgc tgt gag tac ctt cac cag aaa ttg tcc cac att      1214
Glu Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile
      335                                340                                345
aaa ggt ctc atc ctg gag ttt gag gaa aag aac agg ggc agc      1256
Lys Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
      350                                355                                360
tgaagttatc aaggggaattt ttgagcctct gcttagtgaa acacaaagga acaaagcagc      1316
tataaactaa atagaatgca actatctgct tttcttatgc tgaccactgg agtccatgg      1376
ggcaagtaga gagctgctct aggttcttga gggttggttt tcattattaa tttttagggt      1436
atgggcactg tgcaaagact ccatagctgt gcctaggagt ctaggaaaag tgacagaggc      1496
ttggcttttt taccttttagt tcagccaagt cattttcaag tcctgagaaa tgacatcatc      1556
ttcaggataa aataatgagg acattagaca aaccaaacta agtgaatttt agcctggtag      1616
cctctctaag gaaacagtaa taataacttc tgataagagt taaaagaact tgtagcatac      1676
ctggatataa tgggaaaggg cctgggtgtt acccatgtac tgaaaatgaa cttttaccaa      1736
catggctaaa aaattaaaaa aaaaaaaaaa aa      1768

```

```

<210> 8
<211> 1510
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 190..1398

```

```

<220>
<221> sig_peptide
<222> 190..252
<223> Von Heijne matrix
      score 5.8172934575094
      seq ALLWAQEVGQVLA/GR

```

```

<400> 8
acggttgccc tggcagcgcg cgaggetggg gagtcggcag ccctgtggca gccggcgggc      60
tggtttccat ggttgacga ttaggaacca ccagctgctg catcccatgg ccaggggtgg      120
cgtccaggtg gcagagcagc taggaacgca aggcctgaac ctggggccag acaccctgct      180
ctcccggcc atg gtc aac gac cct cca gta cct gcc tta ctg tgg gcc cag      231
      Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln
      -20                                -15                                -10
gag gtg ggc caa gtc ttg gca ggc cgt gcc cgc agg ctg ctg ctg cag      279
Glu Val Gly Gln Val Leu Ala Gly Arg Ala Arg Leu Leu Leu Gln
      -5                                1                                5
ttt ggg gtg ctc ttc tgc acc atc ctc ctt ttg ctc tgg gtg tct gtc      327

```

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Phe | Gly | Val | Leu | Phe | Cys | Thr | Ile | Leu | Leu | Leu | Leu | Trp | Val | Ser | Val | |
| 10 | | | | | 15 | | | | | 20 | | | | | 25 | |
| ttc | ctc | tat | ggc | tcc | ttc | tac | tat | tcc | tat | atg | ccg | aca | gtc | agc | cac | 375 |
| Phe | Leu | Tyr | Gly | Ser | Phe | Tyr | Tyr | Ser | Tyr | Met | Pro | Thr | Val | Ser | His | |
| | | | | 30 | | | | | 35 | | | | | 40 | | |
| ctc | agc | cct | gtg | cat | ttc | tac | tac | agg | acc | gac | tgt | gat | tcc | tcc | acc | 423 |
| Leu | Ser | Pro | Val | His | Phe | Tyr | Tyr | Arg | Thr | Asp | Cys | Asp | Ser | Ser | Thr | |
| | | | 45 | | | | | 50 | | | | | 55 | | | |
| acc | tca | ctc | tgc | tcc | ttc | cct | gtt | gcc | aat | gtc | tcg | ctg | act | aag | ggc | 471 |
| Thr | Ser | Leu | Cys | Ser | Phe | Pro | Val | Ala | Asn | Val | Ser | Leu | Thr | Lys | Gly | |
| | | 60 | | | | | 65 | | | | | 70 | | | | |
| gga | cgt | gat | cgg | gtg | ctg | atg | tat | gga | cag | ccg | tat | cgt | gtt | acc | tta | 519 |
| Gly | Arg | Asp | Arg | Val | Leu | Met | Tyr | Gly | Gln | Pro | Tyr | Arg | Val | Thr | Leu | |
| | 75 | | | | | 80 | | | | | 85 | | | | | |
| gag | ctt | gag | ctg | cca | gag | tcc | cct | gtg | aat | caa | gat | ttg | ggc | atg | ttc | 567 |
| Glu | Leu | Glu | Leu | Pro | Glu | Ser | Pro | Val | Asn | Gln | Asp | Leu | Gly | Met | Phe | |
| | 90 | | | | 95 | | | | 100 | | | | | 105 | | |
| ttg | gtc | acc | att | tcc | tgc | tac | acc | aga | ggc | ggc | cga | atc | atc | tcc | act | 615 |
| Leu | Val | Thr | Ile | Ser | Cys | Tyr | Thr | Arg | Gly | Gly | Arg | Ile | Ile | Ser | Thr | |
| | | | | 110 | | | | | 115 | | | | | 120 | | |
| tct | tcg | cgt | tcg | gtg | atg | ctg | cat | tac | cgc | tca | gac | ctg | ctc | cag | atg | 663 |
| Ser | Ser | Arg | Ser | Val | Met | Leu | His | Tyr | Arg | Ser | Asp | Leu | Leu | Gln | Met | |
| | | | 125 | | | | | 130 | | | | | 135 | | | |
| ctg | gac | aca | ctg | gtc | ttc | tct | agc | ctc | ctg | cta | ttt | ggc | ttt | gca | gag | 711 |
| Leu | Asp | Thr | Leu | Val | Phe | Ser | Ser | Leu | Leu | Leu | Phe | Gly | Phe | Ala | Glu | |
| | 140 | | | | | 145 | | | | | | 150 | | | | |
| cag | aag | cag | ctg | ctg | gag | gtg | gaa | ctc | tac | gca | gac | tat | aga | gag | aac | 759 |
| Gln | Lys | Gln | Leu | Leu | Glu | Val | Glu | Leu | Tyr | Ala | Asp | Tyr | Arg | Glu | Asn | |
| | 155 | | | | 160 | | | | | | 165 | | | | | |
| tcg | gtg | agt | gag | tac | gtg | ccg | acc | act | gga | gcg | atc | att | gag | atc | cac | 807 |
| Ser | Val | Ser | Glu | Tyr | Val | Pro | Thr | Thr | Gly | Ala | Ile | Ile | Glu | Ile | His | |
| | 170 | | | | 175 | | | | | 180 | | | | | 185 | |
| agc | aag | cgc | atc | cag | ctg | tat | gga | gcc | tac | ctc | cgc | atc | cac | gcg | cac | 855 |
| Ser | Lys | Arg | Ile | Gln | Leu | Tyr | Gly | Ala | Tyr | Leu | Arg | Ile | His | Ala | His | |
| | | | 190 | | | | | 195 | | | | | | 200 | | |
| ttc | act | ggg | ctc | aga | tac | ctg | cta | tac | aac | ttc | ccg | atg | acc | tgc | gcc | 903 |
| Phe | Thr | Gly | Leu | Arg | Tyr | Leu | Leu | Tyr | Asn | Phe | Pro | Met | Thr | Cys | Ala | |
| | | | 205 | | | | | 210 | | | | | 215 | | | |
| ttc | ata | ggc | gtt | gcc | agc | aac | ttc | acc | ttc | ctc | agc | gtc | atc | gtg | ctc | 951 |
| Phe | Ile | Gly | Val | Ala | Ser | Asn | Phe | Thr | Phe | Leu | Ser | Val | Ile | Val | Leu | |
| | 220 | | | | | | 225 | | | | | 230 | | | | |
| ttc | agc | tac | atg | cag | tgg | gtg | tgg | ggg | ggc | atc | tgg | ccc | cga | cac | cgc | 999 |
| Phe | Ser | Tyr | Met | Gln | Trp | Val | Trp | Gly | Gly | Ile | Trp | Pro | Arg | His | Arg | |
| | 235 | | | | 240 | | | | | | 245 | | | | | |
| ttc | tct | ttg | cag | gtt | aac | atc | cga | aaa | aga | gac | aat | tcc | cgg | aag | gaa | 1047 |
| Phe | Ser | Leu | Gln | Val | Asn | Ile | Arg | Lys | Arg | Asp | Asn | Ser | Arg | Lys | Glu | |
| | 250 | | | | 255 | | | | | 260 | | | | | 265 | |
| gtc | caa | cga | agg | atc | tct | gct | cat | cag | cca | ggc | gca | ggg | cct | gaa | ggc | 1095 |
| Val | Gln | Arg | Arg | Ile | Ser | Ala | His | Gln | Pro | Gly | Ala | Gly | Pro | Glu | Gly | |
| | | | 270 | | | | | 275 | | | | | | 280 | | |
| cag | gag | gag | tca | act | ccg | caa | tca | gat | gtt | aca | gag | gat | ggc | gag | agc | 1143 |
| Gln | Glu | Glu | Ser | Thr | Pro | Gln | Ser | Asp | Val | Thr | Glu | Asp | Gly | Glu | Ser | |
| | | | 285 | | | | | 290 | | | | | 295 | | | |
| cct | gaa | gat | ccc | tca | ggg | aca | gag | ggc | cag | ctg | tcc | gag | gag | gag | aaa | 1191 |
| Pro | Glu | Asp | Pro | Ser | Gly | Thr | Glu | Gly | Gln | Leu | Ser | Glu | Glu | Glu | Lys | |
| | 300 | | | | | | 305 | | | | | 310 | | | | |
| cca | gat | cag | cag | ccc | ctg | agc | gga | gaa | gag | gag | cta | gag | cct | gag | gcc | 1239 |
| Pro | Asp | Gln | Gln | Pro | Leu | Ser | Gly | Glu | Glu | Glu | Leu | Glu | Pro | Glu | Ala | |

```

      315              320              325
    agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg acg gag gcc      1287
    Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu Thr Glu Ala
    330              335              340              345
    aac ctg cct gct cct gct cct gct tct gct tct gcc cct gtc cta gag      1335
    Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu
      350              355              360
    act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga cag cgc ccc      1383
    Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro
      365              370              375
    acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc agcactttcc      1438
    Thr Cys Ser Ser Ser
      380
    cacctgactc ctctcccctc gtttttcctt caataaacta ttttgtgtca gctccaaaaa      1498
    aaaaaaaaaa aa      1510

<210> 9
<211> 882
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..410

<220>
<221> sig_peptide
<222> 78..155
<223> Von Heijne matrix
      score 10.0731536331164
      seq LWLALVSCILTQA/SA

<400> 9
    atggctggcc agaggaggaa cgctttgtgt tctcatcgga gctgcatggg aagtctgcat      60
    acagcaaagt gacctgc atg cct cac ctt atg gaa agg atg gtg ggc tct      110
                      Met Pro His Leu Met Glu Arg Met Val Gly Ser
                      -25                      -20
    ggc ctc ctg tgg ctg gcc ttg gtc tcc tgc att ctg acc cag gca tct      158
    Gly Leu Leu Trp Leu Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser
    -15              -10              -5              1
    gca gtg cag cga ggt tat gga aac ccc att gaa gcc agt tcg tat ggg      206
    Ala Val Gln Arg Gly Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly
      5              10              15
    ctg gac ctg gac tgc gga gct cct ggc acc cca gag gct cat gtc tgt      254
    Leu Asp Leu Asp Cys Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys
      20              25              30
    ttt gac ccc tgt cag aat tac acc ctc cta gat ttg ggg ccc atc act      302
    Phe Asp Pro Cys Gln Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr
      35              40              45
    cgg aga ggt gca cag tct ccc ggt gtc atg aat gga acc cct agc act      350
    Arg Arg Gly Ala Gln Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr
      50              55              60              65
    gca ggg ttc ctg gtg gcc tgg cct atg gtc ctc ctg act gtc ctc ctg      398
    Ala Gly Phe Leu Val Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu
      70              75              80
    gct tgg ctg ttc tgagagctcc gctgagcatc tggccttgaa gtttgtgttc      450
    Ala Trp Leu Phe
      85

```

[illegible]

```
<220>  
<221> CDS  
<222> 84..299
```

[illegible]

```

gttggtgaag ggtaggcttt gttgaaaaag aaagaaagat tgaactacag gtgcatagca 1319
agcactcttt ctgggtaact aggctgctgg ttttaattac cctcagattt caccataaaa 1379
aacgcacaat tgtattatatt tacagagatg tgtccagcgc cccctgtggt gtgtgagaga 1439
aagcagctgc aactcaagtg actagggtggg cccagctggc ttcgtgcagg agggcacggt 1499
gggtgagcca ttctcgccat tctcatgtca gactgaaagg agggcctggg ccagctttga 1559
aaaggcagga tgaaatggaa aggtcaccac acttagggat ttttagacctt gactaacaag 1619
ctccagggtg agaaaaattc aaaacaaaat gtcaggaatc tagcagtgtt gtctgccctg 1679
gagcaaacaa acagtatgtg attttgcttc gcctatTTTT tttttctttt ttgggggaag 1739
ataattaaag gcagaatgac tgcgtttgta aaagaaggac caccaactat actgacattt 1799
ataaatgaac ctttattaaa gacacttcaa tgcaaaaaaa aaaaaaaaaa 1849

```

```

<210> 11
<211> 565
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 55..468

```

```

<220>
<221> sig_peptide
<222> 55..99
<223> Von Heijne matrix
      score 8.96936032049195
      seq FTLLFLAAVAGA/LV

```

```

<400> 11
attccccaga ctttctgcag attctgtggt tatactcact cctcatccca aaga atg      57
                                                    Met
                                                    -15
aaa ttt acc act ctc ctc ttc ttg gca gct gta gca ggg gcc ctg gtc      105
Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu Val
                    -10                    -5                    1
tat gct gaa gat gcc tcc tct gac tcg acg ggt gct gat cct gcc cag      153
Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala Gln
      5                    10                    15
gaa gct ggg acc tct aag cct aat gaa gag atc tca ggt cca gca gaa      201
Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala Glu
      20                    25                    30
cca gct tca ccc cca gag aca acc aca aca gcc cag gag act tcg gcg      249
Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser Ala
      35                    40                    45                    50
gca gca gtt cag ggg aca gcc aag gtc acc tca agc agg cag gaa cta      297
Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu Leu
                    55                    60                    65
aac ccc ctg aaa tcc ata gtg gag aaa agt atc tta cta aca gaa caa      345
Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu Gln
                    70                    75                    80
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga      393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly
                    85                    90                    95
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag      441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys
                    100                    105                    110
aaa ttc agt cta tta aaa cca tgg gca tgagaagctg aataatggga      488
Lys Phe Ser Leu Leu Lys Pro Trp Ala
115                    120

```

tcattggact taaagcctta aatacccttg tagcccagag ctattaaaac gaaagcatcc 548
 aaaaaaaaaa aaaaaaa 565

<210> 12
 <211> 1663
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 152..475

<220>
 <221> sig_peptide
 <222> 152..244
 <223> Von Heijne matrix
 score 10.0910253445132
 seq LVLLLVTRSPVNA/CL

<400> 12
 atgtgtctgc tgccgccatt gtgcggcgct ggtccctca gagggttcct gctgctgccg 60
 gtgccttgga ccctccccct cgcttctcgt tctactgccc caggagcccg gcgggtccgg 120
 gactcccgtc cgtgccggtg cgggcgcgcg c atg tgg ctg tgg gag gac cag 172
 Met Trp Leu Trp Glu Asp Gln
 -30 -25
 ggc ggc ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg 220
 Gly Gly Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu
 -20 -15 -10
 gtg acg cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc 268
 Val Thr Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe
 -5 1 5
 gtt cta ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc 316
 Val Leu Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala
 10 15 20
 ctg cag gtg ctc aag ccc ccg gac cgc att tct gcc atc gcc cac cgt 364
 Leu Gln Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg
 25 30 35 40
 ggc ggc agc aam sag gcg ccc gag aac acg ctg gcg gcc att ccg cag 412
 Gly Gly Ser Xaa Xaa Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln
 45 50 55
 cta aga atg gag caa cag gcg tgg agt tgg aca ttg agt tta ctt ctg 460
 Leu Arg Met Glu Gln Gln Ala Trp Ser Trp Thr Leu Ser Leu Leu Leu
 60 65 70
 acg gga ttc ctg tct taatgcacga taacacagta gataggacga ctgatgggac 515
 Thr Gly Phe Leu Ser
 75
 tgggcgattg tgtgatttga catttgaaca aattaggaag ctgaatcctg cagcaaacca 575
 cagactcagg aatgatttcc ctgatgaaaa gatccctacc ctaagggaag ctgttgcaga 635
 gtgcctaaac cataacctca caatcttctt tgatgtcaaa ggccatgcac acaaggctac 695
 tgaggctcta aagaaaatgt atatggaatt tcctcaactg tataataata gtgtggtctg 755
 ttctttcttg ccagaagtta tctacaaggt aacattcggg atttttcttg tacatattag 815
 atgagacaaa cagatcggga tgtaataaca gcattaactc acagaccttg gagcctaagc 875
 catacaggag atgggaaacc acgctatgat actttctgga aacattttat atttgttatg 935
 atggacattt tgctcgattg gagcatgcat aatatcttgt ggtacctgtg tggaatttca 995
 gctttcctca tgcaaaagga ttttgtatcc ccggcctact tgaagaagtg gtcagctaaa 1055
 ggaatccagg ttgttggttg gactgttaat acctttgatg aaaagagtta ctacgaatcc 1115
 catcttggtt ccagctatat cactgacagc atggtagaag actgcgaacc tcacttctag 1175
 actttcacgg tgggacgaaa cgggttcaga aactgccagg ggccatcac agggatatca 1235

```

aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca aatgcaatag 1295
ttggtcactg catttttacc tgaaccaaag ctaaaccggg tgttgccacc atgcaccatg 1355
gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa cgcacaagag 1415
cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag cacagattga 1475
attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcattgataa ctcagagttg 1535
acattttaaa acttgccaca cttattttcaa atattttgtac tcagctatgt taacatgtac 1595
tntagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
aaaaaaaaa 1663

```

```

<210> 13
<211> 744
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 112..552

```

```

<220>
<221> sig_peptide
<222> 112..183
<223> Von Heijne matrix
      score 11.7298925418815
      seq FVLGLGLTPPTLA/QD

```

```

<400> 13
tcacaactgg aacccatctc caggaacaaa cagctggaac ccattctccg ttgaaggga 60
actgccagat ttttgtaaga ttcttctctc tgggagcctg tgttggaaga g atg gtg 117
                                     Met Val

atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
      -20              -15              -10

acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
      -5              1              5              10

acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
      15              20              25

gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
      30              35              40

aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa 357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu
      45              50              55

aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct 405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser
      60              65              70

tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct 453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
      75              80              85              90

cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct 501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala
      95              100             105

tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt 549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg
      110             115             120

ccg taaccagcgg gccctgggc aagtgtggc tctgtgtcc ttgccttcca 602
Pro

```

```

tttccctct gcacccagaa cagtgggtggc aacattcatt gccaaagggcc caaagaaaga 662
gctacctgga ccttttggtt tctgtttgac aacatgttta ataaataaaa atgtcttgat 722
atcagcaaaa aaaaaaaaaa aa 744

```

```

<210> 14
<211> 1759
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 101..1243

```

```

<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57142340200611
      seq FLCLGMALCPRQA/TR

```

```

<400> 14
gtagagtgct gaaggctctg ccaacggctc tcttggcgct tcaacgttcg gatcagcagc 60
ttttttccat tctctctctc cactttttca gtgagcagcc atg agt tgg act gtg 115
                                     Met Ser Trp Thr Val
                                     -30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe
                                     -25 -20 -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro
                                     -10 -5 1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5 10 15 20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
25 30 35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
40 45 50
atc agc atc tta tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
55 60 65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70 75 80
agc cct ttc acg aaa atg cca aat att gtt tgt agc aaa gat tac ttt 499
Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys Ser Lys Asp Tyr Phe
85 90 95 100
gtc aca gca aac tcc aac cta gtg att atc aca gca ggt gca cgc caa 547
Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr Ala Gly Ala Arg Gln
105 110 115
gaa aag gga gaa acg cgc ctt aat tta gtc cag cga aat gtg gcc atc 595
Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln Arg Asn Val Ala Ile
120 125 130
ttc aag tta atg att tcc agt att gtc cag tac agc ccc cac tgc aaa 643
Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr Ser Pro His Cys Lys
135 140 145

```


| | | | | | | | | | | | | | | | | |
|------------|-----|-----|--------------|-----|-----|------------|-----|-------|-------|------------|------|------------|-------|------------|-----|------|
| ctg | att | att | gtt | tcc | aat | cca | gtg | gat | atc | tta | act | tat | gta | gct | tgg | 691 |
| Leu | Ile | Ile | Val | Ser | Asn | Pro | Val | Asp | Ile | Leu | Thr | Tyr | Val | Ala | Trp | |
| | 150 | | | | | 155 | | | | | 160 | | | | | |
| aag | ttg | agt | gca | ttt | ccc | aaa | aac | cgt | att | att | gga | agc | ggc | tgt | aat | 739 |
| Lys | Leu | Ser | Ala | Phe | Pro | Lys | Asn | Arg | Ile | Ile | Gly | Ser | Gly | Cys | Asn | |
| | 165 | | | | | 170 | | | | | 175 | | | | 180 | |
| ctg | gat | act | gct | cgt | ttt | cgt | ttc | ttg | att | gga | caa | aag | ctt | ggt | atc | 787 |
| Leu | Asp | Thr | Ala | Arg | Phe | Arg | Phe | Leu | Ile | Gly | Gln | Lys | Leu | Gly | Ile | |
| | | | | 185 | | | | | 190 | | | | | 195 | | |
| cat | tct | gaa | agc | tgc | cat | gga | tgg | atc | ctc | gga | gag | cat | gga | gac | tca | 835 |
| His | Ser | Glu | Ser | Cys | His | Gly | Trp | Ile | Leu | Gly | Glu | His | Gly | Asp | Ser | |
| | | | 200 | | | | | 205 | | | | | 210 | | | |
| agt | gtt | cct | gtg | tgg | agt | gga | gtg | aac | ata | gct | ggg | gtc | cct | ttg | aag | 883 |
| Ser | Val | Pro | Val | Trp | Ser | Gly | Val | Asn | Ile | Ala | Gly | Val | Pro | Leu | Lys | |
| | | 215 | | | | | 220 | | | | 225 | | | | | |
| gat | ctg | aac | tct | gat | ata | gga | act | gat | aaa | gat | cct | gag | caa | tgg | aaa | 931 |
| Asp | Leu | Asn | Ser | Asp | Ile | Gly | Thr | Asp | Lys | Asp | Pro | Glu | Gln | Trp | Lys | |
| | | 230 | | | | 235 | | | | | 240 | | | | | |
| aat | gtc | cac | aaa | gaa | gtg | act | gca | act | gcc | tat | gag | att | att | aaa | atg | 979 |
| Asn | Val | His | Lys | Glu | Val | Thr | Ala | Thr | Ala | Tyr | Glu | Ile | Ile | Lys | Met | |
| | | | | | 250 | | | | | 255 | | | | | 260 | |
| aaa | ggg | tat | act | tct | tgg | gcc | att | ggc | cta | tct | gtg | gcc | gat | tta | aca | 1027 |
| Lys | Gly | Tyr | Thr | Ser | Trp | Ala | Ile | Gly | Leu | Ser | Val | Ala | Asp | Leu | Thr | |
| | | | | 265 | | | | | 270 | | | | | 275 | | |
| gaa | agt | att | ttg | aag | aat | ctt | agg | aga | ata | cat | cca | gtt | tcc | acc | ata | 1075 |
| Glu | Ser | Ile | Leu | Lys | Asn | Leu | Arg | Arg | Ile | His | Pro | Val | Ser | Thr | Ile | |
| | | | 280 | | | | | 285 | | | | | 290 | | | |
| att | aag | ggc | ctc | tat | gga | ata | gat | gaa | gaa | gta | ttc | ctc | agt | att | cct | 1123 |
| Ile | Lys | Gly | Leu | Tyr | Gly | Ile | Asp | Glu | Glu | Val | Phe | Leu | Ser | Ile | Pro | |
| | | 295 | | | | | 300 | | | | | 305 | | | | |
| tgt | atc | ctg | gga | gag | aac | ggg | att | acc | aac | ctt | ata | aag | ata | aag | ctg | 1171 |
| Cys | Ile | Leu | Gly | Glu | Asn | Gly | Ile | Thr | Asn | Leu | Ile | Lys | Ile | Lys | Leu | |
| | | 310 | | | | 315 | | | | | 320 | | | | | |
| acc | cct | gaa | gaa | gag | gcc | cat | ctg | aaa | aaa | agt | gca | aaa | aca | ctc | tgg | 1219 |
| Thr | Pro | Glu | Glu | Glu | Ala | His | Leu | Lys | Lys | Ser | Ala | Lys | Thr | Leu | Trp | |
| | | | | | 330 | | | | | 335 | | | | | 340 | |
| gaa | att | cag | aat | aag | ctt | aag | ctt | taaag | ttgcc | taaaact | tacc | attccc | gaaat | | | 1273 |
| Glu | Ile | Gln | Asn | Lys | Leu | Lys | Leu | | | | | | | | | |
| | | | | 345 | | | | | | | | | | | | |
| tattgaagag | | | atcatagata | | | caggattata | | | | taacgaaatt | | ttgaataaac | | ttgaattcct | | 1333 |
| aaaagatgga | | | aacaggaaag</ | | | | | | | | | | | | | |

```
<210> 15
<211> 1755
<212> DNA
<213> Homo sapiens
```

```

<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57613483592743
      seq FLCLGMALCLRQA/TR

<400> 15
gtagagtgct gaaggtcctg ccaacggctc tcttggcgtc tcaacgttcg gatcagcagc      60
ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg      115
                                         Met Ser Trp Thr Val
                                         -30
cct gtt gtg cgg gcc agc cag aga atg agc tcg gtg gga gcg aat ttc      163
Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe
      -25                      -20                      -15
cta tgc ctg ggg atg gcc ctg tgt ctg cgt caa gca acg cgc atc ccg      211
Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro
      -10                      -5                      1
ctc aac ggc acc tgg ctc ttc aca ccc gtg agc aag atg gcg act gtg      259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5                      10                      15                      20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac      307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
      25                      30                      35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct      355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
      40                      45                      50
atc agc atc ttg tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat      403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
      55                      60                      65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc      451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
      70                      75                      80
agc cct ttc acg aaa atg cca ata ttg ttt gta gca aag att act ttg      499
Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu
85                      90                      95                      100
tca cag caa act cca acc tagtgattat cacagcaggt gcacgccaag      547
Ser Gln Gln Thr Pro Thr
      105
aaaagggaga aacgcgcctt aatttagtcc agcgaaatgt ggccatcttc aagtaatgat      607
ttccagtatt gtccagtaca gccccactg caaactgatt attgtttcca atccagtgga      667
tatcttaact tatgtagctt ggaagttgag tgcatttccc aaaaaccgta ttattggaag      727
cggctgtaat ctggatactg ctcgttttcg tttcttgatt ggacaaaagc ttggtatcca      787
ttctgaaagc tgccatggat ggatcctcgg agagcatgga gactcaagtg ttcctgtgtg      847
gagtggagtg aacatagctg gtgtcccttt gaaggatctg aactctgata taggaactga      907
taaatagctt gagcaggaaa aatgtccaca aagaagtgac tgcaactgcc tatgagatta      967
ttaaaatgaa aggttatact tcttgggcca ttggcctatc tgtggccgat ttaacagaaa      1027
gtattttgaa gaatcttagg agaatacatc cagtttccac cataactaag ggcctctatg      1087
gaatagatga agaagtattc ctcatgattc cttgtatcct gggagagaaac ggtattacca      1147
accttataaa gataaagctg acccctgaag aagaggccca tctgaaaaaa agtgcaaaaa      1207
cactctggga aattcagaat aagcttaagc tttaaagttg cctaaaaacta ccattccgaa      1267
attattgaag agatcataga tacaggatta tataacgaaa ttttgaataa acttgaattc      1327
ctaaaagatg gaaacaggaa agtaggtaga gtgattttcc tatttattta gtcctccagc      1387
tctttttatg agcatccacg tgctggacga tacttattta caattcctaa gtatttttgg      1447
tacctctgat gtagcagcac ttgccatggt atatatatgt agttggcatt tggttcccaa      1507
aaagttagat taggtattt attgtgttct agaaattccg actcttttca ttagatatat      1567
gctattttct tcatctttgc tggtttatac ctatgttcat ttatatgctg taaaaaagta      1627
gtagcttctt ctacaatgta aaaataaatg tacatacaaa aaaatgcagt agtatatata      1687

```

```
atcttttgtt ttgcttcctt tgatagttaa taaattccgt ttgttgaatc aataaaaaaa 1747
aaaaaaaaa 1755
```

```
<210> 16
<211> 936
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 59..853
```

```
<220>
<221> sig_peptide
<222> 59..100
<223> Von Heijne matrix
      score 5.2402423806254
      seq NFILFIFIPGVFS/LK
```

```
<400> 16
agaaaggagg ctctgggtag acgcactaga ttactggata aatcacttca atttccca 58
atg aat ttt ata ttg ttt att ttt ata cct gga gtt ttt tcc tta aaa 106
Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
      -10      -5      1
agt agc act ttg aag cct act att gaa gca ttg cct aat gtg cta cct 154
Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
      5      10      15
tta aat gaa gat gtt aat aag cag gaa gaa aag aat gaa gat cat act 202
Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
      20      25      30
ccc aat tat gct cct gct aat gag aaa aat ggc aat tat tat aaa gat 250
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
      35      40      45      50
ata aaa caa tat gtg ttc aca aca caa aat cca aat ggc act gag tct 298
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
      55      60      65
gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac 346
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
      70      75      80
gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct 394
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
      85      90      95
ata aat gga aca gca gtg gtc atg gat gat aaa gat caa tta ttt cac 442
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
      100      105      110
cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca 490
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
      115      120      125      130
gat cta gag gat ctg aag atc aaa ata atg ctg gga atc tcg ttg atg 538
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
      135      140      145
acc ctc ctc ctc ttt gtg gtc ctc ttg gca ttc tgt agt gct aca ctg 586
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
      150      155      160
tac aaa ctg agg cat ctg agt tat aaa agt tgt gag agt cag tac tct 634
Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser
      165      170      175
gtc aac cca gag ctg gcc acg atg tct tac ttt cat cca tca gaa ggt 682
```

| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|------------|------------|-----|-----|-----|-----|-----|-----|--|
| Val | Asn | Pro | Glu | Leu | Ala | Thr | Met | Ser | Tyr | Phe | His | Pro | Ser | Glu | Gly | | |
| 180 | | | | | | 185 | | | | | 190 | | | | | | |
| ggt | tca | gat | aca | tcc | ttt | tcc | aag | agt | gca | gag | agc | agc | aca | ttt | ttg | 730 | |
| Val | Ser | Asp | Thr | Ser | Phe | Ser | Lys | Ser | Ala | Glu | Ser | Ser | Thr | Phe | Leu | | |
| 195 | | | | | 200 | | | | | 205 | | | | | 210 | | |
| ggt | acc | act | tct | tca | gat | atg | aga | aga | tca | ggc | aca | aga | aca | tca | gaa | 778 | |
| Gly | Thr | Thr | Ser | Ser | Asp | Met | Arg | Arg | Ser | Gly | Thr | Arg | Thr | Ser | Glu | | |
| | | | | 215 | | | | | 220 | | | | | 225 | | | |
| tct | aag | ata | atg | acg | gat | atc | att | tcc | ata | ggc | tca | gat | aat | gag | atg | 826 | |
| Ser | Lys | Ile | Met | Thr | Asp | Ile | Ile | Ser | Ile | Gly | Ser | Asp | Asn | Glu | Met | | |
| | | | 230 | | | | | 235 | | | | | 240 | | | | |
| cat | gaa | aac | gat | gag | tcg | ggt | acc | cgg | tgaagaaatc | aaggaacccg | | | | | | 873 | |
| His | Glu | Asn | Asp | Glu | Ser | Val | Thr | Arg | | | | | | | | | |
| | | 245 | | | | | 250 | | | | | | | | | | |
| gtgaagaaat | cttattgatg | aataaataac | tttaattatt | ttgtcatcaa | aaaaaaaaaa | | | | | | | | | | | 933 | |
| aaa | | | | | | | | | | | | | | | | 936 | |

<210> 17
 <211> 747
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..672

<220>
 <221> sig_peptide
 <222> 73..132
 <223> Von Heijne matrix
 score 5.21332530399231
 seq SPVFLVFPPEITA/SE

| | | | | | | | | | | | | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 17 | | | | | | | | | | | | | | | | | |
| acaagaaaag | aacatgggtct | agactgaagt | accaactaaa | tcattctcctt | tcaaattatc | | | | | | | | | | | 60 | |
| accgacacca | tc | atg | gat | tca | agc | acc | gca | cac | agt | ccg | gtg | ttt | ctg | gta | | 111 | |
| | Met | Asp | Ser | Ser | Thr | Ala | His | Ser | Pro | Val | Phe | Leu | Val | | | | |
| | -20 | | | | -15 | | | | | | -10 | | | | | | |
| ttt | cct | cca | gaa | atc | act | gct | tca | gaa | tat | gag | tcc | aca | gaa | ctt | tca | 159 | |
| Phe | Pro | Pro | Glu | Ile | Thr | Ala | Ser | Glu | Tyr | Glu | Ser | Thr | Glu | Leu | Ser | | |
| | -5 | | | | | 1 | | | | 5 | | | | | | | |
| gcc | acg | acc | ttt | tca | act | caa | agc | ccc | ttg | caa | aaa | tta | ttt | gct | aga | 207 | |
| Ala | Thr | Thr | Phe | Ser | Thr | Gln | Ser | Pro | Leu | Gln | Lys | Leu | Phe | Ala | Arg | | |
| 10 | | | | | 15 | | | | 20 | | | | | 25 | | | |
| aaa | atg | aaa | atc | tta | ggg | act | atc | cag | atc | ctg | ttt | gga | att | atg | acc | 255 | |
| Lys | Met | Lys | Ile | Leu | Gly | Thr | Ile | Gln | Ile | Leu | Phe | Gly | Ile | Met | Thr | | |
| | | | 30 | | | | | 35 | | | | | 40 | | | | |
| ttt | tct | ttt | gga | ggt | atc | ttc | ctt | ttc | act | ttg | tta | aaa | cca | tat | cca | 303 | |
| Phe | Ser | Phe | Gly | Val | Ile | Phe | Leu | Phe | Thr | Leu | Leu | Lys | Pro | Tyr | Pro | | |
| | | 45 | | | | 50 | | | | | | 55 | | | | | |
| agg | ttt | ccc | ttt | ata | ttt | ctt | tca | gga | tat | cca | ttc | tgg | ggc | tct | ggt | 351 | |
| Arg | Phe | Pro | Phe | Ile | Phe | Leu | Ser | Gly | Tyr | Pro | Phe | Trp | Gly | Ser | Val | | |
| | 60 | | | | | 65 | | | | | | 70 | | | | | |
| ttg | ttc | att | aat | tct | gga | gcc | ttc | cta | att | gca | gtg | aaa | aga | aaa | acc | 399 | |
| Leu | Phe | Ile | Asn | Ser | Gly | Ala | Phe | Leu | Ile | Ala | Val | Lys | Arg | Lys | Thr | | |
| | 75 | | | | | 80 | | | | | 85 | | | | | | |
| aca | gaa | act | ctg | ata | ata | ttg | agc | cga | ata | atg | aat | ttt | ctt | agt | gcc | 447 | |
| Thr | Glu | Thr | Leu | Ile | Ile | Leu | Ser | Arg | Ile | Met | Asn | Phe | Leu | Ser | Ala | | |

```

90          95          100          105
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu

          110          115          120
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys

          125          130          135
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe

          140          145          150
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys

          155          160          165
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys

170          175          180
aagatgtgtt aaaatattaa aaaaaaaaaa aaaaaaaaag aaaaaaaaaa aaaaa 747

<210> 18
<211> 1884
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 94..1275

<220>
<221> sig_peptide
<222> 94..210
<223> Von Heijne matrix
      score 4.55778392992629
      seq LVLVKRLLAIVSVS/CI

<400> 18
acagcgcgtg cagcctcgtg cagctcttct ggtctccggc gcccgcccct cagacgtaat 60
gttgaattaa agaaaatact ttatcagaag aag atg gcc act gcc cag ttg cag 114
                        Met Ala Thr Ala Gln Leu Gln
                        -35
agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa 162
Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu
      -30          -25          -20
cac cag tct ttg gtg tta gtg aag agg ctt cta gca gtt tca gta tcc 210
His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser
      -15          -10          -5
tgt atc acg tat ttg agg gga ata ttc cca gaa tgc gct tat gga aca 258
Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr
1          5          10          15
aga tat cta gat gat ctt tgt gtc aaa ata ctg aga gaa gat aaa aat 306
Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn
      20          25          30
tgc cca gga tct aca cag tta gtg aaa tgg att cta gga tgt tat gat 354
Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Ile Leu Gly Cys Tyr Asp
      35          40          45
gct tta cag aaa aaa tat cta agg atg gtt gtt cta gct gta tac aca 402
Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val Leu Ala Val Tyr Thr
      50          55          60
aac cca gaa gat cct cag aca att tca gaa tgt tac caa ttc aaa ttc 450

```

| | | | | | | | | | | | | | | | | |
|-------------|------------|--------------|-------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Asn | Pro | Glu | Asp | Pro | Gln | Thr | Ile | Ser | Glu | Cys | Tyr | Gln | Phe | Lys | Phe | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| aaa | tac | acc | aat | aat | gga | cca | ctc | atg | gac | ttc | ata | agt | aaa | aac | caa | 498 |
| Lys | Tyr | Thr | Asn | Asn | Gly | Pro | Leu | Met | Asp | Phe | Ile | Ser | Lys | Asn | Gln | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| agc | aac | gaa | tct | agc | atg | ttg | tct | act | gac | acc | aag | aaa | gca | agc | att | 546 |
| Ser | Asn | Glu | Ser | Ser | Met | Leu | Ser | Thr | Asp | Thr | Lys | Lys | Ala | Ser | Ile | |
| | | | | 100 | | | | | 105 | | | | 110 | | | |
| ctc | ctc | att | cgc | aag | att | tat | atc | cta | atg | caa | aat | ctg | ggg | cct | tta | 594 |
| Leu | Leu | Ile | Arg | Lys | Ile | Tyr | Ile | Leu | Met | Gln | Asn | Leu | Gly | Pro | Leu | |
| | | | | 115 | | | | | 120 | | | | 125 | | | |
| cct | aat | gat | gtt | tgt | ttg | acc | atg | aaa | ctt | ttt | tac | tat | gat | gaa | gtt | 642 |
| Pro | Asn | Asp | Val | Cys | Leu | Thr | Met | Lys | Leu | Phe | Tyr | Tyr | Asp | Glu | Val | |
| | | | | 130 | | | | | 135 | | | | 140 | | | |
| aca | ccc | cca | gat | tac | cag | cct | ccc | ggg | ttt | aag | gat | ggg | gat | tgt | gaa | 690 |
| Thr | Pro | Pro | Asp | Tyr | Gln | Pro | Pro | Gly | Phe | Lys | Asp | Gly | Asp | Cys | Glu | |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | | |
| gga | gtt | ata | ttt | gaa | ggg | gaa | cct | atg | tat | tta | aat | gtg | gga | gaa | gtc | 738 |
| Gly | Val | Ile | Phe | Glu | Gly | Glu | Pro | Met | Tyr | Leu | Asn | Val | Gly | Glu | Val | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| tca | aca | cct | ttt | cac | atc | ttc | aaa | gta | aaa | gtg | acc | act | gag | aga | gaa | 786 |
| Ser | Thr | Pro | Phe | His | Ile | Phe | Lys | Val | Lys | Val | Thr | Thr | Glu | Arg | Glu | |
| | | | | 180 | | | | | 185 | | | | 190 | | | |
| cga | atg | gaa | aat | att | gac | tca | act | ata | cta | tca | cca | aaa | caa | ata | aaa | 834 |
| Arg | Met | Glu | Asn | Ile | Asp | Ser | Thr | Ile | Leu | Ser | Pro | Lys | Gln | Ile | Lys | |
| | | | | 195 | | | | | 200 | | | | 205 | | | |
| aca | cca | ttt | caa | aaa | atc | ctg | agg | gac | aaa | gat | gta | gaa | gat | gaa | cag | 882 |
| Thr | Pro | Phe | Gln | Lys | Ile | Leu | Arg | Asp | Lys | Asp | Val | Glu | Asp | Glu | Gln | |
| | | | | 210 | | | | | 215 | | | | 220 | | | |
| gag | cat | tat | aca | agt | gat | gat | ttg | gac | att | gaa | act | aaa | atg | gaa | gaa | 930 |
| Glu | His | Tyr | Thr | Ser | Asp | Asp | Leu | Asp | Ile | Glu | Thr | Lys | Met | Glu | Glu | |
| 225 | | | | | 230 | | | | 235 | | | | | 240 | | |
| cag | gaa | aaa | aac | cct | gca | tct | tct | gaa | ctt | gaa | gaa | cca | agt | tta | gtt | 978 |
| Gln | Glu | Lys | Asn | Pro | Ala | Ser | Ser | Glu | Leu | Glu | Glu | Pro | Ser | Leu | Val | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| tgt | gag | gaa | gat | gaa | att | atg | agg | tct | aaa | gaa | agt | cca | gat | ctt | tct | 1026 |
| Cys | Glu | Glu | Asp | Glu | Ile | Met | Arg | Ser | Lys | Glu | Ser | Pro | Asp | Leu | Ser | |
| | | | | 260 | | | | | 265 | | | | 270 | | | |
| att | tct | cat | tct | cag | gtt | gag | cag | tta | gtc | aat | aaa | aca | tct | gaa | ctt | 1074 |
| Ile | Ser | His | Ser | Gln | Val | Glu | Gln | Leu | Val | Asn | Lys | Thr | Ser | Glu | Leu | |
| | | | | 275 | | | | | 280 | | | | 285 | | | |
| gat | atg | tct | gaa | agc | aaa | aca | aga | agt | gga | aaa | gtc | ttt | cag | aat | aaa | 1122 |
| Asp | Met | Ser | Glu | Ser | Lys | Thr | Arg | Ser | Gly | Lys | Val | Phe | Gln | Asn | Lys | |
| | | | | 290 | | | | | 295 | | | | 300 | | | |
| atg | gca | aat | gga | aat | caa | cca | gta | aaa | tct | tcc | aaa | gaa | aat | cgg | aag | 1170 |
| Met | Ala | Asn | Gly | Asn | Gln | Pro | Val | Lys | Ser | Ser | Lys | Glu | Asn | Arg | Lys | |
| 305 | | | | | 310 | | | | 315 | | | | | 320 | | |
| aga | agt | caa | cat | gaa | tct | ggg | aga | ata | gtc | ctc | cat | cac | ttt | gat | tct | 1218 |
| Arg | Ser | Gln | His | Glu | Ser | Gly | Arg | Ile | Val | Leu | His | His | Phe | Asp | Ser | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| tct | agt | caa | gag | tca | gtg | cca | aaa | agg | aga | aag | ttt | agt | gaa | cca | aag | 1266 |
| Ser | Ser | Gln | Glu | Ser | Val | Pro | Lys | Arg | Arg | Lys | Phe | Ser | Glu | Pro | Lys | |
| | | | | 340 | | | | | 345 | | | | 350 | | | |
| gaa | cat | ata | taaaaatttat | ttttgttctg | caggcttgca | gagttcttct | | | | | | | | | | 1315 |
| Glu | His | Ile | | | | | | | | | | | | | | |
| | | | | 355 | | | | | | | | | | | | |
| caccattttaa | actgaaggac | cctatatattat | atttccctaa | ctctgaagat | gtatatgtag | | | | | | | | | | | 1375 |
| tttaaagcag | tttatacact | aaaactaagt | ttttggctga | ctgtcatatt | gtggctccta | | | | | | | | | | | 1435 |

```

atcttgagat aaatccaata gaacttttga ataaaagcaa aagtacaaat gtcataattg 1495
attcggtaat aagtaaaatt tcaaaattga ttttgttcat tacctactta atatttcctt 1555
taaatatata ctaactgtta aggccctcta atgccatttt tctaaacagt aatgtttact 1615
ttggtatata aatttgggat tgattcactt tttacttatg ttaaaattat accatttaac 1675
tggtcttttt gtcattgtgc tgttattaaa acaatgttct tcaatatttt gacataatgt 1735
attaacattt taatatataa tgtacaattt aagaattggg gctttacctt tactatgctt 1795
tttttacagg acaaaaagac tgatttttaa agtatggcat tttttgcagc ataaataaaa 1855
tattgttcag tacgaaaaaa aaaaaaaaaa 1884

```

```

<210> 19
<211> 691
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 42..515

```

```

<220>
<221> sig_peptide
<222> 42..92
<223> Von Heijne matrix
      score 10.7019149919754
      seq VLMLLAVLIWTGA/EN

```

```

<400> 19
gagttgtcct gtgctggagg tctgctcaga cgaaggctctc c atg gcg tta gaa gtc 56
                                         Met Ala Leu Glu Val
                                         -15
ttg atg ctc ctc gct gtc ttg att tgg acc ggt gct gag aac ctc cat 104
Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
      -10      -5      1
gtg aaa ata agt tgc tct ctg gac tgg ttg atg gtc tca gtt atc cca 152
Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
      5      10      15      20
gtt gca gaa agc aga aat ctg tat ata ttt gcg gat gaa tta cat ctg 200
Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
      25      30      35
gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt 248
Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
      40      45      50
ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag 296
Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
      55      60      65
gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata 344
Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
      70      75      80
gat cat gac cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa 392
Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
      85      90      95      100
tca gtg tgg ctt aca cca gtt tct act gag aat gaa ata aaa ttg gat 440
Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
      105      110      115
cct agt cct ttt att gct gac ttt cag aca aca gca gaa gag tta gga 488
Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly
      120      125      130
tta tta tct tct agt cca aac ttg ctc tgagctaaag gagaaatgga 535
Leu Leu Ser Ser Ser Pro Asn Leu Leu

```

```

135          140
aacttgaagc tgggtgttatg tattttgcag gaaaacagtt tcatttttttc atagcaaaaa 595
tatagtgggt gtatatctct ccttaagtct ctgggtttcta aaaaccctac ttcagtaaag 655
gtcctgatta gttgattagc gaaaaaaaaa aaaaaa 691

```

```

<210> 20
<211> 1138
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 271..969

```

```

<220>
<221> sig_peptide
<222> 271..366
<223> Von Heijne matrix
      score 5.6680378526706
      seq WMGLACFRSLAAS/SP

```

```

<220>
<221> misc_feature
<222> 989
<223> n=a, g, c or t

```

```

<400> 20
aaaaaccttt caagtgtccc ctccttttct taaagtcttt tataggggtc cccttcttgg 60
ccatctccat cctgtgagtc aggactgaaa gggcacagac aggtcactgc cagcattgtt 120
ggggcaagcc tgcaagcacg catcactggg gatctgacat gacaatggcc gcctgcccc 180
tctgagggct acaggactta cccagtgagg aagcagctaa gcaggctctga ccagccgacc 240
tggacctggc caagggtcct gtcacccctc atg gcc acc ccg cca ttc cgg ctg 294
                                Met Ala Thr Pro Pro Phe Arg Leu
                                -30 -25

ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc 342
Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala
                                -20 -15 -10

tgc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa 390
Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys
                                -5 1 5

cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa 438
Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys
                                10 15 20

att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc 486
Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe
25 30 35 40

cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa 534
Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu
                                45 50 55

gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa 582
Glu Glu Arg Pro Phe Trp Glu Glu Glu Lys Thr Phe Trp Lys Glu Glu
                                60 65 70

aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act 630
Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr
                                75 80 85

ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg 678
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp
90 95 100

```



```

aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag      726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu
105                      110                      115                      120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
                      125                      130                      135
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
                      140                      145                      150
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
                      155                      160                      165
gag aac aat ggc cac att gcc gga gag cag atg ctc gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
                      170                      175                      180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185                      190                      195                      200
gcg tagccagcat gcaggtgcan gggccctgtg gtccagactc ccctggggtg      1019
Ala
ggattcaagt ccagggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaga tccaataaag tcctgaggca aggtttggaa aaccaaaaaa aaaaaaaaaa      1138

```

```

<210> 21
<211> 468
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 76..276

```

```

<220>
<221> sig_peptide
<222> 76..135
<223> Von Heijne matrix
      score 5.21332530399231
      seq SPVFLVFPPEITA/SE

```

```

<400> 21
agcacaagaa aagaacatgg tctagactga agtaccaact aaatcatctc ctttcaaatt      60
atcaccgaca ccatac atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
      Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
      -20                      -15                      -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
      -5                      1                      5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
      10                      15                      20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
      25                      30                      35                      40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306
Ser Leu Ile Leu Glu Pro Ser
      45
ctctgggaat tttgattaca ttgatgactt tcagcattat tgaattatc atttctctgc      366
ctttctcaat tttgggggtgc cactcagagg attgtgattg tgaacaatgt tgttgactag      426

```

cactgtgaga ataaagatgt gttaaaataa aaaaaaaaaa aa

468

<210> 22
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..287

<220>
<221> sig_peptide
<222> 6..80
<223> Von Heijne matrix
score 4.17710408129886
seq ISLSHLFLDLSRS/LW

<400> 22
atttg atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg 50
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu
-25 -20 -15
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt 98
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys
-10 -5 1 5
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc 146
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu
10 15 20
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc 194
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val
25 30 35
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc 242
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu
40 45 50
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc 287
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
55 60 65
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaaa 347
atagtaagta aaatcttgct tgcctctcag taaaataaag ctctatTTTT cgtttttttt 407
ttttccaact tcctgtacaa aaaagggaaa acttttagctt ttgggggaaa tttggagcta 467
gcctgttggt actgttgagc ttagtgtatc tataactata tattattcca caatatctta 527
aatactttat aaagatatatt tcataaatta cagcaatcct ggcttttagat gattgatggc 587
cattttttaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta 647
gtttcttaga aagtctccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa 707
aaaaaaaaaa aaa 720

<210> 23
<211> 727
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 171..692

<220>
<221> sig_peptide
<222> 171..227

<223> Von Heijne matrix
 score 4.17573075349936
 seq LLLGQRCSLKVSG/QE

<400> 23
 attgtgacat caccgtgcac tagccaatgg ctgcctgcct aagctgggtc cctgggtctcc 60
 tgggactact agccctttgt tgatagggag aagccaacat ctcccgcagg accccctaata 120
 cttcagggca gctcccagag catggatccc tcctgattcc actcagcccg atg ttc 176
 Met Phe
 ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca 224
 Leu Thr Val Lys Leu Leu Leu Gln Arg Cys Ser Leu Lys Val Ser
 -15 -10 -5
 ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg 272
 Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu
 1 5 10 15
 aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg 320
 Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu
 20 25 30
 gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct 368
 Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser
 35 40 45
 atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc 416
 Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala
 50 55 60
 cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta 464
 His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu
 65 70 75
 gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta 512
 Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu
 80 85 90 95
 agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg 560
 Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His Leu
 100 105 110
 gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca 608
 Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro
 115 120 125
 gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt 656
 Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys
 130 135 140
 gac atg gag gag aag gag gag gca gca gct gat cag taaacggggc 702
 Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155
 atcctaccgc aaaaaaaaaa aaaaa 727

<210> 24
 <211> 470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 137..454

<220>
 <221> sig_peptide
 <222> 137..187
 <223> Von Heijne matrix
 score 10.7019149919754

seq VLMLLAVLIWTGA/EN

```

<400> 24
atcctgtgaa ctacccaaaa ggaggaaaac gaacgcagct gagcatggga tgccatataa      60
aaatcactta aaccagtcgc cactccttgt ttcctgagtt gtcctgtgct ggaggtctgc      120
tcagacgaag gtctcc atg gcg tta gaa gtc ttg atg ctc ctc gct gtc ttg      172
          Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu
                    -15                      -10
att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg      220
Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu
-5                      1                      5                      10
gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg      268
Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu
          15                      20                      25
tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat      316
Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn
          30                      35                      40
cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt      364
Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys
          45                      50                      55
ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc      412
Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys
60                      65                      70                      75
atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt      454
Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe
          80                      85
taaaaaaaaa aaaaaa      470

```

<210> 25
 <211> 987
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 238..609

<220>
 <221> sig_peptide
 <222> 238..291
 <223> Von Heijne matrix
 score 10.0374888212272
 seq LLLLVMALPPGTT/GV

```

<400> 25
attccattca cagactcttg ttgggcagca gccacccgct cacctccatc cccaggactt      60
agagggacgc agggcggttg gaacagagga cactccaggc gctgaccctg ggaggccagg      120
accagggcca aagtcccgtg ggcaagagga gtcctcagag gtccttcatt cagcggttcc      180
gggaggtctg ggaagccac ggccctggctg gggcagggtc aacgccgcca ggccgcc      237
atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc      285
Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
          -15                      -10                      -5
acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg      333
Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
          1                      5                      10
cag tgt cct ggt acc tac atg cac tgt ggc gat gac gag gac tgc ttc      381
Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
15                      20                      25                      30

```

```

aca ggc cac ggg gtc gcc ccg ggc act ggt ccg gtc atc aac aaa ggc      429
Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
          35                      40                      45
tgc ctg cga gcc acc agc tgc ggc ctt gag gaa ccc gtc agc tac agg      477
Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
          50                      55                      60
ggc gtc acc tac agc ctc acc acc aac tgc tgc acc ggc cgc ctg tgt      525
Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
          65                      70                      75
aac aga gcc ccg agc agc cag aca gtg ggg gcc acc acc agc ctg gca      573
Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
          80                      85                      90
ctg ggg ctg ggt atg ctg ctt cct cca cgt ttg ctg tgaccaacag      619
Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
          95                      100                      105
ggaggacagg gcctgggact gttctcccag atccgccact ccccatgtcc ccatgtcctt      679
ccccactaa atggccagag aggccctgga caacctcttg cggccctggc ttcacccctt      739
ctaaggctgt ccaccaggag cccggtgcta ggggaagcat cccagggcct gactgagcgg      799
caggggagca cggcccgctgg gtttgattgt attactctgt tccactgggt ctaagacgca      859
gagcttctca catctcaatc aggatgcttc tctccattgg tagcacttta gattccatga      919
aatatggtaa aaaatatata tatatcataa taaatgacag ctgatgttca tggaaaaaaaa      979
aaaaaaaaa

```

```

<210> 26
<211> 908
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 80..862

<220>
<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
      score 3.66725851505537
      seq FSLLSISGPPISS/SA

```

```

<400> 26
gaatgtttat cctctggaca aaccagccag cctctccaga gcaggcgtgt gatctctgta      60
ccccgcagtg ggtcagaat atg gag aac ttc tca ctc ctc agc atc tct gga      112
              Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly
              -15                      -10
cct cca atc tct tcc tcc gcc ctg agt gct ttt ccc gac att atg ttc      160
Pro Pro Ile Ser Ser Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe
-5                      1                      5                      10
tct cgt gcc acc agc ctg cca gac att gca aag aca gca gta ccc act      208
Ser Arg Ala Thr Ser Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr
          15                      20                      25
gag gca tcc agc cca gct cag gcc ctg cca ccc cag tac caa agc atc      256
Glu Ala Ser Ser Pro Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile
          30                      35                      40
att gtc agg caa ggg ata cag aac aca gtg ctc tca cca gac tgc agc      304
Ile Val Arg Gln Gly Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser
          45                      50                      55
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc      352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile

```

| | | | | | | | |
|---|-----|----|-----|----|-----|----|-----|
| 60 | | 65 | | 70 | | 75 | |
| tac cgg ccc tgg ttc tcc ccc tac agc tac ttc gtg tgt gca gac aaa | | | | | | | 400 |
| Tyr Arg Pro Trp Phe Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys | | | | | | | |
| | 80 | | 85 | | 90 | | |
| gag agc cag ctg gag gcc tat gac ttc cca gag gtg cag cag gat gag | | | | | | | 448 |
| Glu Ser Gln Leu Glu Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu | | | | | | | |
| | 95 | | 100 | | 105 | | |
| ggc aag tgg gac aac tgc ctt tct gag gac atg gct gag aac atc tgt | | | | | | | 496 |
| Gly Lys Trp Asp Asn Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys | | | | | | | |
| | 110 | | 115 | | 120 | | |
| tcg tcc tct tcc tcc cca gag aac act tgc cct cga gaa gcc acc aag | | | | | | | 544 |
| Ser Ser Ser Ser Ser Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys | | | | | | | |
| | 125 | | 130 | | 135 | | |
| aaa tcc agg cat ggc ctg gac tcc atc aca tcc cag gac atc cta atg | | | | | | | 592 |
| Lys Ser Arg His Gly Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met | | | | | | | |
| | 140 | | 145 | | 150 | | 155 |
| gct tcc aga tgg cac cca gca cag cag aat ggc tac aag tgc gtg gcc | | | | | | | 640 |
| Ala Ser Arg Trp His Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala | | | | | | | |
| | 160 | | 165 | | 170 | | |
| tgc tgc cgc atg tac ccc acc ctg gac ttc ctc aag agc cac atc aag | | | | | | | 688 |
| Cys Cys Arg Met Tyr Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys | | | | | | | |
| | 175 | | 180 | | 185 | | |
| agg ggc ttc agg gag ggc ttc agc tgc aag gtg tac tac cgc aag ctc | | | | | | | 736 |
| Arg Gly Phe Arg Glu Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu | | | | | | | |
| | 190 | | 195 | | 200 | | |
| aaa gcc ctc tgg agc aag gag cag aag gcc cgg ctg gga gac agg ctc | | | | | | | 784 |
| Lys Ala Leu Trp Ser Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu | | | | | | | |
| | 205 | | 210 | | 215 | | |
| tcc tcc ggc agc tgc cag gcc ttc aat agt cct gct gaa cac ctt agg | | | | | | | 832 |
| Ser Ser Gly Ser Cys Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg | | | | | | | |
| | 220 | | 225 | | 230 | | 235 |
| caa att ggc ggt gaa gcc tac tta tgt ctc tagagagatg ccaataaagt | | | | | | | 882 |
| Gln Ile Gly Gly Glu Ala Tyr Leu Cys Leu | | | | | | | |
| | 240 | | 245 | | | | |
| tagtcacagc caaaaaaaaaa aaaaaa | | | | | | | 908 |

<210> 27
 <211> 762
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 83..310

 <220>
 <221> sig_peptide
 <222> 83..157
 <223> Von Heijne matrix
 score 4.72955689475746
 seq LCALLSNFCPSTT/VK

 <400> 27
 ttttttctac tacaaacgcc atgggggatgc ggggtctggga acagcggaaa accctaccct 60
 gccctgaaaa gtccctggct ca atg tgc atg tcc ctt tct atg aaa gtt cct 112
 Met Cys Met Ser Leu Ser Met Lys Val Pro
 -25 -20
 tgc tgc cta tgc gcc ttg ctc tct aac ttc tgt ccc tcc aca act gtg 160

| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Cys | Cys | Leu | Cys | Ala | Leu | Leu | Ser | Asn | Phe | Cys | Pro | Ser | Thr | Thr | Val | | |
| -15 | | | | | -10 | | | | | -5 | | | | | 1 | | |
| aaa | gga | gac | gtc | gtg | act | tcc | ttc | ttt | cgt | gct | gac | tat | gac | tta | gcc | 208 | |
| Lys | Gly | Asp | Val | Val | Thr | Ser | Phe | Phe | Arg | Ala | Asp | Tyr | Asp | Leu | Ala | | |
| | | 5 | | | | | 10 | | | | | 15 | | | | | |
| agt | agg | tct | gca | gat | cag | tcc | tcc | cag | aaa | gtg | aag | ttg | cgc | atg | ttc | 256 | |
| Ser | Arg | Ser | Ala | Asp | Gln | Ser | Ser | Gln | Lys | Val | Lys | Leu | Arg | Met | Phe | | |
| | | 20 | | | | 25 | | | | | 30 | | | | | | |
| act | ggg | cgt | ctt | ccc | atc | ggc | ccc | ttc | gcc | agt | gtg | ggg | aac | gcg | gcg | 304 | |
| Thr | Gly | Arg | Leu | Pro | Ile | Gly | Pro | Phe | Ala | Ser | Val | Gly | Asn | Ala | Ala | | |
| | 35 | | | | 40 | | | | | 45 | | | | | | | |
| gag | ctg | tgagccggcg | actcgggtcc | ctgaggtctg | gattctttct | ccgctactga | | | | | | | | | | 360 | |
| Glu | Leu | | | | | | | | | | | | | | | | |
| 50 | | | | | | | | | | | | | | | | | |
| gacacggcgg | acacacacaa | acacagaacc | acacagccag | ttccaggagc | ccagtaatgg | | | | | | | | | | | 420 | |
| agagcccca | aaagaagaac | cagcagctga | aagtcgggat | cctacacctg | ggcagcagac | | | | | | | | | | | 480 | |
| agaagaagat | caggatacag | ctgagatccc | agtgcgcgac | atggaagggtg | atctgcaaga | | | | | | | | | | | 540 | |
| gctgcatcag | tcaaacaccg | gggataaatc | tggatttggg | ttccggcgctc | aaggtgaaga | | | | | | | | | | | 600 | |
| taatacctaa | agaggaacac | tgtaaaatgc | cagaagcagg | tgaagagcaa | ccacaagttt | | | | | | | | | | | 660 | |
| aatgaagac | aagctgaaac | aacgcaagct | ggttttatat | tagatatattg | acttaaacta | | | | | | | | | | | 720 | |
| tctcaataaa | gttttgcagc | tttcaccaaa | aaaaaaaaaa | aa | | | | | | | | | | | | 762 | |

<210> 28
 <211> 1102
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 310..906

<220>
 <221> sig_peptide
 <222> 310..357
 <223> Von Heijne matrix
 score 11.0931109030915
 seq FPLLLLSLGLVLA/EA

| | | | | | | | | | | | | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|--|--|--|----|--|--|--|--|--|--|-----|--|
| <400> 28 | | | | | | | | | | | | | | | | | |
| atacagtgac | ctagagcagg | catgggtggg | tcacaggctt | tggagagcac | tctctgtcct | | | | | | | | | | | 60 | |
| gatcttttca | gttgagagac | ttcagctgtt | cattgtctcat | ttggacttag | ttcaagggtca | | | | | | | | | | | 120 | |
| tgtcaaagaa | gaagggtgcac | ttacgctagt | tgtagctct | gtcttttgta | accatcaagt | | | | | | | | | | | 180 | |
| tccatgcgat | tgatcagatt | taggaggggg | cgttggggga | taatcaattt | tgggtgtcac | | | | | | | | | | | 240 | |
| caggtaaaca | gagccctcag | catctgaata | gaaactgaac | aggaacagaa | gagattcact | | | | | | | | | | | 300 | |
| acatctgag | atg gag acc | ttt cct ctg | ctg ctg ctg | ctc agc ctg | ggc ctg gtt | | | | | | | | | | | 351 | |
| | Met Glu Thr | Phe Pro Leu | Leu Leu Ser | Leu Gly Leu | Val | | | | | | | | | | | | |
| | -15 | | -10 | | -5 | | | | | | | | | | | | |
| ctt gca gaa | gca tca gaa | agc aca atg | aag ata att | aaa gaa gaa | ttt | | | | | | | | | | | 399 | |
| Leu Ala Glu | Ala Ser Glu | Ser Thr Met | Lys Ile Ile | Lys Glu Glu | Phe | | | | | | | | | | | | |
| | 1 | | 5 | | 10 | | | | | | | | | | | | |
| aca gac gaa | gag atg caa | tat gac atg | gca aaa agt | ggc caa gaa | aaa | | | | | | | | | | | 447 | |
| Thr Asp Glu | Glu Met Gln | Tyr Asp Met | Ala Lys Ser | Gly Gln Glu | Lys | | | | | | | | | | | | |
| | 15 | | 20 | | 25 | | | | 30 | | | | | | | | |
| cag acc att | gag ata tta | atg aac ccg | atc ctg tta | gtt aaa aat | acc | | | | | | | | | | | 495 | |
| Gln Thr Ile | Glu Ile Leu | Met Asn Pro | Ile Leu Leu | Val Lys Asn | Thr | | | | | | | | | | | | |
| | 35 | | 40 | | 45 | | | | | | | | | | | | |
| agc ctc agc | atg tcc aag | gat gat atg | tct tcc aca | tta ctg aca | ttc | | | | | | | | | | | 543 | |
| Ser Leu Ser | Met Ser Lys | Asp Asp Met | Ser Ser Thr | Leu Leu Thr | Phe | | | | | | | | | | | | |

| | | | | | | |
|--|-------------------------------------|------|----|--|----|--|
| | 50 | | 55 | | 60 | |
| aga agt tta cat tat aat gac | ccc aag gga aac agt tcg ggt aat gac | 591 | | | | |
| Arg Ser Leu His Tyr Asn Asp | Pro Lys Gly Asn Ser Ser Gly Asn Asp | | | | | |
| 65 | 70 | 75 | | | | |
| aaa gag tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca | 639 | | | | | |
| Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala | | | | | | |
| 80 | 85 | 90 | | | | |
| aac gga tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa | 687 | | | | | |
| Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu | | | | | | |
| 95 | 100 | 105 | | | | |
| gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat | 735 | | | | | |
| Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn | | | | | | |
| 115 | 120 | 125 | | | | |
| cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc | 783 | | | | | |
| Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys | | | | | | |
| 130 | 135 | 140 | | | | |
| cag ttc act aca ggc aaa caa ttc ccc agg tgc caa tac cat agt gtt | 831 | | | | | |
| Gln Phe Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val | | | | | | |
| 145 | 150 | 155 | | | | |
| acc tca tta gag aag ata ttg aca gtg ctg aca ggt cat tct ctg atg | 879 | | | | | |
| Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met | | | | | | |
| 160 | 165 | 170 | | | | |
| agc tgg tta gtt tgt ggc tct aag ttg taaatccac agagcttttag | 926 | | | | | |
| Ser Trp Leu Val Cys Gly Ser Lys Leu | | | | | | |
| 175 | 180 | | | | | |
| gactaggggtc ttactaaaga aggacctctt cttgttcatt cttgtttaaa cctttcctta | | 986 | | | | |
| atatctactc tttagcacta tagtgaactc ctgattattt attctaactg gaggagtga | | 1046 | | | | |
| aaatccaaaa ttgtggataa ttcaattaaa agttatgact gaaaaaaaaa aaaaaa | | 1102 | | | | |

<210> 29
 <211> 436
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..287

<220>
 <221> sig_peptide
 <222> 24..131
 <223> Von Heijne matrix
 score 3.79790641648006
 seq ILMRDFSPSGIFG/AF

| | |
|---|-----|
| <400> 29 | |
| acagcggaca ccaggactcc aaa atg gcg tca gtt gta cca gtg aag gac aag | 53 |
| Met Ala Ser Val Val Pro Val Lys Asp Lys | |
| -35 | -30 |
| aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc tgg atc ttg atg | 101 |
| Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser Trp Ile Leu Met | |
| -25 | -20 |
| cggtac ttc agt cct agt ggc att ttc gga gcg ttt caa aga ggt tac | 149 |
| Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr | |
| -10 | -5 |
| tac cggtac tac aac aag tac atc aat gtg aag aag ggg agc atc tcg | 197 |
| Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser | |
| 10 | 15 |
| | 20 |


```

ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt agc tac tcc ttt      245
Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe
      25              30              35
tcc tac aag cat ctc aag cac gag cgg ctc cgc aaa tac cac      287
Ser Tyr Lys His Leu Lys His Glu Arg Leu Arg Lys Tyr His
      40              45              50
tgaagaggac acactctgca cccccccacc ccacgacctt ggcccagagcc cctccgtgag      347
gaacacaatc tcaatcggtg ctgaatcctt tcatatccta ataggaatta acctccaaat      407
aaaacatgac tggtaaaaaa aaaaaaaaaa      436

```

<210> 30
 <211> 1938
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 132..1574

<220>
 <221> sig_peptide
 <222> 132..206
 <223> Von Heijne matrix
 score 11.1130239236827
 seq LALLLTSTPEALG/AN

```

<400> 30
ctcccccttcc cgctcccagg aaccatcca gcctcaggaa ctgccccag ccacgagcc      60
ttggctactt aagggacctg ggcccaatcc acagctggga cagtcctggc ccaactgcact      120
gggaatctag g atg ggg gcc ttg gcc aga gcc ctg ccg tcc ata ctg ctg      170
      Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu
      -25              -20              -15
gca ttg ctg ctt acg tcc acc cca gag gct ctg ggt gcc aac ccc ggc      218
Ala Leu Leu Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly
      -10              -5              1
ttg gtc gcc agg atc acc gac aag gga ctg cag tat gcg gcc cag gag      266
Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu
      5              10              15              20
ggg cta ttg gct ctg cag agt gag ctg ctc agg atc acg ctg cct gac      314
Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp
      25              30              35
ttc acc ggg gac ttg agg atc ccc cac gtc ggc cgt ggg cgc tat gag      362
Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu
      40              45              50
ttc cac agc ctg aac atc cac agc tgt gag ctg ctt cac tct gcg ctg      410
Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu
      55              60              65
agg cct gtc cct ggc cag ggc ctg agt ctc agc atc tcc gac tcc tcc      458
Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser
      70              75              80
atc cgg gtc cag ggc agg tgg aag gtg cgc aag tca ttc ttc aaa cta      506
Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu
      85              90              95              100
cag ggc tcc ttt gat gtc agt gtc aag ggc atc agc att tcg gtc aac      554
Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn
      105              110              115
ctc ctg ttg ggc agc gat tcc tcc ggg agg ccc aca gtt act gcc tcc      602
Leu Leu Leu Gly Ser Asp Ser Ser Gly Arg Pro Thr Val Thr Ala Ser

```



```

ggg ctg cag atc cat aag gac ttc ctg ttc ttg ggt gcc aat gtc caa      1562
Gly Leu Gln Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln
      440              445              450
tac atg aga gtt tgaggacaag aaagatgaag cttggagggtc acagctggat      1614
Tyr Met Arg Val
      455
ctgcttgttg catttccagc tgtgcagcac gtctcagaga ttcttgaaga atgaagacat      1674
ttctgctctc agctccgggg gtgaggtgtg cctggcctct gcctccaccc tcctcctctt      1734
caccaggtgc atgcatgccc tctctgagtc tggactttgc ttcccctcca ggagggacca      1794
ccctccctga ctggcctggg atatctttac aagcaggcac tgtatttttt tattcgccat      1854
ctgatcccca tgcctagcag agtgctggca cttagtaggt cctcaataaa tatttattaa      1914
atgatgacaa aaaaaaaaaa aaaa      1938

```

```

<210> 31
<211> 1116
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 117..545

```

```

<220>
<221> sig_peptide
<222> 117..245
<223> Von Heijne matrix
      score 5.65876793443964
      seq VVSFALIATLVYA/LF

```

```

<400> 31
ataaggggac gtctagtggg ttgcccggga ggggtggcgg gagcggtcct ggaaataatc      60
tgtcctctgt cgccgggaac tggcgaggta gttccttcgc ggtggagaga cctgga atg      119
                                     Met
gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca      167
Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser
      -40              -35              -30
gtt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt      215
Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser
      -25              -20              -15
ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat      263
Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His
      -10              -5              1              5
caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa      311
Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu
      10              15              20
cag ctt caa aca gaa cag gat gca cct gct gcc act cga cag cag ttc      359
Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln Phe
      25              30              35
tac act gac atg tac tgt ccc atc tgc ctg cac caa gcc tcc ttc ccg      407
Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe Pro
      40              45              50
gtg gag acc aac tgt gga cat ctt ttt tgt ggt gcc tgc att att gct      455
Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile Ala
      55              60              65              70
tac tgg cga tat ggt tca tgg ctt ggg gca atc agt tgt cca atc tgt      503
Tyr Trp Arg Tyr Gly Ser Trp Leu Gly Ala Ile Ser Cys Pro Ile Cys
      75              80              85
aga caa acg aga cat ggc cac att gca ttg tcc aga aca gct      545

```

| Arg | Gln | Thr | Arg | His | Gly | His | Ile | Ala | Leu | Ser | Arg | Thr | Ala | |
|-------------|-------------|------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 90 | | | 95 | | | 100 | | | | | | | | |
| tagaccatga | cagtttagcat | cgaagccacc | tgaggagggga | ggcagtaacc | ttactcctaa | | | | | | | | | 605 |
| cagtatttgg | tgaagatgat | cagtctcagg | atgttctgag | attgcatcag | gatattaatg | | | | | | | | | 665 |
| attataaccg | gagatttctca | gggcaaccca | gatctgtaag | taatgctaaa | gcatgttcaa | | | | | | | | | 725 |
| agtttagagga | agacacattt | cttctctttt | gtaaagttag | gtttaccaac | aagtattcct | | | | | | | | | 785 |
| tgactatgag | aaatcttggc | caggcacagt | agctaacgcc | tataatccta | gcactttggg | | | | | | | | | 845 |
| aggccaaggc | aggtggatca | cttgagccca | ggagtttgag | accagccttg | gaaacatgat | | | | | | | | | 905 |
| gaaaccccat | ctctagaaaa | aacaccaaaa | aattggacaa | gagtgttggc | acatgcctgt | | | | | | | | | 965 |
| agtccctgct | tcttgggagg | ctgaaatggg | aggatcacct | gagcccagga | ggttgaggct | | | | | | | | | 1025 |
| atagttagcc | atgatcgac | tattgcactc | ccacctgggt | ggcagtgaga | cccttctca | | | | | | | | | 1085 |
| aaaaacaaga | aaagaaaaaa | aaaaaaaaaa | a | | | | | | | | | | | 1116 |

<210> 32
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 117..362

| <400> 32 | | | | | | | | | | | | | | |
|----------------|-------------|-------------|-------------|-------------|------------|--|--|--|--|--|--|--|--|------|
| ataagggggac | gtctagtggg | ttgcccggga | ggggtggcgg | gagcggtcct | ggaaataatc | | | | | | | | | 60 |
| tgctctctgt | cgccgggaac | tggcgaggta | gttccttcgc | ggtggagaga | cctgga atg | | | | | | | | | 119 |
| | | | | | Met | | | | | | | | | |
| | | | | | 1 | | | | | | | | | |
| gcc aaa tat | caa ggt gaa | ggt gtt caa | agt ttg aaa | ctg gat gat | gat tca | | | | | | | | | 167 |
| Ala Lys Tyr | Gln Gly Glu | Val Gln Ser | Leu Lys Leu | Asp Asp Asp | Ser | | | | | | | | | |
| | 5 | 10 | 15 | | | | | | | | | | | |
| ggt ata gaa | gga gta agc | gac caa gta | ctt gtg gca | ggt gtg gtc | agt | | | | | | | | | 215 |
| Val Ile Glu | Gly Val Ser | Asp Gln Val | Leu Val Ala | Val Val Val | Ser | | | | | | | | | |
| | 20 | 25 | 30 | | | | | | | | | | | |
| ttc gct ttg | att gct acc | ctg gta tat | gca ctt ttc | aga aat gta | cat | | | | | | | | | 263 |
| Phe Ala Leu | Ile Ala Thr | Leu Val Tyr | Ala Leu Phe | Arg Asn Val | His | | | | | | | | | |
| | 35 | 40 | 45 | | | | | | | | | | | |
| caa aac att | cac cca gaa | aac cag gag | cta gta agg | gta ctt cga | gaa | | | | | | | | | 311 |
| Gln Asn Ile | His Pro Gln | Asn Gln Glu | Leu Val Arg | Val Leu Arg | Glu | | | | | | | | | |
| | 50 | 55 | 60 | 65 | | | | | | | | | | |
| cag ctt caa | aca gaa cag | gat gca cct | gct gac tcg | aca gca gtt | cta | | | | | | | | | 359 |
| Gln Leu Gln | Thr Glu Gln | Asp Ala Pro | Ala Asp Ser | Thr Ala Val | Leu | | | | | | | | | |
| | 70 | 75 | 80 | | | | | | | | | | | |
| cac tgacatgtac | tgtcccatct | gcctgcacca | agcctccttc | ccggtggaga | | | | | | | | | | 412 |
| His | | | | | | | | | | | | | | |
| ccaactgtgg | acatcttttt | tgtggtgcct | gcattattgc | ttactggcga | tatggttcat | | | | | | | | | 472 |
| ggcttggggc | aatcagttgt | ccaatctgta | gacaaacgag | acatggccac | attgcattgt | | | | | | | | | 532 |
| ccagaacagc | ttagaccatg | acagtttagca | tcgaagccac | ctgaggaggg | aggcagtaac | | | | | | | | | 592 |
| cttactccta | acagtatttg | gtgaagatga | tcagtctcag | gatgttctga | gattgcatca | | | | | | | | | 652 |
| ggatattaat | gattataaacc | ggagattctc | agggcaaccc | agatctgtaa | gtaatgctaa | | | | | | | | | 712 |
| agcatgttca | aagtttagagg | aagacacatt | tcttctcttt | tgtaaagtga | ggtttaccac | | | | | | | | | 772 |
| caagtattct | ttgactatga | gaaatcttgg | ccaggcacag | tagctaacgc | ctataatcct | | | | | | | | | 832 |
| agcacttttg | gaggccaagg | cagggtggatc | acttgagccc | aggagtttga | gaccagcctt | | | | | | | | | 892 |
| ggaaacatga | tgaaacccca | tctctagaaa | aaacacccaaa | aaattggaca | agagtgttgg | | | | | | | | | 952 |
| cacatgcctg | tagtccctgc | ttcttgggag | gctgaaatgg | gaggatcacc | tgagcccagg | | | | | | | | | 1012 |
| aggttgaggc | tatagtgagc | catgatcgca | ctattgcact | cccacctggg | tggcagtgag | | | | | | | | | 1072 |
| acccttcctc | aaaaacaag | aaaagaaaaa | aaaaaaaaaa | aa | | | | | | | | | | 1114 |

<210> 33

<211> 2072
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 144..1262

<220>
 <221> sig_peptide
 <222> 144..224
 <223> Von Heijne matrix
 score 5.14258625256317
 seq FLCQRLVLSTLSG/RP

<400> 33
 acgtggacgc gtctgggctg ctggaggcag cccgagccgc cgccgtcggc gtcgccgccca 60
 ccaccaccat cggagtcacg agtcccgcgt ctgtccgaag tcgccgtctt cgggctgctc 120
 acgtctcttc ggagagcgcg cac atg gcg act cag gcg cac tcc ctc agc tac 173
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr
 -25 -20
 gca ggg tgc aac ttc ttg tgc caa cgt ctg gtc ctg tct acc ctg agc 221
 Ala Gly Cys Asn Phe Leu Cys Gln Arg Leu Val Leu Ser Thr Leu Ser
 -15 -10 -5
 ggg cgc ccc gtc aaa atc cga aag att cgg gcc aga gac gac aac ccg 269
 Gly Arg Pro Val Lys Ile Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro
 1 5 10 15
 ggc ctc cga gat ttt gaa gcc agc ttc ata agg cta ttg gac aaa ata 317
 Gly Leu Arg Asp Phe Glu Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile
 20 25 30
 acg aat ggt tct cga att gaa ata aac caa aca gga aca acc tta tat 365
 Thr Asn Gly Ser Arg Ile Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr
 35 40 45
 tat cag cct ggc ctc ctg tat ggt gga tct gtg gaa cat gac tgt agc 413
 Tyr Gln Pro Gly Leu Leu Tyr Gly Gly Ser Val Glu His Asp Cys Ser
 50 55 60
 gtc ctt cgt ggc att ggg tat tac ctg gag agt ctt ctt tgc ttg gct 461
 Val Leu Arg Gly Ile Gly Tyr Leu Glu Ser Leu Leu Cys Leu Ala
 65 70 75
 cca ttt atg aag cac ccg tta aaa ata gtt cta cga gga gtg acc aat 509
 Pro Phe Met Lys His Pro Leu Lys Ile Val Leu Arg Gly Val Thr Asn
 80 85 90 95
 gat cag att gac cct tca gtt gat gtt ctt aag gca aca gca ctc cct 557
 Asp Gln Ile Asp Pro Ser Val Asp Val Leu Lys Ala Thr Ala Leu Pro
 100 105 110
 ttg ttg aaa caa ttt ggg att gat ggt gaa tca ttt gaa ctg aag att 605
 Leu Leu Lys Gln Phe Gly Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile
 115 120 125
 gtg cga cgg gga atg cct ccc gga gga gga ggc gaa gtg gtt ttc tca 653
 Val Arg Arg Gly Met Pro Pro Gly Gly Gly Glu Val Val Phe Ser
 130 135 140
 tgt cct gtg agg aag gtc ttg aag ccc att caa ctc aca gat cca gga 701
 Cys Pro Val Arg Lys Val Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly
 145 150 155
 aaa atc aaa cgt att aga gga atg gcg tac tct gta cgt gtg tca cct 749
 Lys Ile Lys Arg Ile Arg Gly Met Ala Tyr Ser Val Arg Val Ser Pro
 160 165 170 175
 cag atg gcg aac cgg att gtg gat tct gca agg agc atc ctc aac aag 797

| | |
|--|---------|
| Gln Met Ala Asn Arg Ile Val Asp Ser Ala Arg Ser Ile Leu Asn Lys | |
| 180 | 185 190 |
| ttc ata cct gat atc tat att tac aca gat cac att aaa gga gtc aac | 845 |
| Phe Ile Pro Asp Ile Tyr Ile Tyr Thr Asp His Ile Lys Gly Val Asn | |
| 195 200 205 | |
| tct ggg aag tct ccg ggc ttt ggg ttg tca ctg gtt gct gag acc acc | 893 |
| Ser Gly Lys Ser Pro Gly Phe Gly Leu Ser Leu Val Ala Glu Thr Thr | |
| 210 215 220 | |
| agt ggc acc ttc ctc agt gct gaa ctg gcc tcc aac ccc cag ggc cag | 941 |
| Ser Gly Thr Phe Leu Ser Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln | |
| 225 230 235 | |
| gga gca gca gta ctt cca gag gac ctt ggc agg aac tgt gcc cgg ctg | 989 |
| Gly Ala Ala Val Leu Pro Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu | |
| 240 245 250 255 | |
| ctg ctg gag gaa atc tac agg ggt gga tgc gta gac tcg acc aac caa | 1037 |
| Leu Leu Glu Glu Ile Tyr Arg Gly Gly Cys Val Asp Ser Thr Asn Gln | |
| 260 265 270 | |
| agc ctg gcg cta cta ctc atg acc ctt gga cag cag gat gtt tcc aaa | 1085 |
| Ser Leu Ala Leu Leu Leu Met Thr Leu Gly Gln Gln Asp Val Ser Lys | |
| 275 280 285 | |
| gtc ctg cta ggc cct ctc tct ccc tac acg ata gaa ttt ttg cgg cat | 1133 |
| Val Leu Leu Gly Pro Leu Ser Pro Tyr Thr Ile Glu Phe Leu Arg His | |
| 290 295 300 | |
| ttg aag agc ttt ttc cag att atg ttt aaa att gaa acc aag cca tgt | 1181 |
| Leu Lys Ser Phe Phe Gln Ile Met Phe Lys Ile Glu Thr Lys Pro Cys | |
| 305 310 315 | |
| ggt gaa gaa ctc aag ggt ggg gat aaa gtg ctg atg acc tgt gtt ggc | 1229 |
| Gly Glu Glu Leu Lys Gly Gly Asp Lys Val Leu Met Thr Cys Val Gly | |
| 320 325 330 335 | |
| att ggt ttc tcc aac ctt agc agg acc ctc aag tgataaccat cacaagataa | 1282 |
| Ile Gly Phe Ser Asn Leu Ser Arg Thr Leu Lys | |
| 340 345 | |
| ggccccagtg cctacagaca aagcagaagc tgccacggac accaatggga ccaagtccaa | 1342 |
| atggattaat ccaggacaga atagccactt gcttaatttt ctgtgaagaa atatcaatat | 1402 |
| acaaataaaaa gacatccctg tagcatatgg tttccagctg tttctccagt ggcattgcc | 1462 |
| ttgcccagga ggggcccagt caccatgaga gctcccttgc cttacctgga ggaagaatgt | 1522 |
| gccttcaggc cacagtcgtg ctgctagaac agtctcgtag ctgcagttca gctgtgcttc | 1582 |
| ctcagcctac tatcataggc ttctcagcc ctctgtcata tggctgtttt gcaaacctgt | 1642 |
| ggagtctggt actgttcttt ctgcaaggac tcacctcctt gagccttggt ttttgttgta | 1702 |
| gggattaaat gagataatat gagtggcagc tcttcatgag tcctgcagtg ctaagcaaat | 1762 |
| gtcagaaatt ggtgtattag actatttatc tttgatcttc tgaatggatt gctgtcatgg | 1822 |
| acacggacac ggatcttcat ctgggttcatt gtattttatat gtgagggatg gatggctg | 1882 |
| gggctccaag taagtatttg ggatgttttt atattccagg tgtgctgtac gttcttattt | 1942 |
| tattttcaca atagctctgt gatgtaagtg ctatctccat gagaaaattc ataaaggggtg | 2002 |
| ttttgttcat ttgaaatgta taatgtaaag acattaaatc tcctcattta aggaaaaaaa | 2062 |
| aaaaaaaaa | 2072 |

<210> 34
 <211> 409
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..316

<220>
 <221> sig_peptide

<222> 35..109

<223> Von Heijne matrix

score 5.38058532480537

seq AVTSLLSPTPATA/LA

<400> 34

```
tttttttcga gaccggaagt gagtgatcga aagc atg gcg tcg gtg gtg ttg gcg      55
                               Met Ala Ser Val Val Leu Ala
                               -25                               -20
ctg agg acc cgg aca gcc gtt aca tcc ttg cta agc ccc act ccg gct      103
Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala
          -15          -10          -5
aca gct ctt gct gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc      151
Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser
          1          5          10
aaa aac ctc ggt gga aag tca tca ggc aga cgc caa ggc att aag aaa      199
Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys
15          20          25          30
atg gaa ggt cac tat gtt cat gct ggg aac atc att gca aca cag cgc      247
Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg
          35          40          45
cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc      295
His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala
          50          55          60
ccc ctt ttt cct ttt cta ggt tgacctctcc ttgccctaa gcatggtaat      346
Pro Leu Phe Pro Phe Leu Gly
          65
aacagttgca tgtattgagt gcttaccaaaa tggcaagcat tgtgccaaaa aaaaaaaaaa      406
aaa                                                                409
```

<210> 35

<211> 836

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 177..767

<220>

<221> sig_peptide

<222> 177..236

<223> Von Heijne matrix

score 6.51720597568932

seq LAVILTLLGLAIL/AI

<400> 35

```
aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgccatacaag ggccctccctg      60
acaccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct      120
ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg      179
                               Met
                               -20
aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt      227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
          -15          -10          -5
gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt      275
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
          1          5          10
```

| | |
|---|-----|
| gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg | 323 |
| Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu | |
| 15 20 25 | |
| gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt | 371 |
| Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser | |
| 30 35 40 45 | |
| gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg | 419 |
| Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu | |
| 50 55 60 | |
| tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa | 467 |
| Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys | |
| 65 70 75 | |
| tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg | 515 |
| Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met | |
| 80 85 90 | |
| atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc | 563 |
| Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu | |
| 95 100 105 | |
| tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct | 611 |
| Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro | |
| 110 115 120 125 | |
| gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc | 659 |
| Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu | |
| 130 135 140 | |
| act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc | 707 |
| Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser | |
| 145 150 155 | |
| cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt | 755 |
| His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu | |
| 160 165 170 | |
| ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg | 807 |
| Phe Ser Pro Ala | |
| 175 | |
| atagtgtata aatgaaaaaa aaaaaaaaaa | 836 |

<210> 36

<211> 1323

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 208..1239

<220>

<221> sig_peptide

<222> 208..294

<223> Von Heijne matrix

score 5.73027134157378

seq GLVLICVCSKTHS/LK

<400> 36

| | |
|---|-----|
| agtctcgtat cgcgcccggg aggcgccgga gccagcggc tggcgccaga tccaggctcc | 60 |
| tggaagaacc atgtccggca gctactggtc atgccaggca cacactgctg cccaagagga | 120 |
| gctgctgttt gaattatctg tgaatgttgg gaagaggaat gccagagctg ccggctgaaa | 180 |
| attacccaac caagagaaat ctgcagg atg gac ttt ctg gtc ctc ttc ttg ttc | 234 |
| Met Asp Phe Leu Val Leu Phe Leu Phe | |

-25

| | |
|---|------|
| tac ctg gct tcg gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc tcg | 282 |
| Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys Ser | |
| -20 -15 -10 -5 | |
| aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata ttt | 330 |
| Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile Phe | |
| 1 5 10 | |
| tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg ctt | 378 |
| Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu Leu | |
| 15 20 25 | |
| cat tac ctt ttc cat acg aga aac acc ttc att gtc ctg cac ctg | 426 |
| His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His Leu | |
| 30 35 40 | |
| gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt ggc | 474 |
| Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe Gly | |
| 45 50 55 60 | |
| tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc tat | 522 |
| Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro Tyr | |
| 65 70 75 | |
| ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga acc | 570 |
| Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly Thr | |
| 80 85 90 | |
| aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat gtt | 618 |
| Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His Val | |
| 95 100 105 | |
| tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct act | 666 |
| Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser Thr | |
| 110 115 120 | |
| tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt aac | 714 |
| Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys Asn | |
| 125 130 135 140 | |
| tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac tgc | 762 |
| Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn Cys | |
| 145 150 155 | |
| atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc ttg | 810 |
| Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu | |
| 160 165 170 | |
| acg gcc tcg gct gcc acc gtc gcc att gtg agc acc act ttt ctg gtc | 858 |
| Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser Thr Thr Phe Leu Val | |
| 175 180 185 | |
| cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat gac | 906 |
| His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp | |
| 190 195 200 | |
| ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac ctg | 954 |
| Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr Leu | |
| 205 210 215 220 | |
| ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg gtt | 1002 |
| Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val Val | |
| 225 230 235 | |
| ctg agc ttc ctc ctg ggt ggc tac ctg ttg ttt gtc ctg tat ctg gcg | 1050 |
| Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu Ala | |
| 240 245 250 | |
| gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc tgg | 1098 |
| Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala Trp | |
| 255 260 265 | |
| tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc caa | 1146 |
| Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro Ser Ala Glu Pro Gln | |
| 270 275 280 | |
| gtc cac cgg aac att cac tcc cat ggg ctt cgg agc aac ctt caa gag | 1194 |


```

gtt act gct gtt tcg gag gta ttc ctc tgc tgt gag cag ggc tgg cca 1547
Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
      455                      460                      465
gcc aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act 1595
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
      470                      475                      480
ctc ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg 1643
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
485                      490                      495                      500
act cag tta ggt gtg ccc aga cgc act gac aaa atg aca tgacttcagg 1692
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
      505                      510
gaagcctgga caccgcaggc acctggacca gctatgggta gttctgtggg tggaacacat 1752
tctgtgtaag agccccactg agggctctgc agcggagtga cagcaacccc agagatgagg 1812
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg 1872
ggagtttcat ttttaagtga agaccaaag ccctttaaaa ataatagttt tttatcaaaa 1932
aaaaaaaaaa aaa 1945

```

```

<210> 38
<211> 1330
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 198..998

```

```

<220>
<221> sig_peptide
<222> 198..269
<223> Von Heijne matrix
      score 9.08017839002281
      seq LLLGPGLLATVRA/EC

```

```

<400> 38
agaaatcagc cctttgcaga gggcgcagag ggccctggaaa cctctgggac cttttcccag 60
gaactgttta tggtttcccc ctagggtctag gagacgtaga tgcataggtg gattggatac 120
atcgatggta gctataagag tcgtgtctga acccggtctt tccaattggc ctgctccatc 180
cgaacagcgt caactcc atg gcg cgg ttc ctg aca ctt tgc act tgg ctg 230
      Met Ala Arg Phe Leu Thr Leu Cys Thr Trp Leu
      -20                      -15
ctg ttg ctc ggc ccc ggg ctc ctg gcg acc gtg cgg gcc gaa tgc agc 278
Leu Leu Leu Gly Pro Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser
      -10                      -5                      1
cag gat tgc gcg acg tgc agc tac cgc cta gtg cgc ccg gcc gac atc 326
Gln Asp Cys Ala Thr Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile
      5                      10                      15
aac ttc ctg gct tgc gta atg gaa tgt gaa ggt aaa ctg cct tct ctg 374
Asn Phe Leu Ala Cys Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu
20                      25                      30                      35
aaa att tgg gaa acc tgc aag gag ctc ctg cag ctg tcc aaa cca gat 422
Lys Ile Trp Glu Thr Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp
      40                      45                      50
ctt cct caa gat ggc acc agc acc ctc aga gaa aat agc aaa ccg gaa 470
Leu Pro Gln Asp Gly Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu
      55                      60                      65
gaa agc cat ttg cta gcc aaa agg tat ggg gcc ttc atg aaa agg tat 518
Glu Ser His Leu Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Arg Tyr

```

```

      70      75      80
gga ggc ttc atg aag aaa atg gat gag ctt tat ccc atg gag cca gaa 566
Gly Gly Phe Met Lys Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu
      85      90      95
gaa gag gcc aat gga agt gag atc ctc gcc aag cgg tat ggg ggc ttc 614
Glu Glu Ala Asn Gly Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe
100      105      110      115
atg aag aag gat gca gag gag gac gac tcg ctg gcc aat tcc tca gac 662
Met Lys Lys Asp Ala Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp
      120      125      130
ctg cta aaa gag ctt ctg gaa aca ggg gac aac cga gag cgt agc cac 710
Leu Leu Lys Glu Leu Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His
      135      140      145
cac cag gat ggc agt gat aat gag gaa gaa gtg agc aag aga tat ggg 758
His Gln Asp Gly Ser Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly
      150      155      160
ggc ttc atg aga ggc tta aag aga agc ccc caa ctg gaa gat gaa gcc 806
Gly Phe Met Arg Gly Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala
      165      170      175
aaa gag ctg cag aag cga tat ggg ggc ttc atg aga aga gta ggt cgc 854
Lys Glu Leu Gln Lys Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg
180      185      190      195
cca gag tgg tgg atg gac tac cag aaa cgg tat gga ggt ttc ctg aag 902
Pro Glu Trp Trp Met Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys
      200      205      210
cgc ttt gcc gag gct ctg ccc tcc gac gaa gaa ggc gaa agt tac tcc 950
Arg Phe Ala Glu Ala Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser
      215      220      225
aaa gaa gtt cct gaa atg gaa aaa aga tac gga gga ttt atg aga ttt 998
Lys Glu Val Pro Glu Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe
      230      235      240
taatattttt cccactagtg gccccaggcc ccagcaagcc tccctccatc ctccagtggg 1058
aaactgttga tgggtgtttta ttgtcatgtg ttgcttgcc tgtatagttg acttcattgt 1118
ctggataact atacaacctg aaaactgtca ttccagggtc tgtgctcttt ttggagtctt 1178
taagctcagt attagtctat tgcagctatc tcgttttcat gctaaaatag tttttgttat 1238
cttgtctctt atttttgaca aacatcaata aatgcttact tgtatataga gataataaac 1298
ctattacccc aagtgcacaaa aaaaaaaaaa aa 1330

```

<210> 39
 <211> 2124
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 505..1590

<220>
 <221> sig_peptide
 <222> 505..624
 <223> Von Heijne matrix
 score 8.5056444915604
 seq VVMLMLLTLLVLG/MV

```

<400> 39
cctggcataa ctgataggca tgtatgggag gaccacattc ctggggacag cctgggtatg 60
tgacatggca ggtgaccagg ttcccatgaa tgcccagggc tgtgcccata ccatgagctg 120
gggcttcctt ggaggtaaag agctaggggtg ggggtggcagt gggtagaacc ccagctggac 180

```

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| agctccttcc | ttagctctgt | gattgctaca | gctggttctg | gaagccacag | gcgcctcag | 240 | | | | | | | | | | |
| gacaaatggg | gcttcttcag | cacagggtag | tgagtgcga | gctaagcaag | gacactgtcc | 300 | | | | | | | | | | |
| ccttctctgc | ccaggctcga | gctgtgcacc | tttaccctgg | caattgccct | gggtgctgtc | 360 | | | | | | | | | | |
| ctgtcctgc | ccttctccat | catcagcaat | gaggtgctgc | tctccctgcc | tcggaactac | 420 | | | | | | | | | | |
| tacatccagt | ggctcaacgg | ctccctcatc | catggcctct | ggaaccttgt | ttttctcttc | 480 | | | | | | | | | | |
| tccaacctgt | ccctcatctt | cctc | atg | ccc | ttt | gca | tat | ttc | ttc | act | gag | 531 | | | | |
| | | | Met | Pro | Phe | Ala | Tyr | Phe | Phe | Thr | Glu | | | | | |
| | | | -40 | | | | -35 | | | | | | | | | |
| tct | gag | ggc | ttt | gct | ggc | tcc | aga | aag | ggg | gtc | ctg | ggc | cgg | gtc | tat | 579 |
| Ser | Glu | Gly | Phe | Ala | Gly | Ser | Arg | Lys | Gly | Val | Leu | Gly | Arg | Val | Tyr | |
| | -30 | | | | | -25 | | | | | -20 | | | | | |
| gag | aca | gtg | gtg | atg | ttg | atg | ctc | ctc | act | ctg | ctg | gtg | cta | ggg | atg | 627 |
| Glu | Thr | Val | Val | Met | Leu | Met | Leu | Leu | Thr | Leu | Leu | Val | Leu | Gly | Met | |
| | -15 | | | | -10 | | | | | -5 | | | | | 1 | |
| gtg | tgg | gtg | gca | tca | gcc | att | gtg | gac | aag | aac | aag | gcc | aac | aga | gag | 675 |
| Val | Trp | Val | Ala | Ser | Ala | Ile | Val | Asp | Lys | Asn | Lys | Ala | Asn | Arg | Glu | |
| | | | 5 | | | | | 10 | | | | 15 | | | | |
| tca | ctc | tat | gac | ttt | tgg | gag | tac | tat | ctc | ccc | tac | ctc | tac | tca | tgc | 723 |
| Ser | Leu | Tyr | Asp | Phe | Trp | Glu | Tyr | Tyr | Leu | Pro | Tyr | Leu | Tyr | Ser | Cys | |
| | | 20 | | | | | 25 | | | | 30 | | | | | |
| atc | tcc | ttc | ctt | ggg | gtt | ctg | ctg | ctc | ctg | gtg | tgt | act | cca | ctg | ggg | 771 |
| Ile | Ser | Phe | Leu | Gly | Val | Leu | Leu | Leu | Leu | Val | Cys | Thr | Pro | Leu | Gly | |
| | 35 | | | | | 40 | | | | | 45 | | | | | |
| ctc | gcc | cgc | atg | ttc | tcc | gtc | act | ggg | aag | ctg | cta | gtc | aag | ccc | cgg | 819 |
| Leu | Ala | Arg | Met | Phe | Ser | Val | Thr | Gly | Lys | Leu | Leu | Val | Lys | Pro | Arg | |
| | 50 | | | | 55 | | | | | 60 | | | | 65 | | |
| ctg | ctg | gaa | gac | ctg | gag | gag | cag | ctg | tac | tgc | tca | gcc | ttt | gag | gag | 867 |
| Leu | Leu | Glu | Asp | Leu | Glu | Glu | Gln | Leu | Tyr | Cys | Ser | Ala | Phe | Glu | Glu | |
| | | | | 70 | | | | 75 | | | | | 80 | | | |
| gca | gcc | ctg | acc | cgc | agg | atc | tgt | aat | cct | act | tcc | tgc | tgg | ctg | cct | 915 |
| Ala | Ala | Leu | Thr | Arg | Arg | Ile | Cys | Asn | Pro | Thr | Ser | Cys | Trp | Leu | Pro | |
| | | | 85 | | | | | 90 | | | | 95 | | | | |
| tta | gac | atg | gag | ctg | cta | cac | aga | cag | gtc | ctg | gct | ctg | cag | aca | cag | 963 |
| Leu | Asp | Met | Glu | Leu | Leu | His | Arg | Gln | Val | Leu | Ala | Leu | Gln | Thr | Gln | |
| | 100 | | | | | | 105 | | | | 110 | | | | | |
| agg | gtc | ctg | ctg | gag | aag | agg | cgg | aag | gct | tca | gcc | tgg | caa | cgg | aac | 1011 |
| Arg | Val | Leu | Leu | Glu | Lys | Arg | Lys | Ala | Ser | Ala | Trp | Gln | Arg | Asn | | |
| | 115 | | | | | 120 | | | | | 125 | | | | | |
| ctg | ggc | tac | ccc | ctg | gct | atg | ctg | tgc | ttg | ctg | gtg | ctg | acg | ggc | ctg | 1059 |
| Leu | Gly | Tyr | Pro | Leu | Ala | Met | Leu | Cys | Leu | Leu | Val | Leu | Thr | Gly | Leu | |
| | 130 | | | | 135 | | | | | 140 | | | | 145 | | |
| tct | gtg | ctc | att | gtg | gcc | atc | cac | atc | ctg | gag | ctg | ctc | atc | gat | gag | 1107 |
| Ser | Val | Leu | Ile | Val | Ala | Ile | His | Ile | Leu | Glu | Leu | Leu | Ile | Asp | Glu | |
| | | | | 150 | | | | | 155 | | | | 160 | | | |
| gct | gcc | atg | ccc | cga | ggc | atg | cag | ggg | acc | tcc | tta | ggc | cag | gtc | tcc | 1155 |
| Ala | Ala | Met | Pro | Arg | Gly | Met | Gln | Gly | Thr | Ser | Leu | Gly | Gln | Val | Ser | |
| | | | 165 | | | | | 170 | | | | 175 | | | | |
| ttc | tcc | aag | ctg | ggc | tcc | ttt | ggg | gcc | gtc | att | cag | gtt | gta | ctc | atc | 1203 |
| Phe | Ser | Lys | Leu | Gly | Ser | Phe | Gly | Ala | Val | Ile | Gln | Val | Val | Leu | Ile | |
| | | 180 | | | | | 185 | | | | | 190 | | | | |
| ttt | tac | cta | atg | gtg | tcc | tca | gtt | gtg | ggc | ttc | tat | agc | tct | cca | ctc | 1251 |
| Phe | Tyr | Leu | Met | Val | Ser | Ser | Val | Val | Gly | Phe | Tyr | Ser | Ser | Pro | Leu | |
| | 195 | | | | | 200 | | | | | 205 | | | | | |
| ttc | cgg | agc | ctg | cgg | ccc | aga | tgg | cac | gac | act | gcc | atg | acg | cag | ata | 1299 |
| Phe | Arg | Ser | Leu | Arg | Pro | Arg | Trp | His | Asp | Thr | Ala | Met | Thr | Gln | Ile | |
| | 210 | | | | 215 | | | | | 220 | | | | 225 | | |
| att | ggg | aac | tgt | gtc | tgt | ctc | ctg | gtc | cta | agc | tca | gca | ctt | cct | gtc | 1347 |
| Ile | Gly | Asn | Cys | Val | Cys | Leu | Leu | Val | Leu | Ser | Ser | Ala | Leu | Pro | Val | |

| | | | | |
|--|-----|-----|-----|------|
| | 230 | 235 | 240 | |
| ttc tct cga acc ctg ggg ctc act cgc ttt gac ctg ctg ggt gac ttt | | | | 1395 |
| Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu Leu Gly Asp Phe | | | | |
| | 245 | 250 | 255 | |
| gga cgc ttc aac tgg ctg ggc aat ttc tac att gtg ttc ctc tac aac | | | | 1443 |
| Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile Val Phe Leu Tyr Asn | | | | |
| | 260 | 265 | 270 | |
| gca gcc ttt gca ggc ctc acc aca ctc tat ctg gtg aag acc ttc act | | | | 1491 |
| Ala Ala Phe Ala Gly Leu Thr Thr Leu Tyr Leu Val Lys Thr Phe Thr | | | | |
| | 275 | 280 | 285 | |
| gca gct gtg cgg gca gag ctg atc cgg gcc ttt ggg ctg gac aga ctg | | | | 1539 |
| Ala Ala Val Arg Ala Glu Leu Ile Arg Ala Phe Gly Leu Asp Arg Leu | | | | |
| | 290 | 295 | 300 | 305 |
| ccg ctg ccc gtc tcc ggt ttc ccc cag gca tct agg aag acc cag cac | | | | 1587 |
| Pro Leu Pro Val Ser Gly Phe Pro Gln Ala Ser Arg Lys Thr Gln His | | | | |
| | 310 | 315 | 320 | |
| cag tgacctccag ctgggggtgg gaagaaaaaa actggacact gccatctgct | | | | 1640 |
| Gln | | | | |
| gcctaggcct ggaggggaagc ccaaggctac ttggacctca ggacctggaa tctgagaggg | | | | 1700 |
| tgggtggcag aggggagcag agccatctgc actattgcat aatctgagcc agagtgtggg | | | | 1760 |
| accaggacct cctgcttttc cataacttaac tgtggcctca gcatggggta gggctgggtg | | | | 1820 |
| actgggtcta gcccctgata ccaaactctgt ttacacatca atctgcctca ctgctgttct | | | | 1880 |
| gggccatccc catagccatg ttacatgat ttgatgtgca atagggtggg gtaggggcag | | | | 1940 |
| ggaaaggact gggccagggc aggcctcggga gatagattgt ctcccttgcc tctggcccag | | | | 2000 |
| cagagcctaa gcaactgtgct atcctggagg ggctttggac cacctgaaag accaagggga | | | | 2060 |
| tagggaggag gaggcttcag ccatcagcaa taaagttgat cccaggcaaa aaaaaaaaaa | | | | 2120 |
| aaaa | | | | 2124 |

<210> 40
 <211> 1159
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..326

<220>
 <221> sig_peptide
 <222> 84..146
 <223> Von Heijne matrix
 score 6.39000252120129
 seq LGLSVLLTAATVA/GV

| | |
|---|-----|
| <400> 40 | |
| agtacaggcg gcggtgcgca ctctcgggcg gcctctgcgc ctcgggcggg cgggagagag | 60 |
| aggccgcggc cgccagcgtg ggg atg tct agg agc tcg aag gtg gtg ctg ggc | 113 |
| Met Ser Arg Ser Ser Lys Val Val Leu Gly | |
| -20 -15 | |
| ctc tcg gtg ctg ctg acg gcg gcc aca gtg gcc ggc gta cat gtg aag | 161 |
| Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val Lys | |
| -10 -5 1 5 | |
| cag cag tgg gac cag cag agg ctt cgt gac gga gtt atc aga gac att | 209 |
| Gln Gln Trp Asp Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile | |
| 10 15 20 | |
| gag agg caa att cgg aaa aaa gaa aac att cgt ctt ttg gga gaa cag | 257 |
| Glu Arg Gln Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln | |
| 25 30 35 | |

| | |
|--|------|
| att att ttg act gag caa ctt gaa gca gaa aga gag aag atg tta ttg | 305 |
| Ile Ile Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu | |
| 40 45 50 | |
| gca aaa gga tct caa aaa tca tgacttgaat gtgaaatattc tgttggacag | 356 |
| Ala Lys Gly Ser Gln Lys Ser | |
| 55 60 | |
| acaacacgag tttgtgtgtg tgtgttgatg gagagtagct tagtagtatc ttcattctttt | 416 |
| tttttgggtca ctgtcctttt aaacttgatc aaataaagga cagtgggtca tataagttac | 476 |
| tgcttttcagg gtcccttata tctgaataaa ggagtgtggg cagacacttt ttggaagagt | 536 |
| ctgtctgggt gatcctggta gaagcccat tagggctact gtccagtgtc tagggttgtt | 596 |
| actgagaagc actgccgagc ttgtgagaag gaaggatgg atagtagcat ccacctgagt | 656 |
| agtctgatca gtcggcatga tgacgaagcc acgagaacat cgacctcaga aggactggag | 716 |
| gaagggtgaaa gtggaggagg agacgtcct gatcgtcgaa tyccgaggat caggkcatca | 776 |
| gtggacttat cgcacgacca gagtggggat tccctcaaca gtgatgaagg agacgtgtct | 836 |
| tggatggagg agcagctgtc ctacttctgt gacaagtgcc aaaaatggat accagccagt | 896 |
| aaggagcttc tcaattcctt tgatttgtca attcctgtgt gaaggtttgt ttttccaacc | 956 |
| tgtgaaagaa acgtgaatgt aaaagagacc taaataaaag gataattata tttattctct | 1016 |
| agttgatcag ctataaattt atataaaaca taggcattgtt tgtactaatg aaacgtactg | 1076 |
| tcaacctcta tcacattgtt aaattaacac ttttgggtgt aactcaataa aattgagaaa | 1136 |
| attgcaaaaa aaaaaaaaaaaa aaa | 1159 |

<210> 41
 <211> 1953
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..1678

<220>
 <221> sig_peptide
 <222> 56..139
 <223> Von Heijne matrix
 score 3.75144398608723
 seq SGLLLQVLFRLIT/FV

| | |
|---|-----|
| <400> 41 | |
| agactaaacg gagtggcggc ggcatttctt ggtgtctgag cctggcgcgaggaggct atg | 58 |
| | Met |
| ggc agc cag gag gtg ctg ggc cac gcg gcc cgg ctg gcc tcc tcc ggt | 106 |
| Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser Gly | |
| -25 -20 -15 | |
| ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat gca | 154 |
| Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn Ala | |
| -10 -5 1 5 | |
| ttt att ctt cgc ttc ctg tca aag gaa atc gtt ggc gta gta aat gta | 202 |
| Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn Val | |
| 10 15 20 | |
| aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag gcc | 250 |
| Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala | |
| 25 30 35 | |
| ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc cag | 298 |
| Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln | |
| 40 45 50 | |
| acc ctc aac ctg ctg tgg cta aca gtc ccc ctg ggt gtg ttt tgg tcc | 346 |
| Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp Ser | |
| 55 60 65 | |

| | |
|---|------|
| tta ttc ctg ggc tgg atc tgg ttg cag ctg ctt gaa gtg cct gat cct | 394 |
| Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp Pro | |
| 70 75 80 85 | |
| aat gtt gtc cct cac tat gca act gga gtg gtg ctg ttt ggt ctc tcg | 442 |
| Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu Ser | |
| 90 95 100 | |
| gca gtg gtg gag ctt cta gga gag ccc ttt tgg gtc ttg gca caa gca | 490 |
| Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln Ala | |
| 105 110 115 | |
| cat atg ttt gtg aag ctc aag gtg att gca gag agc ctg tcg gta att | 538 |
| His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val Ile | |
| 120 125 130 | |
| ctt aag agc gtt ctg aca gct ttt ctc gtg ctg tgg ttg cct cac tgg | 586 |
| Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His Trp | |
| 135 140 145 | |
| gga ttg tac att ttc tct ttg gcc cag ctt ttc tat acc aca gtt ctg | 634 |
| Gly Leu Tyr Ile Phe Ser Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu | |
| 150 155 160 165 | |
| gtg ctc tgc tat gtt att tat ttc aca aag tta ctg ggt tcc cca gaa | 682 |
| Val Leu Cys Tyr Val Ile Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu | |
| 170 175 180 | |
| tca acc aag ctt caa act ctt cct gtc tcc aga ata aca gat ctg tta | 730 |
| Ser Thr Lys Leu Gln Thr Leu Pro Val Ser Arg Ile Thr Asp Leu Leu | |
| 185 190 195 | |
| ccc aat att aca aga aat gga gcg ttt ata aac tgg aaa gag gct aaa | 778 |
| Pro Asn Ile Thr Arg Asn Gly Ala Phe Ile Asn Trp Lys Glu Ala Lys | |
| 200 205 210 | |
| ctg act tgg agt ttt ttc aaa cag tct ttc ttg aaa cag att ttg aca | 826 |
| Leu Thr Trp Ser Phe Phe Lys Gln Ser Phe Leu Lys Gln Ile Leu Thr | |
| 215 220 225 | |
| gaa ggc gag cga tat gtg atg aca ttt ttg aat gta ttg aac ttt ggt | 874 |
| Glu Gly Glu Arg Tyr Val Met Thr Phe Leu Asn Val Leu Asn Phe Gly | |
| 230 235 240 245 | |
| gat cag ggt gtg tat gat ata gtg aat aat ctt ggc tcc ctt gtg gcc | 922 |
| Asp Gln Gly Val Tyr Asp Ile Val Asn Asn Leu Gly Ser Leu Val Ala | |
| 250 255 260 | |
| aga tta att ttc cag cca ata gag gaa agt ttt tat ata ttt ttt gct | 970 |
| Arg Leu Ile Phe Gln Pro Ile Glu Glu Ser Phe Tyr Ile Phe Phe Ala | |
| 265 270 275 | |
| aag gtg ctg gag agg gga aag gat gcc aca ctt cag aag cag gag gac | 1018 |
| Lys Val Leu Glu Arg Gly Lys Asp Ala Thr Leu Gln Lys Gln Glu Asp | |
| 280 285 290 | |
| gtt gct gtg gct gct gca gtc ttg gag tcc ctg ctc aag ctg gcc ctg | 1066 |
| Val Ala Val Ala Ala Val Leu Glu Ser Leu Leu Lys Leu Ala Leu | |
| 295 300 305 | |
| ctg gcc ggc ctg acc atc act gtt ttt ggc ttt gcc tat tct cag ctg | 1114 |
| Leu Ala Gly Leu Thr Ile Thr Val Phe Gly Phe Ala Tyr Ser Gln Leu | |
| 310 315 320 325 | |
| gct ctg gat atc aac gga ggg acc atg ctt agc tca gga tcc ggt cct | 1162 |
| Ala Leu Asp Ile Asn Gly Gly Thr Met Leu Ser Ser Gly Ser Gly Pro | |
| 330 335 340 | |
| gtt ttg ctg cgt tcc tac tgt ctc tat gtt ctc ctg ctt gcc atc aat | 1210 |
| Val Leu Leu Arg Ser Tyr Cys Leu Tyr Val Leu Leu Leu Ala Ile Asn | |
| 345 350 355 | |
| gga gtg aca gag tgt ttc aca ttt gct gcc atg agc aaa gag gag gtc | 1258 |
| Gly Val Thr Glu Cys Phe Thr Phe Ala Ala Met Ser Lys Glu Glu Val | |
| 360 365 370 | |
| gac agg tac aat ttt gtg atg ctg gcc ctg tcc tcc tca ttc ctg gtg | 1306 |

| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|------------|-----|-----|-----|------|--|
| Asp | Arg | Tyr | Asn | Phe | Val | Met | Leu | Ala | Leu | Ser | Ser | Ser | Phe | Leu | Val | | |
| 375 | | | | | | 380 | | | | 385 | | | | | | | |
| tta | tcc | tat | ctc | ttg | acc | cgt | tgg | tgt | ggc | agc | gtg | ggc | ttc | atc | ttg | 1354 | |
| Leu | Ser | Tyr | Leu | Leu | Thr | Arg | Trp | Cys | Gly | Ser | Val | Gly | Phe | Ile | Leu | | |
| 390 | | | | | 395 | | | | 400 | | | | | | 405 | | |
| gcc | aac | tgc | ttt | aac | atg | ggc | att | cgg | atc | acg | cag | agc | ctt | tgc | ttc | 1402 | |
| Ala | Asn | Cys | Phe | Asn | Met | Gly | Ile | Arg | Ile | Thr | Gln | Ser | Leu | Cys | Phe | | |
| | | | | 410 | | | | | 415 | | | | | 420 | | | |
| atc | cac | cgc | tac | tac | cga | agg | agc | ccc | cac | agg | ccc | ctg | gct | ggc | ctg | 1450 | |
| Ile | His | Arg | Tyr | Tyr | Arg | Arg | Ser | Pro | His | Arg | Pro | Leu | Ala | Gly | Leu | | |
| | | | 425 | | | | 430 | | | | | | 435 | | | | |
| cac | cta | tgc | cca | gtc | ctg | ctc | ggg | aca | ttt | gcc | ctc | agt | ggt | ggg | gtt | 1498 | |
| His | Leu | Ser | Pro | Val | Leu | Leu | Gly | Thr | Phe | Ala | Leu | Ser | Gly | Gly | Val | | |
| | | | 440 | | | | 445 | | | | | | 450 | | | | |
| act | gct | gtt | tgc | gag | gta | ttc | ctc | tgc | tgt | gag | cag | ggc | tgg | cca | gcc | 1546 | |
| Thr | Ala | Val | Ser | Glu | Val | Phe | Leu | Cys | Cys | Glu | Gln | Gly | Trp | Pro | Ala | | |
| | | | 455 | | | | 460 | | | | | | 465 | | | | |
| aga | ctg | gca | cac | att | gct | gtg | ggg | gcc | ttc | tgt | ctg | gga | gca | act | ctc | 1594 | |
| Arg | Leu | Ala | His | Ile | Ala | Val | Gly | Ala | Phe | Cys | Leu | Gly | Ala | Thr | Leu | | |
| 470 | | | | | 475 | | | | | 480 | | | | | 485 | | |
| ggg | aca | gca | ttc | ctc | aca | gag | acc | aag | ctg | atc | cat | ttc | ctc | agg | act | 1642 | |
| Gly | Thr | Ala | Phe | Leu | Thr | Glu | Thr | Lys | Leu | Ile | His | Phe | Leu | Arg | Thr | | |
| | | | | 490 | | | | | 495 | | | | | 500 | | | |
| cag | tta | ggt | gtg | ccc | aga | cgc | act | gac | aaa | atg | acg | tgacttcagg | | | | 1688 | |
| Gln | Leu | Gly | Val | Pro | Arg | Arg | Thr | Asp | Lys | Met | Thr | | | | | | |
| | | | 505 | | | | | | 510 | | | | | | | | |
| gaagcctgga | cacccgaggc | acctggacca | gctatgggta | gttctgtggg | tggaacacat | | | | | | | | | | | 1748 | |
| tctgtgtaag | agccccactg | agggctctgc | agcggagtga | cagcaacccc | agagatgagg | | | | | | | | | | | 1808 | |
| caccagagag | tgccactgca | tgagacacct | gtgaccattc | gaagtctgaa | atgcgggggg | | | | | | | | | | | 1868 | |
| ggagtttcat | ttttaagtga | agaccaaag | ccctttaaaa | ataatagttt | tttatcattt | | | | | | | | | | | 1928 | |
| tatagtga | aaaaaaaaa | aaaaa | | | | | | | | | | | | | | 1953 | |

<210> 42
 <211> 1688
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..1522

<220>
 <221> sig_peptide
 <222> 119..181
 <223> Von Heijne matrix
 score 11.6921972463885
 seq LLLCLALSGAET/KP

| | | | | | | | | | | | | | | | | | |
|-------------|-------------|-------------|-------------|-------------|------------|--|--|--|--|--|--|--|--|--|----|-----|--|
| <400> | 42 | | | | | | | | | | | | | | | | |
| aaaaggctgc | aggctgccag | gtgtgcttgg | agagccccct | tcttccgccg | ggcctcgcaa | | | | | | | | | | | 60 | |
| gcagcgtagg | actgtggaga | agggcggtgg | gcaaggaggg | aactcgagag | cagcctcc | | | | | | | | | | | 118 | |
| atg ggc aca | cag gag ggc | tgg tgc ctg | ctg ctg ctc | tgc ctg gct | cta tct | | | | | | | | | | | 166 | |
| Met Gly Thr | Gln Glu Gly | Trp Cys Leu | Leu Leu Leu | Cys Leu Ala | Leu Ser | | | | | | | | | | | | |
| -20 | | -15 | | -10 | | | | | | | | | | | | | |
| gga gca gca | gaa acc aag | ccc cac cca | gca gag ggg | cag tgg cgg | gca | | | | | | | | | | | 214 | |
| Gly Ala Ala | Glu Thr Lys | Pro His Pro | Ala Glu Gly | Gln Trp Arg | Ala | | | | | | | | | | | | |
| -5 | | 1 | | 5 | | | | | | | | | | | 10 | | |
| gtg gac gtg | gtc cta gac | tgt ttc ctg | gtg aag gac | ggt gcg cac | cgt | | | | | | | | | | | 262 | |


```

          320          325          330
tcc agc ctc agg caa agc gtg gca ggc acc tac agc atc tcc tcc tct      1222
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser
          335          340          345
ctc acc gca gaa cct ggc tct gca ggt gcc act tac acc tgc cag gtc      1270
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val
          350          355          360
aca cac atc tct ctg gag gag ccc ctt ggg gcc agc acc cag gtt gtc      1318
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val
          365          370          375
cca cca gag cgg aga aca gcc ttg gga gtc atc ttt gcc agc agt ctc      1366
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
380          385          390          395
ttc ctt ctt gca ctg atg ttc ctg ggg ctt cag aga cgg caa gca cct      1414
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro
          400          405          410
aca gga ctt ggg ctg ctt cag gct gaa cgc tgg gag acc act tcc tgt      1462
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
          415          420          425
gct gac aca cag agc tcc cat ctc cat gaa gac cgc aca gcg cgt gta      1510
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val
          430          435          440
agc cag ccc agc tgacctaaag cgacatgaga ctactagaaa gaaacgacac      1562
Ser Gln Pro Ser
          445
ccttccccaa gccccacag ctactccaac ccaaacaaca accaagccag tttaatggta      1622
ggaatttgta ttttttgct ttgttcagaa tacatgacat tggtaaataa aaaaaaaaaa      1682
aaaaaa      1688

<210> 43
<211> 1942
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 334..1551

<220>
<221> sig_peptide
<222> 334..426
<223> Von Heijne matrix
      score 4.0554926521937
      seq TVFLLVTLQALDT/VE

<400> 43
gctcataggg agaaaggaag ctgcgctgcg ttctgcggga cgaaccctgc tccgcgcgag      60
aatttttttg attccttctt atttgagaaa atctccagct gctctgatca tagcctaaga      120
agactgcatg ctgcttcctc tcgatgccaa gccagacctt ctcacaacct cggatctcag      180
tccttcatgg agacctggtc ccagcaggaa tggcagtgca ggaaattggc gcccagatgg      240
ttcttccatg tgaagttgtc tcgggctctg ggctgacgag agaacacctg gtaaccaggt      300
tagccctctg tcagtcaccc agggcagggc agc atg gtg cgg att cag agg agg      354
      Met Val Arg Ile Gln Arg Arg
      -30          -25
aag ctt ttg gca tct tgc ctg tgc gtc aca gcc acc gtc ttt ctg ctt      402
Lys Leu Leu Ala Ser Cys Leu Cys Val Thr Ala Thr Val Phe Leu Leu
      -20          -15          -10
gtc aca ctc cag gcc ttg gat acc gtt gag aat cta atg aaa gtc acg      450

```



```

      300      305      310
gtc cct gta tat tac gga tcc ccc agc atc aca gac tgg ctt cca agt      1410
Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser
      315      320      325
aac aaa agt gct att ctt gta tca gaa ttt tct cac ccc agg gaa ctg      1458
Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu
      330      335      340
gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc      1506
Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala
      345      350      355      360
tat gta gaa tgg aag ctg aag ggt aga tct cta acc agc gac ttc      1551
Tyr Val Glu Trp Lys Leu Lys Gly Arg Ser Leu Thr Ser Asp Phe
      365      370      375
tgacagctct caggaacgg aaatggggag tgcaagacgt caaccaggac aattacatcg      1611
atgcatttga gtgtatggtg tgcaccaagg tgtgggctaa tatcaggctt caggaaaagg      1671
gcttaccacc caaaagatgg gaggcagaag ataccacct gagttgccca gagcccacag      1731
tgtttgcttt ctcaccactc cggactccac ctttgagctc tttgcgagag atgtggattt      1791
ccagctttga acaatccaag aaagaagccc aggactaag gtggctgggt gataggaatc      1851
aaaacttttc atctcaagag ttttggggcc tagtattcaa ggactgattt caaaaatgat      1911
cagaatgaaa cagaaaaaaa aaaaaaaaaa a      1942

<210> 44
<211> 1657
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..986

<220>
<221> sig_peptide
<222> 72..149
<223> Von Heijne matrix
      score 6.33091407142367
      seq GVGLVTLGLAVG/SY

<400> 44
ctccgaccgc ccccgcggcg cattgtggga tctgtcggct tgtcagggtg tggaggaaaa      60
ggcgctccgt c atg ggg atc cag acg agc ccc gtc ctg ctg gcc tcc ctg      110
      Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu
      -25      -20      -15
ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc tac ttg      158
Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu
      -10      -5      1
gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg gac ccc aat gaa      206
Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu
      5      10      15
aag tac ctg cta cga ctg cta gac aag acg act gtg agc cac aac acc      254
Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr
      20      25      30      35
aag agg ttc cgc ttt gcc ctg ccc acc gcc cac cac act ctg ggg ctg      302
Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu
      40      45      50
cct gtg ggc aaa cat atc tac ctc tcc acc cga att gat ggc agc ctg      350
Pro Val Gly Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu
      55      60      65
gtc atc agg cca tac act cct gtc acc agt gat gag gat caa ggc tat      398

```

| | | | | | | | | | | | | | | | | | |
|-------------|-------------|-------------|------------|------------|-------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|------|--|
| Val | Ile | Arg | Pro | Tyr | Thr | Pro | Val | Thr | Ser | Asp | Glu | Asp | Gln | Gly | Tyr | | |
| | | 70 | | | | | 75 | | | | 80 | | | | | | |
| gtg | gat | ctt | gtc | atc | aag | gtc | tac | ctg | aag | ggg | gtg | cac | ccc | aaa | ttt | 446 | |
| Val | Asp | Leu | Val | Ile | Lys | Val | Tyr | Leu | Lys | Gly | Val | His | Pro | Lys | Phe | | |
| | | 85 | | | | 90 | | | | | 95 | | | | | | |
| cct | gag | gga | ggg | aag | atg | tct | cag | tac | ctg | gat | agc | ctg | aag | gtt | ggg | 494 | |
| Pro | Glu | Gly | Gly | Lys | Met | Ser | Gln | Tyr | Leu | Asp | Ser | Leu | Lys | Val | Gly | | |
| 100 | | | | | 105 | | | | | 110 | | | | | 115 | | |
| gat | gtg | gtg | gag | ttt | cgg | ggg | cca | agc | ggg | ttg | ctc | act | tac | act | gga | 542 | |
| Asp | Val | Val | Glu | Phe | Arg | Gly | Pro | Ser | Gly | Leu | Leu | Thr | Tyr | Thr | Gly | | |
| | | | | 120 | | | | | 125 | | | | | 130 | | | |
| aaa | ggg | cat | ttt | aac | att | cag | ccc | aac | aag | aaa | tct | cca | cca | gaa | ccc | 590 | |
| Lys | Gly | His | Phe | Asn | Ile | Gln | Pro | Asn | Lys | Lys | Ser | Pro | Pro | Glu | Pro | | |
| | | | 135 | | | | | 140 | | | | | 145 | | | | |
| cga | gtg | gag | aag | aaa | ctg | gga | atg | att | gcc | ggc | ggg | aca | gga | atc | acc | 638 | |
| Arg | Val | Ala | Lys | Lys | Leu | Gly | Met | Ile | Ala | Gly | Gly | Thr | Gly | Ile | Thr | | |
| | | 150 | | | | | 155 | | | | | 160 | | | | | |
| cca | atg | cta | cag | ctg | atc | cgg | gcc | atc | ctg | aaa | gtc | cct | gaa | gat | cca | 686 | |
| Pro | Met | Leu | Gln | Leu | Ile | Arg | Ala | Ile | Leu | Lys | Val | Pro | Glu | Asp | Pro | | |
| | | 165 | | | | 170 | | | | | 175 | | | | | | |
| acc | cag | tgc | ttt | ctg | ctt | ttt | gcc | aac | cag | aca | gaa | aag | gat | atc | atc | 734 | |
| Thr | Gln | Cys | Phe | Leu | Leu | Phe | Ala | Asn | Gln | Thr | Glu | Lys | Asp | Ile | Ile | | |
| 180 | | | | | 185 | | | | | 190 | | | | | 195 | | |
| ttg | cgg | gag | gac | tta | gag | gaa | ctg | cag | gcc | cgc | tat | ccc | aat | cgc | ttt | 782 | |
| Leu | Arg | Glu | Asp | Leu | Glu | Glu | Leu | Gln | Ala | Arg | Tyr | Pro | Asn | Arg | Phe | | |
| | | | | 200 | | | | | 205 | | | | | 210 | | | |
| aag | ctc | tgg | ttc | act | ctg | gat | cat | ccc | cca | aaa | gat | tgg | gcc | tac | agc | 830 | |
| Lys | Leu | Trp | Phe | Thr | Leu | Asp | His | Pro | Pro | Lys | Asp | Trp | Ala | Tyr | Ser | | |
| | | | 215 | | | | 220 | | | | | | 225 | | | | |
| aag | ggc | ttt | gtg | act | gcc | gac | atg | atc | cgg | gaa | cac | ctg | ccc | gct | cca | 878 | |
| Lys | Gly | Phe | Val | Thr | Ala | Asp | Met | Ile | Arg | Glu | His | Leu | Pro | Ala | Pro | | |
| | | 230 | | | | 235 | | | | | | 240 | | | | | |
| ggg | gat | gat | gtg | ctg | gta | ctg | ctt | tgt | ggg | cca | ccc | cca | atg | gtg | cag | 926 | |
| Gly | Asp | Asp | Val | Leu | Val | Leu | Leu | Cys | Gly | Pro | Pro | Pro | Met | Val | Gln | | |
| | | 245 | | | | 250 | | | | 255 | | | | | | | |
| ctg | gcc | tgc | cat | ccc | aac | ttg | gac | aaa | ctg | ggc | tac | tca | caa | aag | atg | 974 | |
| Leu | Ala | Cys | His | Pro | Asn | Leu | Asp | Lys | Leu | Gly | Tyr | Ser | Gln | Lys | Met | | |
| 260 | | | | | 265 | | | | 270 | | | | | 275 | | | |
| cga | ttc | acc | tac | tgagc | atcct | ccagcttccc | tggtgctggt | cgctgcagtt | | | | | | | | 1026 | |
| Arg | Phe | Thr | Tyr | | | | | | | | | | | | | | |
| gttccccatc | agtactcaag | cactataagc | cttagattcc | tttcctcaga | gtttcagggtt | | | | | | | | | | | 1086 | |
| ttttcagtta | catctagagc | tgaaatctgg | atagtacctg | caggaacaat | attcctgtag | | | | | | | | | | | 1146 | |
| ccatggaaga | gggccaaggc | tcagtcactc | cttgatgggc | ctcctaaatc | tccccgtggc | | | | | | | | | | | 1206 | |
| aacaggtcca | ggagaggccc | atggagcagt | ctcttccatg | gagtaagaag | gaaggaggca | | | | | | | | | | | 1266 | |
| tgtacgcttg | gtccaagatt | ggctagttcc | ttgatagcat | cttactctca | ccttctttgt | | | | | | | | | | | 1326 | |
| gtctgtgatg | aaaggaacag | tctgtgcaat | gggttttact | taaacttcac | tgttcaacct | | | | | | | | | | | 1386 | |
| atgagcaaat | ctgtatgtgt | gagtataagt | tgagcatagc | atacttccag | aggtggtctt | | | | | | | | | | | 1446 | |
| atggagatgg | caagaaaagg | ggaaatgatt | tcttcagatc | tcaaaggagt | ctgaaatatc | | | | | | | | | | | 1506 | |
| atattttctgt | gtgtgtctct | ctcagccccct | gccagggcta | gagggaaaca | gctactgata | | | | | | | | | | | 1566 | |
| atcgaaaact | gctgtttgtg | gcaggaaccc | ctggctgtgc | aaataaatgg | ggctgaggcc | | | | | | | | | | | 1626 | |
| cctgtgtgat | attaaaaaaaa | aaaaaaaaaaa | a | | | | | | | | | | | | | 1657 | |

<210> 45
 <211> 1733
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 157..1482

<220>
 <221> sig_peptide
 <222> 157..219
 <223> Von Heijne matrix
 score 11.6921972463885
 seq LLLCLALSGAAET/KP

<400> 45
 aaagaaaagt cggcagcaga gggaacaggg aagaaaccta aaggctgcag gctgccaggt 60
 gtgcttggag agcccccttc ttccgccggg cctcgcaagc agcgtaggac tgtggagaag 120
 ggcggtgggc aaggaggggaa ctcgagagca gcctcc atg ggc aca cag gag ggc 174
 Met Gly Thr Gln Glu Gly
 -20
 tgg tgc ctg ctg ctc tgc ctg gct cta tct gga gca gca gaa acc aag 222
 Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys
 -15 -10 -5 1
 ccc cac cca gca gag ggg cag ttg cgg gca gtg gac gtg gtc cta gac 270
 Pro His Pro Ala Glu Gly Gln Leu Arg Ala Val Asp Val Val Leu Asp
 5 10 15
 tgc ttc ctg gcg aag gac ggt gcg cac cgt gga gct ctc gcc agc agt 318
 Cys Phe Leu Ala Lys Asp Gly Ala His Arg Gly Ala Leu Ala Ser Ser
 20 25 30
 gag gac agg gca agg gcc tcc ctt gtg ctg aag cag gtg cca gtg ctg 366
 Glu Asp Arg Ala Arg Ala Ser Leu Val Leu Lys Gln Val Pro Val Leu
 35 40 45
 gag gat ggc tcc ctg gag gac ttc acc gat ttc caa ggg ggc aca ctg 414
 Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp Phe Gln Gly Gly Thr Leu
 50 55 60 65
 gcc caa gat gac cca cct att atc ttt gag gcc tca gtg gac ctg gtc 462
 Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu Ala Ser Val Asp Leu Val
 70 75 80
 cag att ccc cag gcc gag gcc ttg ctc cat gct gac tgc agt ggg aag 510
 Gln Ile Pro Gln Ala Glu Ala Leu Leu His Ala Asp Cys Ser Gly Lys
 85 90 95
 gag gtg acc tgt gag atc tcc cgc tac ttt ctc cag atg aca gag acc 558
 Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe Leu Gln Met Thr Glu Thr
 100 105 110
 act gtt aag aca gca gct tgg ttc atg gcc aac atg cag gtc tct gga 606
 Thr Val Lys Thr Ala Ala Trp Phe Met Ala Asn Met Gln Val Ser Gly
 115 120 125
 ggg gga cst agc atc tcc ttg gtg atg aag act ccc agg gtc acc aag 654
 Gly Gly Xaa Ser Ile Ser Leu Val Met Lys Thr Pro Arg Val Thr Lys
 130 135 140 145
 aat gag gcg ctc tgg cac ccg acg ctg aac ttg cca ctg agc ccc cag 702
 Asn Glu Ala Leu Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln
 150 155 160
 ggg act gtg cga act gca gtg gag ttc cag gtg atg aca cag acc caa 750
 Gly Thr Val Arg Thr Ala Val Glu Phe Gln Val Met Thr Gln Thr Gln
 165 170 175
 tcc ctg agc ttc ctg ctg ggg tcc tca gcc tcc ttg gac tgt ggc ttc 798
 Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe
 180 185 190
 tcc atg gca ccg ggc ttg gac ctc atc agt gtg gag tgg cga ctg cag 846
 Ser Met Ala Pro Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln
 195 200 205

| | |
|---|------|
| cac aag ggc agg ggt cag ttg gtg tac agc tgg acc gca ggg cag ggg | 894 |
| His Lys Gly Arg Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly | |
| 210 215 220 225 | |
| cag gct gtg cgg aag ggc gct acc ctg gag cct gca caa ctg ggc atg | 942 |
| Gln Ala Val Arg Lys Gly Ala Thr Leu Glu Pro Ala Gln Leu Gly Met | |
| 230 235 240 | |
| gcc agg gat gcc tcc ctc acc ctg ccc ggc ctc act ata cag gac gag | 990 |
| Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu | |
| 245 250 255 | |
| ggg acc tac att tgc cag atc acc acc tct ctg tac cga gct cag cag | 1038 |
| Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln | |
| 260 265 270 | |
| atc atc cag ctc aac atc caa gct tcc cct aaa gta cga ctg agc ttg | 1086 |
| Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu | |
| 275 280 285 | |
| gca aac gaa gct ctg ctg ccc acc ctc atc tgc gac att gct ggc tat | 1134 |
| Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr | |
| 290 295 300 305 | |
| tac cct ctg gat gtg gtg gtg acg tgg acc cga gag gag ctg ggt gga | 1182 |
| Tyr Pro Leu Asp Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly | |
| 310 315 320 | |
| tcc cca gcc caa gtc tct ggt gcc tcc ttc tcc agc ctc agg caa agc | 1230 |
| Ser Pro Ala Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser | |
| 325 330 335 | |
| gtg gca ggc acc tac agc atc tcc tcc tct ctc acc gca gaa cct ggc | 1278 |
| Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly | |
| 340 345 350 | |
| tct gca ggt gcc act tac acc tgc cag gtc aca cac atc tct ctg gag | 1326 |
| Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val Thr His Ile Ser Leu Glu | |
| 355 360 365 | |
| gag ccc ctt ggg gcc agc acc cag gtt gtc cca cca gag cgg aga aca | 1374 |
| Glu Pro Leu Gly Ala Ser Thr Gln Val Val Pro Pro Glu Arg Arg Thr | |
| 370 375 380 385 | |
| gcc ttg gga gtc atc ttt gcc agc agt ctc ttc ctt ctt gca ctg atg | 1422 |
| Ala Leu Gly Val Ile Phe Ala Ser Ser Leu Phe Leu Leu Ala Leu Met | |
| 390 395 400 | |
| ttc ctg ggg ctt cag aga cgg caa gca cct aca gga ctt ggg ctg ctt | 1470 |
| Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro Thr Gly Leu Gly Leu Leu | |
| 405 410 415 | |
| cag gct gaa cgc taggagacca cttcctgtgc tgacacacag agctcccatc | 1522 |
| Gln Ala Glu Arg | |
| 420 | |
| tccatgaaga ccgcacagcg cgtgtaagcc agcccagctg acctaaagcg acatgagact | 1582 |
| actagaaaga aacgacaccc ttcccccaagc cccacagct actccaaccc aaacaacaac | 1642 |
| caagccagtt taatggtagg aatttgtatt ttttgccctt gttcagaata catgacattg | 1702 |
| gtaaatatgc cacaaaaaaaa aaaaaaaaaa a | 1733 |

<210> 46

<211> 1871

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 195..1052

<220>

<221> sig_peptide

<222> 195..338

<223> Von Heijne matrix

score 3.50178852790004

seq LGVFFVCHQLSSS/LN

<400> 46

| | | | | | | |
|---|--|-------------|------------|------------|------------|-----|
| agtgactgcc | gggagtcctg | cagggggcggg | gcggcgccaa | gcgcagggag | cccggctgag | 60 |
| tggcagccca | gattgaagat | ggatacgtga | caatcccagg | gaccgctgca | ctgacttcat | 120 |
| ttccttagac | aagacacagt | gtagggcccg | gcccgtgttg | gccccaggac | tcctttggaa | 180 |
| tatagctgtg | gaca atg aat cct gcg agc gat ggg ggc aca tca gag agc | 230 | | | | |
| | Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser | | | | | |
| | -45 | -40 | | | | |
| att ttt gac ctg gac tat gca tcc tgg ggg atc cgc tcc acg ctg atg | 278 | | | | | |
| Ile Phe Asp Leu Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met | | | | | | |
| -35 | -30 | -25 | | | | |
| gtc gct ggc ttt gtc ttc tac ttg ggc gtc ttt gtg gtc tgc cac cag | 326 | | | | | |
| Val Ala Gly Phe Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln | | | | | | |
| -20 | -15 | -10 | -5 | | | |
| ctg tcc tct tcc ctg aat gcc act tac cgt tct ttg gtg gcc aga gag | 374 | | | | | |
| Leu Ser Ser Ser Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu | | | | | | |
| | 1 | 5 | 10 | | | |
| aag gtc ttc tgg gac ctg gcg gcc acg cgt gca gtc ttt ggt gtt cag | 422 | | | | | |
| Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln | | | | | | |
| | 15 | 20 | 25 | | | |
| agc aca gcc gca ggc ctg tgg gct ctg ctg ggg gac cct gtg ctg cat | 470 | | | | | |
| Ser Thr Ala Ala Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His | | | | | | |
| | 30 | 35 | 40 | | | |
| gcc gac aag gcg cgt ggc cag cag aac tgg tgc ttt cac atc acg | 518 | | | | | |
| Ala Asp Lys Ala Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr | | | | | | |
| | 45 | 50 | 55 | 60 | | |
| aca gca acg gga ttc ttt tgc ttt gaa aat gtt gca gtc cac ctg tcc | 566 | | | | | |
| Thr Ala Thr Gly Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser | | | | | | |
| | 65 | 70 | 75 | | | |
| aac ttg atc ttc cgg aca ttt gac ttg ttt ctg gtt atc cac cat ctc | 614 | | | | | |
| Asn Leu Ile Phe Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu | | | | | | |
| | 80 | 85 | 90 | | | |
| ttt gcc ttt ctt ggg ttt ctt ggc tgc ttg gtc aat ctc caa gct ggc | 662 | | | | | |
| Phe Ala Phe Leu Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly | | | | | | |
| | 95 | 100 | 105 | | | |
| cac tat cta gct atg acc acg ttg ctc ctg gag atg agc acg ccc ttt | 710 | | | | | |
| His Tyr Leu Ala Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe | | | | | | |
| | 110 | 115 | 120 | | | |
| acc tgc gtt tcc tgg atg ctc tta aag gcg ggc tgg tcc gag tct ctg | 758 | | | | | |
| Thr Cys Val Ser Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu | | | | | | |
| | 125 | 130 | 135 | 140 | | |
| ttt tgg aag ctc aac cag tgg ctg atg att cac atg ttt cac tgc cgc | 806 | | | | | |
| Phe Trp Lys Leu Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg | | | | | | |
| | 145 | 150 | 155 | | | |
| atg gtt cta acc tac cac atg tgg tgg gtg tgt ttc tgg cac tgg gac | 854 | | | | | |
| Met Val Leu Thr Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp | | | | | | |
| | 160 | 165 | 170 | | | |
| ggc ctg gtc agc agc ctg tat ctg cct cat ttg aca ctg ttc ctt gtc | 902 | | | | | |
| Gly Leu Val Ser Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val | | | | | | |
| | 175 | 180 | 185 | | | |
| gga ctg gct ctg ctt acg cta atc att aat cca tat tgg acc cat aag | 950 | | | | | |
| Gly Leu Ala Leu Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys | | | | | | |
| | 190 | 195 | 200 | | | |
| aag act cag cag ctt ctc aat ccg gtg gac tgg aac ttc gca cag cca | 998 | | | | | |

Lys Thr Gln Gln Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro
 205 210 215 220
 gaa gcc aag agc agg cca gaa ggc aac ggg cag ctg ctg cgg aag aag 1046
 Glu Ala Lys Ser Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys
 225 230 235
 agg cca tagctgctcc agccggggct ccggggcgcc agcagagctg gcacaccgat 1102
 Arg Pro
 tctgggaagc cccgcgaatg atggcttttg aattaatgag gcagtgaatg ttttgtgttt 1162
 acttctaagg gaaatactaa ctttctttcg cattagtatt aattttgaag tagctacaaa 1222
 gtatttttaa gaaattataa ttttatgact gtctggcagg ctctgtcagt ttagccgcgc 1282
 cggaccgtgt caagcatcta ggagaggagt ccatgggtgc caggcatcgg ggcgtcacac 1342
 ctgttgagga gtgggggtggc tttgaatgct ggaaatggct tcatagtga gtgcctccca 1402
 cagggcggtt gggtcagcgt tgactctttc cagctgcaca ctcatatgcc gtgtgtctta 1462
 ttcagaagtc acattctttt cagttggaga gaattgggct aagatagaaa ataacatgat 1522
 ttgttcctta ttaaagtttc ccagcgtatg aaattctaag ctgggtgggg tggctcacac 1582
 ccgacgtaat cccagcacgt tgggaggccg aggcagggtg atcacttgag gccaggagtt 1642
 cgagaccagc ctgggtcaaga tgggtgaaacc ccatctctac taaaattaca aaaattagcc 1702
 ggggtgtcgtg gcacacacct gtaatcccag ctatttggga ggccaaggca ggagaattgc 1762
 ctgaacccgg gaggcggagg ttgcagttag ctgagatcgc accactgcac tccagcactc 1822
 cagcctgggt gacggagcaa cactctctcg caaaaaaaaa aaaaaaaaaa 1871

 <210> 47
 <211> 1523
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 217..1410

 <220>
 <221> sig_peptide
 <222> 217..279
 <223> Von Heijne matrix
 score 5.8172934575094
 seq ALLWAEVGVLA/GR

 <400> 47
 acttccccgg gagccggaag tcccgtctca cggttgccct ggcagcgccg gaggctggtg 60
 agtcggcagc cctgtggcag ccggcgggct ggtttccatg gttgcacgat taggaaccac 120
 cagctgctgc atcccatggc caggggtggc gtccagggtg cagagcagct aggaacgcaa 180
 ggctgaacc tggggccaga caccctctc ccggcc atg gtc aac gac cct cca 234
 Met Val Asn Asp Pro Pro
 -20
 gta cct gcc tta ctg tgg gcc cag gag gtg ggc caa gtc ttg gca ggc 282
 Val Pro Ala Leu Leu Trp Ala Gln Glu Val Gly Gln Val Leu Ala Gly
 -15 -10 -5 1
 cgt gcc cgc agg ctg ctg ctg cag ttt ggg gtg ctc ttc tgc acc atc 330
 Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly Val Leu Phe Cys Thr Ile
 5 10 15
 ctc ctt ttg ctc tgg gtg tct gtc ttc ctc tat ggc tcc ttc tac tat 378
 Leu Leu Leu Leu Trp Val Ser Val Phe Leu Tyr Gly Ser Phe Tyr Tyr
 20 25 30
 tcc tat atg ccg aca gtc agc cac ctc agc cct gtg cat ttc tac tac 426
 Ser Tyr Met Pro Thr Val Ser His Leu Ser Pro Val His Phe Tyr Tyr
 35 40 45
 agg acc gac tgt gat tcc tcc acc acc tca ctc tgc tcc ttc cct gtt 474
 Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser Leu Cys Ser Phe Pro Val

| | | | | | | | | |
|---|---|-----|---|----|-----------------------------|----|---------|-----|
| 50 | gcc aat gtc tcg ctg act aag ggt gga cgt gat cgg gtg ctg atg tat | 55 | aag ggt gga cgt gat cgg gtg ctg atg tat | 60 | cgt gat cgg gtg ctg atg tat | 65 | atg tat | 522 |
| Ala Asn Val Ser Leu Thr Lys Gly Gly Arg Asp Arg Val Leu Met Tyr | | | | | | | | |
| | 70 | 75 | 80 | | | | | |
| gga cag ccg tat cgt gtt acc tta gag ctt gag ctg cca gag tcc cct | 570 | | | | | | | |
| Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu Glu Leu Pro Glu Ser Pro | | | | | | | | |
| | 85 | 90 | 95 | | | | | |
| gtg aat caa gat ttg ggc atg ttc ttg gtc acc att tcc tgc tac acc | 618 | | | | | | | |
| Val Asn Gln Asp Leu Gly Met Phe Leu Val Thr Ile Ser Cys Tyr Thr | | | | | | | | |
| | 100 | 105 | 110 | | | | | |
| aga ggt ggc cga atc atc tcc act tct tcg cgt tcg gtg atg ctg cat | 666 | | | | | | | |
| Arg Gly Arg Ile Ile Ser Thr Ser Ser Arg Ser Val Met Leu His | | | | | | | | |
| | 115 | 120 | 125 | | | | | |
| tac cgc tca gac ctg ctc cag atg ctg gac aca ctg gtc ttc tct agc | 714 | | | | | | | |
| Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp Thr Leu Val Phe Ser Ser | | | | | | | | |
| | 130 | 135 | 140 | | | | | |
| ctc ctg cta ttt ggc ttt gca gag cag aag cag ctg ctg gag gtg gaa | 762 | | | | | | | |
| Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys Gln Leu Leu Glu Val Glu | | | | | | | | |
| | 150 | 155 | 160 | | | | | |
| ctc tac gca gac tat aga gag aac tcg tac gtg ccg acc act gga gcg | 810 | | | | | | | |
| Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr Val Pro Thr Thr Gly Ala | | | | | | | | |
| | 165 | 170 | 175 | | | | | |
| atc att gag atc cac agc aag cgc atc cag ctg tat gga gcc tac ctc | 858 | | | | | | | |
| Ile Ile Glu Ile His Ser Lys Arg Ile Gln Leu Tyr Gly Ala Tyr Leu | | | | | | | | |
| | 180 | 185 | 190 | | | | | |
| cgc atc cac gcg cac ttc act ggg ctc aga tac ctg cta tac aac ttc | 906 | | | | | | | |
| Arg Ile His Ala His Phe Thr Gly Leu Arg Tyr Leu Leu Tyr Asn Phe | | | | | | | | |
| | 195 | 200 | 205 | | | | | |
| ccg atg acc tgc gcc ttc ata ggt gtt gcc agc aac ttc acc ttc ctc | 954 | | | | | | | |
| Pro Met Thr Cys Ala Phe Ile Gly Val Ala Ser Asn Phe Thr Phe Leu | | | | | | | | |
| | 210 | 215 | 220 | | | | | |
| agc gtc atc gtg ctc ttc agc tac atg cag tgg gtg tgg ggg ggc atc | 1002 | | | | | | | |
| Ser Val Ile Val Leu Phe Ser Tyr Met Gln Trp Val Trp Gly Gly Ile | | | | | | | | |
| | 230 | 235 | 240 | | | | | |
| tgg ccc cga cac cgc ttc tct ttg cag gtt aac atc cga aaa aga gac | 1050 | | | | | | | |
| Trp Pro Arg His Arg Phe Ser Leu Gln Val Asn Ile Arg Lys Arg Asp | | | | | | | | |
| | 245 | 250 | 255 | | | | | |
| aat tcc cgg aag gaa gtc caa cga agg atc tct gct cat cag cca ggg | 1098 | | | | | | | |
| Asn Ser Arg Lys Glu Val Gln Arg Arg Ile Ser Ala His Gln Pro Gly | | | | | | | | |
| | 260 | 265 | 270 | | | | | |
| cct gaa ggc cag gag gag tca act ccg caa tca gat gtt aca gag gat | 1146 | | | | | | | |
| Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp | | | | | | | | |
| | 275 | 280 | 285 | | | | | |
| ggt gag agc cct gaa gat ccc tca ggg aca gag ggt cag ctg tcc gag | 1194 | | | | | | | |
| Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu | | | | | | | | |
| | 290 | 295 | 300 | | | | | |
| gag gag aaa cca gat cag cag ccc ctg agc gga gag gag cta gag | 1242 | | | | | | | |
| Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu | | | | | | | | |
| | 310 | 315 | 320 | | | | | |
| cct gag gcc agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg | 1290 | | | | | | | |
| Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu | | | | | | | | |
| | 325 | 330 | 335 | | | | | |
| acg gag gcc aac ctg cct gct cct gct cct gct tct gct tct gcc cct | 1338 | | | | | | | |
| Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro | | | | | | | | |
| | 340 | 345 | 350 | | | | | |
| gtc cta gag act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga | 1386 | | | | | | | |
| Val Leu Glu Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg | | | | | | | | |
| | 355 | 360 | 365 | | | | | |

```

cag cgc ccc acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc 1440
Gln Arg Pro Thr Cys Ser Ser Ser
370
agcactttcc cacctgactc ctctcccctc gtttttcctt caataaacta ttttgtgtca 1500
gcttcgaaaa aaaaaaaaaa aaa 1523

```

```

<210> 48
<211> 832
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 103..492

```

```

<220>
<221> sig_peptide
<222> 103..162
<223> Von Heijne matrix
      score 8.21832452871462
      seq LFFCYLLLLFTCSG/VE

```

```

<400> 48
gtttactcgc tgctgtgccc atctatcagc aggctccggg ctgaagattg cttctcttct 60
ctcctccaag gtctagtac ggagcccgcg cgcggcgcca cc atg cgg cag aag 114
                               Met Arg Gln Lys
                               -20
gcg gta tcg ctt ttc ttc tgc tac ctg ctg ctc ttc act tgc agt ggg 162
Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly
      -15                               -10                               -5
gtg gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc 210
Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser
1      5      10      15
ggg ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca 258
Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala
      20      25      30
gtc gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc 306
Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala
      35      40      45
aac tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg 354
Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly
      50      55      60
ggc ggc gtg ccc gcc ggg ggg cta gtg gcc acg ctg cag agc ctc ggg 402
Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly
      65      70      75      80
gct ggt ggc agc agc gtc gtc ata ggt aat att ggt gcc ctg atg ggc 450
Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly
      85      90      95
tac gcc acc cac aag tat ctc gat agt gag gag gat gag gag 492
Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
      100      105      110
tagccagcag ctcccagaac ctcttcttcc ttcttggcct aactcttcca gttaggatct 552
agaactttgc cttttttttt tttttttttt tttttttgag atgggttctc actatattgt 612
ccaggctaga gtgcagtggc tattcacaga tgcgaacata gtacactgca gcctccaact 672
cctagcctca agtgatcctc ctgtctcaac ctcccgaagta ggattacaag catgcgccga 732
cgatgccag aatccagaac tttgtctatc actctcccca acaacctaga tgtgaaaaca 792
gaataaactt caccagaaaa gcaaaaaaaaa aaaaaaaaaa 832

```

<210> 49
 <211> 831
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 234..491

<220>
 <221> sig_peptide
 <222> 234..293
 <223> Von Heijne matrix
 score 4.85037394589162
 seq AVAGLPALGFTGA/GI

<400> 49
 gtttactcgc tgctgtgccc atctatcagc aggctccggg ctgaagattg cttctcttct 60
 ctctccaag gtctagtac ggagcccgcg cgcggcgcca ccatgcggca gaaggcggta 120
 tcgcttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180
 agtgctcgga gagctcggac agcgggtccg ggttctggaa ggccctgacc ttc atg 236
 Met
 -20
 gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284
 Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe
 -15 -10 -5
 acc ggc gcc ggc atc gcg gcc aac tcg gtg gct gcc tcg ctg atg agc 332
 Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser
 1 5 10
 tgg tct gcg atc ctg aat ggg ggc gcc gtg ccc gcc ggg ggg cta gtg 380
 Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val
 15 20 25
 gcc acg ctg cag agc ctc ggg gct ggt gcc agc agc gtc gtc ata ggt 428
 Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly
 30 35 40 45
 aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476
 Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser
 50 55 60
 gag gag gat gag gag tagccagcag ctccagaac ctcttcttcc ttcttggcct 531
 Glu Glu Asp Glu Glu
 65
 aactcttcca gttaggatct agaactttgc cttttttttt tttttttttt tttttttgag 591
 atgggttctc actatattgt ccaggctaga gtgcagtggc tattcacaga tgcgaacata 651
 gtacactgca gcctccaact cctagcctca agtgatcctc ctgtctcaac ctcccaagta 711
 ggattacaag catgcgccga cgatgcccag aatccagaac tttgtctatc actctcccca 771
 acaacctaga tgtgaaaaca gaataaactt caccagaaa gcaaaaaaaaa aaaaaaaaaa 831

<210> 50
 <211> 917
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 180..800

<220>
 <221> sig_peptide

<222> 180..248

<223> Von Heijne matrix

score 14.6828672385356

seq ILLLLWLIAPSRA/CT

<400> 50

```
acccttggt tctgcactga tgggtgggtgg atgagtaatg catccaggaa gcctggaggg 60
ctgtgggtttc cgcacccgct gccacccccg cccctagcgt ggacatttat cctctagcgc 120
tcaggccctg ccgccatcgc cgcagatcca gcgcccagag agacaccaga gaaccacc 179
atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg 227
Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
-20 -15 -10
ctg ata gcc ccc agc agg gcc tgc acc tgt gtc cca ccc cac cca cag 275
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
-5 1 5
acg gcc ttc tgc aat tcc gac ctc gtc atc agg gcc aag ttc gtg ggg 323
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10 15 20 25
aca cca gaa gtc aac cag acc acc tta tac cag cgt tat gag atc aag 371
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
30 35 40
atg acc aag atg tat aaa ggg ttc caa gcc tta ggg gat gcc gct gac 419
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
45 50 55
atc cgg ttc gtc tac acc ccc gcc atg gag agt gtc tgc gga tac ttc 467
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
60 65 70
cac agg tcc cac aac cgc agc gag gag ttt ctc att gct gga aaa ctg 515
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
75 80 85
cag gat gga ctc ttg cac atc act acc tgc agt ttt gtg gct ccc tgg 563
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90 95 100 105
aac agc ctg agc tta gct cag cgc cgg ggc ttc acc aag acc tac act 611
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
110 115 120
gtt ggc tgt gag gaa tgc aca gtg ttt ccc tgt tta tcc ttc ccc tgc 659
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
125 130 135
aaa ctg cag agt ggc act cat tgc ttg tgg acg gac cag ctc ctc caa 707
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
140 145 150
ggc tct gaa aag ggc ttc cag tcc cgt cac ctt gcc tgc ctg cct cgg 755
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
155 160 165
gag cca ggg ctg tgc acc tgg cag tcc ctg cgg tcc cag ata gcc 800
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170 175 180
tgaatcctgc ccggagtggga agctgaagcc tgcacagtgt ccaccctgtt cccactccca 860
tctttcttcc ggacaatgaa ataaagagtt accaccagc aaaaaaaaaa aaaaaaa 917
```

<210> 51

<211> 621

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 140..472

<220>

<221> sig_peptide

<222> 140..211

<223> Von Heijne matrix

score 8.44884907465122

seq FVVFSFLFLICAMA/GD

<400> 51

```
atatttttttt catatctgac atttctatgt cctatgacgg tttcacagct atcctacttt      60
ggagaagatg ctggaaattc agagtttccg ccagagaata tatgcctgaa ctaaaagagg      120
aagtgggtcta taggagaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca      172
                               Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser
                               -20                               -15

ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta      220
Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val
                               -10                               -5                               1

gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg      268
Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala
                               5                               10                               15

ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa      316
Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys
20                               25                               30                               35

tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg      364
Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp
                               40                               45                               50

att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc      412
Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala
                               55                               60                               65

ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg      460
Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val
70                               75                               80

aga ttt aac att tagaggtgac agcatccccc aactggcag ttaatttttt      512
Arg Phe Asn Ile
85

gtctacaaac ttggcaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat      572
acaaatatta gttgaatgaa ttgttgaatt aaaaaaaaaa aaaaaaaaaa      621
```

<210> 52

<211> 673

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..484

<220>

<221> sig_peptide

<222> 68..112

<223> Von Heijne matrix

score 4.93618539864455

seq AVVFVFSLLDCCA/LI

<400> 52

```
ctatcagggg tgggtcgggg catccgagcg gggttgacgg aaggagcggc ggcgacggag      60
gaggagg atg gag gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc      109
```


| | | | | | | | | | | | | | | | | |
|-------------|-------------|------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|------------|-----|-----|-----|
| | Met | Glu | Ala | Val | Val | Phe | Val | Phe | Ser | Leu | Leu | Asp | Cys | Cys | | |
| | -15 | | | | | -10 | | | | -5 | | | | | | |
| gcg | ctc | atc | ttc | ctc | tcg | gtc | tac | ttc | ata | att | aca | ttg | tct | gat | tta | 157 |
| Ala | Leu | Ile | Phe | Leu | Ser | Val | Tyr | Phe | Ile | Ile | Thr | Leu | Ser | Asp | Leu | |
| | 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| gaa | tgt | gat | tac | att | aat | gct | aga | tca | tgt | tgc | tca | aaa | tta | aac | aag | 205 |
| Glu | Cys | Asp | Tyr | Ile | Asn | Ala | Arg | Ser | Cys | Cys | Ser | Lys | Leu | Asn | Lys | |
| | | | 20 | | | | | | 25 | | | | 30 | | | |
| tgg | gta | att | cca | gaa | ttg | att | ggc | cat | acc | att | gtc | act | gta | tta | ctg | 253 |
| Trp | Val | Ile | Pro | Glu | Leu | Ile | Gly | His | Thr | Ile | Val | Thr | Val | Leu | Leu | |
| | | | 35 | | | | | 40 | | | | 45 | | | | |
| ctc | atg | tca | ttg | cac | tgg | ttc | atc | ttc | ctt | ctc | aac | tta | cct | gtt | gcc | 301 |
| Leu | Met | Ser | Leu | His | Trp | Phe | Ile | Phe | Leu | Leu | Asn | Leu | Pro | Val | Ala | |
| | | | 50 | | | 55 | | | | | 60 | | | | | |
| act | tgg | aat | ata | tat | cga | tac | att | atg | gtg | ccg | agt | ggt | aac | atg | gga | 349 |
| Thr | Trp | Asn | Ile | Tyr | Arg | Tyr | Ile | Met | Val | Pro | Ser | Gly | Asn | Met | Gly | |
| | 65 | | | | 70 | | | | | 75 | | | | | | |
| gtg | ttt | gat | cca | aca | gaa | ata | cac | aat | cga | ggg | cag | ctg | aag | tca | cac | 397 |
| Val | Phe | Asp | Pro | Thr | Glu | Ile | His | Asn | Arg | Gly | Gln | Leu | Lys | Ser | His | |
| | 80 | | | | 85 | | | | 90 | | | | | 95 | | |
| atg | aaa | gaa | gcc | atg | atc | aag | ctt | ggt | ttc | cac | ttg | ctc | tgc | ttc | ttc | 445 |
| Met | Lys | Glu | Ala | Met | Ile | Lys | Leu | Gly | Phe | His | Leu | Leu | Cys | Phe | Phe | |
| | | | 100 | | | | | 105 | | | 110 | | | | | |
| atg | tat | ctt | tat | agt | atg | atc | tta | gct | ttg | ata | aat | gac | tgaagctgga | | | 494 |
| Met | Tyr | Leu | Tyr | Ser | Met | Ile | Leu | Ala | Leu | Ile | Asn | Asp | | | | |
| | | | 115 | | | | 120 | | | | | | | | | |
| gaagccggtgg | ttgaagtcag | cctacactac | agtgccacagt | tgaggagcca | gagacttctt | | | | | | | | | | | 554 |
| aaatcatcct | tagaacctg | accatagcag | tatatatttt | cctcttgga | caaaaaacta | | | | | | | | | | | 614 |
| tttttgctgt | attttttacca | tataaagtat | ttaaaaaaca | cgaaaaaaaa | aaaaaaaaaa | | | | | | | | | | | 673 |

<210> 53
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..517

<220>
 <221> sig_peptide
 <222> 38..118
 <223> Von Heijne matrix
 score 7.20400999800742
 seq VLWLSGLSEPGAA/RQ

| | |
|--|-------------------------|
| <400> 53 | |
| agattgggac agtcgccagg gatggctgag cgtgaag atg cag cgg gtg tcc ggg | 55 |
| | Met Gln Arg Val Ser Gly |
| | -25 |
| ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc ggc ctc tct | 103 |
| Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu Ser | |
| | -20 -15 -10 |
| gag ccg gga gct gcc cgg cag ccc cgg atc atg gaa gag aaa gcg cta | 151 |
| Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu Lys Ala Leu | |
| | -5 1 5 10 |
| gag gtt tat gat ttg att aga act atc cgg gac cca gaa aag ccc aat | 199 |
| Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro Asn | |

| | | | | | | | |
|---|-----|--|-----|--|-----|--|-----|
| | 15 | | 20 | | 25 | | |
| act tta gaa gaa ctg gaa gtg gtc tgc gaa agt tgt gtg gaa gtt cag | | | | | | | 247 |
| Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val Gln | | | | | | | |
| | 30 | | 35 | | 40 | | |
| gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca | | | | | | | 295 |
| Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr | | | | | | | |
| | 45 | | 50 | | 55 | | |
| gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta | | | | | | | 343 |
| Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val | | | | | | | |
| | 60 | | 65 | | 70 | | 75 |
| aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att | | | | | | | 391 |
| Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile | | | | | | | |
| | 80 | | 85 | | 90 | | |
| tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat | | | | | | | 439 |
| Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn | | | | | | | |
| | 95 | | 100 | | 105 | | |
| gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa | | | | | | | 487 |
| Asp Lys Glu Arg Val Ala Ala Ala Met Glu Asn Pro Asn Leu Arg Glu | | | | | | | |
| | 110 | | 115 | | 120 | | |
| att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt ttttaagagcc | | | | | | | 537 |
| Ile Val Glu Gln Cys Val Leu Glu Pro Asp | | | | | | | |
| | 125 | | 130 | | | | |
| actggcctgt aattgtttgta tatattttgta actcttttga taatgtcaga gactcatggt | | | | | | | 597 |
| taatacatag gtgattttgta cctcagagca ttttttaaag gattctttcc aagcgagatt | | | | | | | 657 |
| taattataag gtagtaccta atttgttcaa tgtataacat tctcaggatt tgtaacactt | | | | | | | 717 |
| aaatgatcag acagaataat attttctagt tattatgtgt aagatgagtt gctatttttc | | | | | | | 777 |
| tgatgctcat tctgatacaa ctatttttctg tgtcaaatat ctactgtgcc caaatgtact | | | | | | | 837 |
| caatttaaat cattactctg taaaataaat aagcagatga ttctttataaa aaaaaaaaaa | | | | | | | 897 |

<210> 54
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..634

<220>
 <221> sig_peptide
 <222> 92..139
 <223> Von Heijne matrix
 score 7.36306712986597
 seq FLLLTCLFITGTS/VS

| | |
|--|-----|
| <400> 54 | |
| cttaaaaaaaaa aaagtgcttg aaagagaagg ggacaaaagga acaccagtat taagaggatt | 60 |
| ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc | 112 |
| Met Pro Pro Phe Leu Leu Leu | |
| -15 -10 | |
| acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat | 160 |
| Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp | |
| -5 1 5 | |
| cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac | 208 |
| Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp | |
| 10 15 20 | |
| cac cag ttg gat gag tct caa ggt cct cct cta tgt gac aac cat gtg | 256 |
| His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys Asp Asn His Val | |

| | | | |
|---|-----|-----|------|
| 25 | 30 | 35 | |
| aat ggg gag tgg tac cac ttc acg ggc atg gcg gga gat gcc atg cct | | | 304 |
| Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly Asp Ala Met Pro | | | |
| 40 | 45 | 50 | 55 |
| acc ttc tgc ata cca gaa aac cac tgt gga acc cac gca cct gtc tgg | | | 352 |
| Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His Ala Pro Val Trp | | | |
| 60 | 65 | 70 | |
| ctc aat ggc agc cac ccc cta gaa ggc gac ggc att gtg caa cgc cag | | | 400 |
| Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile Val Gln Arg Gln | | | |
| 75 | 80 | 85 | |
| gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg aac acc acg gtg | | | 448 |
| Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp Asn Thr Thr Val | | | |
| 90 | 95 | 100 | |
| gaa gtc aag gct tgc cct gga ggc tac tat gtg tat cgt ctg acc aag | | | 496 |
| Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr Arg Leu Thr Lys | | | |
| 105 | 110 | 115 | |
| ccc agc gtc tgc ttc cac gtc tac tgt ggt cgt gag tac ctt ccc tgt | | | 544 |
| Pro Ser Val Cys Phe His Val Tyr Cys Gly Arg Glu Tyr Leu Pro Cys | | | |
| 120 | 125 | 130 | 135 |
| gct ctt ttt ctc cac caa caa ggc cac agg tgg agt cca aaa gtg ccc | | | 592 |
| Ala Leu Phe Leu His Gln Gln Gly His Arg Trp Ser Pro Lys Val Pro | | | |
| 140 | 145 | 150 | |
| aat tat agg ata tgc agt tac agt ggc aac tat atc tca atc | | | 634 |
| Asn Tyr Arg Ile Cys Ser Tyr Ser Gly Asn Tyr Ile Ser Ile | | | |
| 155 | 160 | 165 | |
| tgaacaacat tgatgtgggg ctaaagatac tctgatttct gagatctctt cttagaactt | | | 694 |
| ctgaaaaatt cctgaagaaa tagaagggga aaggagctat gactttgatc agttcttttt | | | 754 |
| aattttgtct gaattccatt caaacaaaac attagaaaat gaaacattgg gccaggcgca | | | 814 |
| gtggctcatg cctgtaatcc cagcactttg ggaggctgag gcgggtggat cacaagatca | | | 874 |
| ggagtttaag accagcctgg ccaatatggt gaaaccctgt ctctactaga aatacaaaaa | | | 934 |
| ttagacaggc gtggtggcag gcaactgtaa cccagctac ccgggaggct gaggcaggag | | | 994 |
| aattgcttga acccgggagg tggacgttgc ggtcaggcga aaatcgtgcc attgcactcc | | | 1054 |
| agcctgggtg acagagttag actctgattc aaaaaaaaaa aaaaaaaa | | | 1101 |

<210> 55
 <211> 1047
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..767

<220>
 <221> sig_peptide
 <222> 27..80
 <223> Von Heijne matrix
 score 8.96664802487992
 seq LFCLAVLAASSFS/KA

| | |
|--|-----|
| <400> 55 | |
| agcagaggcc ctacacccac cgaggc atg ggg ctc cct ggg ctg ttc tgc ttg | 53 |
| Met Gly Leu Pro Gly Leu Phe Cys Leu | |
| -15 | -10 |
| gcc gtg ctg gct gcc agc agc ttc tcc aag gca cgg gag gaa gaa att | 101 |
| Ala Val Leu Ala Ala Ser Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile | |
| -5 | 1 |
| acc cct gtg gtc tcc att gcc tac aaa gtc ctg gaa gtt ttc ccc aaa | 149 |

| | | | | | | | | | | | | | | | | |
|-------------|------------|-------------|-------------|-------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Thr | Pro | Val | Val | Ser | Ile | Ala | Tyr | Lys | Val | Leu | Glu | Val | Phe | Pro | Lys | |
| | 10 | | | | | | 15 | | | | | 20 | | | | |
| ggc | cgc | tgg | gtg | ctc | ata | acc | tgc | tgt | gca | ccc | cag | cca | cca | ccg | ccc | 197 |
| Gly | Arg | Trp | Val | Leu | Ile | Thr | Cys | Cys | Ala | Pro | Gln | Pro | Pro | Pro | Pro | |
| | 25 | | | | | | 30 | | | | 35 | | | | | |
| atc | acc | tat | tcc | ctc | tgt | gga | acc | aag | aac | atc | aag | gtg | gcc | aag | aag | 245 |
| Ile | Thr | Tyr | Ser | Leu | Cys | Gly | Thr | Lys | Asn | Ile | Lys | Val | Ala | Lys | Lys | |
| | 40 | | | | 45 | | | | | 50 | | | | | 55 | |
| gtg | gtg | aag | acc | cac | gag | ccg | gcc | tcc | ttc | aac | ctc | aac | gtc | aca | ctc | 293 |
| Val | Val | Lys | Thr | His | Glu | Pro | Ala | Ser | Phe | Asn | Leu | Asn | Val | Thr | Leu | |
| | | | | 60 | | | | | 65 | | | | | 70 | | |
| aag | tcc | agt | cca | gac | ctg | ctc | acc | tac | ttc | tgc | cgg | gcg | tcc | tcc | acc | 341 |
| Lys | Ser | Ser | Pro | Asp | Leu | Leu | Thr | Tyr | Phe | Cys | Arg | Ala | Ser | Ser | Thr | |
| | | | 75 | | | | | 80 | | | | | | 85 | | |
| tca | ggg | gcc | cat | gtg | gac | agt | gcc | agg | cta | cag | atg | cac | tgg | gag | ctg | 389 |
| Ser | Gly | Ala | His | Val | Asp | Ser | Ala | Arg | Leu | Gln | Met | His | Trp | Glu | Leu | |
| | 90 | | | | | | 95 | | | | | 100 | | | | |
| tgg | tcc | aag | cca | gtg | tct | gag | ctg | cgg | gcc | aac | ttc | act | ctg | cag | gac | 437 |
| Trp | Ser | Lys | Pro | Val | Ser | Glu | Leu | Arg | Ala | Asn | Phe | Thr | Leu | Gln | Asp | |
| | 105 | | | | | 110 | | | | | 115 | | | | | |
| aga | ggg | gca | ggc | ccc | agg | gtg | gag | atg | atc | tgc | cag | gcg | tcc | tcg | ggc | 485 |
| Arg | Gly | Ala | Gly | Pro | Arg | Val | Glu | Met | Ile | Cys | Gln | Ala | Ser | Ser | Gly | |
| | 120 | | | | 125 | | | | | 130 | | | | | 135 | |
| agc | cca | cct | atc | acc | aac | agc | ctg | atc | ggg | aag | gat | ggg | cag | gtc | cac | 533 |
| Ser | Pro | Pro | Ile | Thr | Asn | Ser | Leu | Ile | Gly | Lys | Asp | Gly | Gln | Val | His | |
| | | | | 140 | | | | | 145 | | | | | 150 | | |
| ctg | cag | cag | aga | cca | tgc | cac | agg | cag | cct | gcc | aac | ttc | tcc | ttc | ctg | 581 |
| Leu | Gln | Gln | Arg | Pro | Cys | His | Arg | Gln | Pro | Ala | Asn | Phe | Ser | Phe | Leu | |
| | | | 155 | | | | | 160 | | | | 165 | | | | |
| ccg | agc | cag | aca | tcg | gac | tgg | ttc | tgg | tgc | cag | gct | gca | aac | aac | gcc | 629 |
| Pro | Ser | Gln | Thr | Ser | Asp | Trp | Phe | Trp | Cys | Gln | Ala | Ala | Asn | Asn | Ala | |
| | | 170 | | | | | 175 | | | | | 180 | | | | |
| aat | gtc | cag | cac | agc | gcc | ctc | aca | gtg | gtg | ccc | cca | gga | ggg | ttg | ccc | 677 |
| Asn | Val | Gln | His | Ser | Ala | Leu | Thr | Val | Val | Pro | Pro | Gly | Gly | Leu | Pro | |
| | 185 | | | | | 190 | | | | 195 | | | | | | |
| agg | gca | ccc | acc | atc | gtg | ctg | gtt | ggc | agc | ctt | gcc | tcc | act | gcg | gcc | 725 |
| Arg | Ala | Pro | Thr | Ile | Val | Leu | Val | Gly | Ser | Leu | Ala | Ser | Thr | Ala | Ala | |
| | 200 | | | | 205 | | | | | 210 | | | | | 215 | |
| atc | acc | tcc | agg | atg | ctg | ggc | tgg | acc | acg | tgg | gcc | agg | tgg | | | 767 |
| Ile | Thr | Ser | Arg | Met | Leu | Gly | Trp | Thr | Thr | Trp | Ala | Arg | Trp | | | |
| | | | 220 | | | | | | | 225 | | | | | | |
| tgaccagaag | atggaggact | ggcagggtcc | cctggagagc | cccattccttg | ccttgccgct | | | | | | | | | | | 827 |
| ctacaggagc | accgcgcgtc | tgagtgaaga | ggagtttggg | gggttcagga | tagggaatgg | | | | | | | | | | | 887 |
| ggagggtcaga | ggacgcaaag | cagcagccat | gtagaatgaa | ccgtccagag | agccaagcac | | | | | | | | | | | 947 |
| ggcagaggac | tgcaggccat | cagcgtgcac | tgttcgtatt | tggagttcat | gcaaaatgag | | | | | | | | | | | 1007 |
| tgtgttttag | ctgctcttgc | cacaaaaaaaa | aaaaaaaaaaa | | | | | | | | | | | | | 1047 |

<210> 56
 <211> 925
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..399

<220>
 <221> sig_peptide

<222> 4..126
 <223> Von Heijne matrix
 score 4.34454795165846
 seq RVVSWLFSIVVFG/SI

<400> 56
 acg atg gaa ggg ggt gcg tac gga gcg ggc aaa gcc ggg ggc gcc ttc 48
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe
 -40 -35 -30
 gac ccc tac acc ctg gtc cgg cag ccg cac acc atc ctg cgc gtc gtg 96
 Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val
 -25 -20 -15
 tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc 144
 Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly
 -10 -5 1 5
 tac ctc aac agc gcc tcc gag ggg gag cag ttc tgc atc tac aac cgc 192
 Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg
 10 15 20
 aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc 240
 Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe
 25 30 35
 ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc 288
 Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile
 40 45 50
 agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc 336
 Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val
 55 60 65 70
 tcg ggt gag ccc cac cca gca ggt acc ccc tgc aca gag tct aca gag 384
 Ser Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu
 75 80 85
 ggc tgt ccc ggg cca taggaggcgg ctgccaccct tcttcccatg tttcagatga 439
 Gly Cys Pro Gly Pro
 90
 gggaaatgag ccttctgggc tttcctctgg ttctgtggat tctgctacct ggccaaccag 499
 tggcaggtct ccaagcccaa ggacaacca ctgaacgaag ggacggacgc agcccgggcc 559
 gccatgcct tctccttttt ctccatcttc acctggagcc tgaccgcagc cctggccgtg 619
 cggagattca aggacctaag cttccaggag gagtacagca cactgttccc tgcttcggca 679
 cagccgtagg cctccccggc ttgcagaggc cggcagccct gtatcacccc tggcagttag 739
 gtggcaggag cagcctagtg ccagaaatgt ccaagatgcc agggcatgca gggcagtgga 799
 aggtggctt gaggaaccaa ttcagggtct ccactgactc attcattcct tcaccgcctc 859
 cttcattgat tcttcattgag ttcattcatt cagtaaacad ttattgagta aaaaaaaaaa 919
 aaaaaa 925

<210> 57
 <211> 1240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 127..879

<220>
 <221> sig_peptide
 <222> 127..198
 <223> Von Heijne matrix
 score 5.38660866264012
 seq ALCSVCSMSVLRA/YP

```

<400> 57
agcttaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg      60
gccaggagag tcccgacagg agtgtcaggt ttcaatctca gcaccagcca ctcagagcag      120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
      -20      -15
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca      216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
-10      -5      1      5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca      264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
      10      15      20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
      25      30      35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
      40      45      50
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
      55      60      65      70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg      456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
      75      80      85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc      504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
      90      95      100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag      552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
      105      110      115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg      600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
      120      125      130
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca      648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
      135      140      145      150
cgg cgg cac acc cgg agc gcc gag gac gac tgc gag cgg gac ccc ctg      696
Arg Arg His Thr Ser Ala Glu Asp Ser Glu Arg Asp Pro Leu
      155      160      165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt      744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
      170      175      180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
      185      190      195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
      200      205      210
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgct      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
      215      220      225
ggaagggcac cctctttaac ccatccctca gcaaacgcag ctcttcccaa ggaccaggtc      949
ccttgacggt ccgaggatgg gaaaggtagc agggggcatgt atggaatttg ctgcttctct      1009
gggggtccctt ccacaggagg tctgtgaga accaaccttt gagggccaaag tcatgggggtt      1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa      1129
ctagaaattt ccccttcctg aaggtagaga gaaggggtct ctcccaacat atttctcttc      1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa a      1240

```

<210> 58
 <211> 902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..566

<220>
 <221> sig_peptide
 <222> 156..221
 <223> Von Heijne matrix
 score 5.67458379966095
 seq LVSMAGRVCLCQG/SA

<400> 58
 atttcccagc gtgcctcagg aagggcgcca ggactgcatt ttgctccgga gcgtccagag 60
 tcctggccct gagcggaat cgcagtggcc gaggtgagc ggcaggcgga tcgccccgac 120
 cctcactcct ggcgtctgag tctctggcgt agccc atg ctg agt ggg cgg ctg 173
 Met Leu Ser Gly Arg Leu
 -20
 gtc ctg ggt ctg gtc tcc atg gct ggc cgc gtt tgt ttg tgc cag ggc 221
 Val Leu Gly Leu Val Ser Met Ala Gly Arg Val Cys Leu Cys Gln Gly
 -15 -10 -5
 agc gcg gga tcc ggg gcc atc ggt ccg gtg gag gcc gcc att cgc acg 269
 Ser Ala Gly Ser Gly Ala Ile Gly Pro Val Glu Ala Ala Ile Arg Thr
 1 5 10 15
 aag ttg gag gag gcc ctg agc ccc gag gtg cta gag ctt cgc aac gag 317
 Lys Leu Glu Glu Ala Leu Ser Pro Glu Val Leu Glu Leu Arg Asn Glu
 20 25 30
 agc ggt ggc cac gcg gtc ccg cca ggc agt gag act cac ttc cgc gtg 365
 Ser Gly Gly His Ala Val Pro Pro Gly Ser Glu Thr His Phe Arg Val
 35 40 45
 gct gtg gtg agc tct cgt ttc gag gga ctg agc ccc cta caa cga cac 413
 Ala Val Val Ser Ser Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His
 50 55 60
 cgg ctg gtc cac gca gcg ctg gcc gag gag ctg gga ggt ccg gtc cat 461
 Arg Leu Val His Ala Ala Leu Ala Glu Glu Leu Gly Gly Pro Val His
 65 70 75 80
 gcg ctg gcc atc cag gca cgg acc ccc gcc cag tgg aga gag aac tct 509
 Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala Gln Trp Arg Glu Asn Ser
 85 90 95
 cag ctg gac act agc ccc cca tgc ctg ggt ggg aac aag aaa act cta 557
 Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly Gly Asn Lys Lys Thr Leu
 100 105 110
 gga acc ccc tgaaccccaa gagagggagg accaggatcc gaatgggctg 606
 Gly Thr Pro
 115
 ggtgagcacg aattaccgag gccttccctt tgatacagtc caggatttgt aagggatgaa 666
 gacccctggg cccattctg ttgggggtcca tacatactct ccgaagatag caacttgctt 726
 caggtcaaag tgaacccgag aaaagagaag aatcactcac tactgctctt gccctggact 786
 attcaggaag ggcagcccgg atgttccatg ttaaatacgtg acagaattgc accagacctg 846
 atgagttgga aacaatccta tacattaaaa gaaattacac taaaaaaaaa aaaaaa 902

<210> 59
 <211> 1969

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..1657

<220>
<221> sig_peptide
<222> 35..118
<223> Von Heijne matrix
score 3.75144398608723
seq SGLLLQVLFRLIT/FV

<400> 59
atttttcctg gtgtctgagc ctggcgcgga ggct atg ggc agc cag gag gtg ctg 55
Met Gly Ser Gln Glu Val Leu
-25
ggc cac gcg gcc cgg ctg gcc tcc tcc ggt ctc ctc ctg cag gtg ttg 103
Gly His Ala Ala Arg Leu Ala Ser Ser Gly Leu Leu Gln Val Leu
-20 -15 -10
ttt cgg ttg atc acc ttt gtc ttg aat gca ttt att ctt cgc ttc ctg 151
Phe Arg Leu Ile Thr Phe Val Leu Asn Ala Phe Ile Leu Arg Phe Leu
-5 1 5 10
tca aag gaa atc gtt ggc gta gta aat gta aga cta acg ctg ctt tac 199
Ser Lys Glu Ile Val Gly Val Val Asn Val Arg Leu Thr Leu Leu Tyr
15 20 25
tca acc acc ctc ttc ctg gcc aga gag gcc ttc cgc aga gca tgt ctc 247
Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala Phe Arg Arg Ala Cys Leu
30 35 40
agt ggg ggc acc cag cga gac tgg agc cag acc ctc aac ctg ctg tgg 295
Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln Thr Leu Asn Leu Leu Trp
45 50 55
cta aca gtc ccc ctg ggt gtg ttt tgg tcc tta ttc ctg ggc tgg atc 343
Leu Thr Val Pro Leu Gly Val Phe Trp Ser Leu Phe Leu Gly Trp Ile
60 65 70 75
tgg ttg cag ctg ctt gaa gtg cct gat cct aat gtt gtc cct cac tat 391
Trp Leu Gln Leu Leu Glu Val Pro Asp Pro Asn Val Val Pro His Tyr
80 85 90
gca act gga gtg gtg ctg ttt ggt ctc tcg gca gtg gtg gag ctt cta 439
Ala Thr Gly Val Val Leu Phe Gly Leu Ser Ala Val Val Glu Leu Leu
95 100 105
gga gag ccc ttt tgg gtc ttg gca caa gca cat atg ttt gtg aag ctc 487
Gly Glu Pro Phe Trp Val Leu Ala Gln Ala His Met Phe Val Lys Leu
110 115 120
aag gtg att gca gag agc ctg tcg gta att ctt aag agc gtt ctg aca 535
Lys Val Ile Ala Glu Ser Leu Ser Val Ile Leu Lys Ser Val Leu Thr
125 130 135
gct ttt ctc gtg ctg tgg ttg cct cac tgg gga ttg tac att ttc tct 583
Ala Phe Leu Val Leu Trp Leu Pro His Trp Gly Leu Tyr Ile Phe Ser
140 145 150 155
ttg gcc cag ctt ttc tat acc aca gtt ctg gtg ctc tgc tat gtt att 631
Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu Val Leu Cys Tyr Val Ile
160 165 170
tat ttc aca aag tta ctg ggt tcc cca gaa tca acc aag ctt caa act 679
Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu Ser Thr Lys Leu Gln Thr
175 180 185
ctt cct gtc tcc aga ata aca gat ctg tta ccc aat att aca aga aat 727

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Leu | Pro | Val | Ser | Arg | Ile | Thr | Asp | Leu | Leu | Pro | Asn | Ile | Thr | Arg | Asn | | |
| | | 190 | | | | | 195 | | | | | 200 | | | | | |
| gga | gcg | ttt | ata | aac | tgg | aaa | gag | gct | aaa | ctg | act | tgg | agt | ttt | ttc | 775 | |
| Gly | Ala | Phe | Ile | Asn | Trp | Lys | Glu | Ala | Lys | Leu | Thr | Trp | Ser | Phe | Phe | | |
| | | 205 | | | | | 210 | | | | 215 | | | | | | |
| aaa | cag | tct | ttc | ttg | aaa | cag | att | ttg | aca | gaa | ggc | gag | cga | tat | gtg | 823 | |
| Lys | Gln | Ser | Phe | Leu | Lys | Gln | Ile | Leu | Thr | Glu | Gly | Glu | Arg | Tyr | Val | | |
| 220 | | | | | 225 | | | | | 230 | | | | | 235 | | |
| atg | aca | ttt | ttg | aat | gta | ttg | aac | ttt | ggt | gat | cag | ggg | gtg | tat | gat | 871 | |
| Met | Thr | Phe | Leu | Asn | Val | Leu | Asn | Phe | Gly | Asp | Gln | Gly | Val | Tyr | Asp | | |
| | | | | 240 | | | | | 245 | | | | | 250 | | | |
| ata | gtg | aat | aat | ctt | ggc | tcc | ctt | gtg | gcc | aga | tta | att | ttc | cag | cca | 919 | |
| Ile | Val | Asn | Asn | Leu | Gly | Ser | Leu | Val | Ala | Arg | Leu | Ile | Phe | Gln | Pro | | |
| | | | | 255 | | | | 260 | | | | | 265 | | | | |
| ata | gag | gaa | agt | ttt | tat | ata | ttt | ttt | gct | aag | gtg | ctg | gag | agg | gga | 967 | |
| Ile | Glu | Glu | Ser | Phe | Tyr | Ile | Phe | Phe | Ala | Lys | Val | Leu | Glu | Arg | Gly | | |
| | | 270 | | | | | 275 | | | | | 280 | | | | | |
| aag | gat | gcc | aca | ctt | cag | aag | cag | gag | gac | gtt | gct | gtg | gct | gct | gca | 1015 | |
| Lys | Asp | Ala | Thr | Leu | Gln | Lys | Gln | Glu | Asp | Val | Ala | Val | Ala | Ala | Ala | | |
| | | 285 | | | | | 290 | | | | 295 | | | | | | |
| gtc | ttg | gag | tcc | ctg | ctc | aag | ctg | gcc | ctg | ctg | ggc | ctg | acc | atc | | 1063 | |
| Val | Leu | Glu | Ser | Leu | Leu | Lys | Leu | Ala | Leu | Leu | Ala | Gly | Leu | Thr | Ile | | |
| 300 | | | | | 305 | | | | | 310 | | | | | 315 | | |
| act | gtt | ttt | ggc | ttt | gcc | tat | tct | cag | ctg | gct | ctg | gat | atc | tac | gga | 1111 | |
| Thr | Val | Phe | Gly | Phe | Ala | Tyr | Ser | Gln | Leu | Ala | Leu | Asp | Ile | Tyr | Gly | | |
| | | | | 320 | | | | 325 | | | | | | 330 | | | |
| ggg | acc | atg | ctt | agc | tca | gga | tcc | ggt | cct | gtt | ttg | ctg | cgt | tcc | tac | 1159 | |
| Gly | Thr | Met | Leu | Ser | Ser | Gly | Ser | Gly | Pro | Val | Leu | Leu | Arg | Ser | Tyr | | |
| | | | 335 | | | | | 340 | | | | | 345 | | | | |
| tgt | ctc | tat | gtt | ctc | ctg | ctt | gcc | atc | aat | gga | gtg | aca | gag | tgt | tta | 1207 | |
| Cys | Leu | Tyr | Val | Leu | Leu | Leu | Ala | Ile | Asn | Gly | Val | Thr | Glu | Cys | Leu | | |
| | | | 350 | | | | 355 | | | | | 360 | | | | | |
| aca | ttt | gct | gcc | atg | agc | aaa | gag | gag | gtc | gac | agg | tac | aat | ttt | gtg | 1255 | |
| Thr | Phe | Ala | Ala | Met | Ser | Lys | Glu | Glu | Val | Asp | Arg | Tyr | Asn | Phe | Val | | |
| | | 365 | | | | 370 | | | | 375 | | | | | | | |
| atg | ctg | gcc | ctg | tcc | tcc | tca | ttc | ctg | gtg | tta | tcc | tat | ctc | ttg | acc | 1303 | |
| Met | Leu | Ala | Leu | Ser | Ser | Ser | Phe | Leu | Val | Leu | Ser | Tyr | Leu | Leu | Thr | | |
| 380 | | | | | 385 | | | | | 390 | | | | | 395 | | |
| cgt | tgg | tgt | ggc | agc | gtg | ggc | ttc | atc | ttg | gcc | aac | tgc | ttt | aac | atg | 1351 | |
| Arg | Trp | Cys | Gly | Ser | Val | Gly | Phe | Ile | Leu | Ala | Asn | Cys | Phe | Asn | Met | | |
| | | | | 400 | | | | 405 | | | | | | 410 | | | |
| ggc | att | cgg | atc | acg | cag | agc | ctt | tgc | ttc | atc | cac | cgc | tac | tac | cga | 1399 | |
| Gly | Ile | Arg | Ile | Thr | Gln | Ser | Leu | Cys | Phe | Ile | His | Arg | Tyr | Tyr | Arg | | |
| | | | 415 | | | | 420 | | | | | 425 | | | | | |
| agg | agc | ccc | cac | agg | ccc | ctg | gct | ggc | ctg | cac | cta | tcg | cca | gtc | ctg | 1447 | |
| Arg | Ser | Pro | His | Arg | Pro | Leu | Ala | Gly | Leu | His | Leu | Ser | Pro | Val | Leu | | |
| | | 430 | | | | 435 | | | | | 440 | | | | | | |
| ctc | ggg | aca | ttt | gcc | ctc | agt | ggg | gtt | act | gct | gtt | tcg | gag | gta | | 1495 | |
| Leu | Gly | Thr | Phe | Ala | Leu | Ser | Gly | Gly | Val | Thr | Ala | Val | Ser | Glu | Val | | |
| | | 445 | | | | 450 | | | | 455 | | | | | | | |
| ttc | ctc | tgc | tgt | gat | cag | ggc | tgg | cca | gcc | aga | ctg | gca | cac | att | gct | 1543 | |
| Phe | Leu | Cys | Cys | Asp | Gln | Gly | Trp | Pro | Ala | Arg | Leu | Ala | His | Ile | Ala | | |
| 460 | | | | | 465 | | | | 470 | | | | | | 475 | | |
| gtg | ggg | gcc | ttc | tgt | ctg | gga | gca | act | ctc | ggg | aca | gca | ttc | ctc | aca | 1591 | |
| Val | Gly | Ala | Phe | Cys | Leu | Gly | Ala | Thr | Leu | Gly | Thr | Ala | Phe | Leu | Thr | | |
| | | | | 480 | | | | 485 | | | | | | 490 | | | |
| gag | acc | aag | ctg | atc | cat | ttc | ctc | agg | act | cag | tta | ggg | gtg | ccc | aga | 1639 | |
| Glu | Thr | Lys | Leu | Ile | His | Phe | Leu | Arg | Thr | Gln | Leu | Gly | Val | Pro | Arg | | |

```

          495          500          505
cgc act gac aaa atg aca tgacttcagg gaagcctgga cacccgaggc 1687
Arg Thr Asp Lys Met Thr
      510
acctggacca gctatgggta gttctgtggg tggaacacat tctgtgtaag agccccactg 1747
agggctctgc agcggagtga cagcaacccc agagatgagg caccagagag tgccactgca 1807
tgagacacct gtgaccattc gaagtctgaa atgcgggggg ggagtttcat ttttaagtga 1867
agaccaaag ccctttaaaa ataatagttt tttatcattt tatagtaatc agcattttct 1927
cttttactaa tatactcatt ccttttgaaa aaaaaaaaaa aa 1969

<210> 60
<211> 1132
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..937

<220>
<221> sig_peptide
<222> 77..127
<223> Von Heijne matrix
      score 3.74817238048175
      seq RIVSAALLAFVQT/HL

<400> 60
gttgggtgggg ctgggggatg agagctgcac cgcgcgggac aagtcgcccg cgccccgacg 60
gagcagaaga gagagc atg gag ctg gag agg atc gtc agt gca gcc ctc ctt 112
      Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu
      -15 -10
gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg gat 160
Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp
-5 1 5 10
gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc ccc 208
Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro
15 20 25
tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag atg 256
Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met
30 35 40
atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca ata 304
Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile
45 50 55
ggg gac atg atg cag aag ctc tca ggg cag ctg agc gat gcc agg aac 352
Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn
60 65 70 75
aaa gag aac ctg caa ccg cag agc tct ggt gtc caa ggt cag gtg ccc 400
Lys Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro
80 85 90
atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag act 448
Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr
95 100 105
agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act ggc 496
Arg Ser Ser Ala Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly
110 115 120
gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg ttc 544
Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe
125 130 135

```

```

cct acc tgt tgc gtg gag cag gcc cag tgg gtg ctg gcc aaa gct cgg      592
Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg
140                               145                               155
ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa gag      640
Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu
                               160                               165                               170
ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc ctc      688
Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu
                               175                               180                               185
aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag tac      736
Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr
190                               195                               200
atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg gct      784
Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala
205                               210                               215
ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag gta      832
Pro Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val
220                               225                               230                               235
gtg agc acc aaa ggg gag cga ttc aaa gat gtg cgg aac cct gag gcc      880
Val Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala
240                               245                               250
gag gag atg aag gcc aca tac atc aac ctc aag cca gcc aga aag tac      928
Glu Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr
255                               260                               265
cgc ttc cat tgaggcactc gccggactct gcccagacct tctaggctca      977
Arg Phe His
270
gatcccagag ggatgcagga gccctatacc cctacacagg ggccccctaa ctctgtccc      1037
ccttctctac tcctttgtct catagtgtta acctactctc ggagctgcct ccatgggcac      1097
agtaaagggtg gcccaaggaa aaaaaaaaaa aaaaa      1132

```

```

<210> 61
<211> 631
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 9..503

```

```

<220>
<221> sig_peptide
<222> 9..113
<223> Von Heijne matrix
      score 10.2506494380376
      seq LLPLVLLPPLAAA/AA

```

```

<400> 61
tgccaggg atg atg cgc tgc tgc cgc cgc cgc tgc tgc tgc cgg caa cca      50
      Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro
      -35                               -30                               -25
ccc cat gcc ctg agg ccg ttg ctg ttg ctg ccc ctc gtc ctt tta cct      98
Pro His Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro
      -20                               -15                               -10
ccc ctg gca gca gct gca gcg ggc cca aac cga tgt gac acc ata tac      146
Pro Leu Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr
      -5                               1                               5                               10
cag ggc ttc gcc gag tgt ctc atc cgc ttg ggg gac agc atg ggc cgc      194

```

| | |
|--|-----|
| Gln Gly Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg | |
| 15 20 25 | |
| gga ggc gag ctg gag acc atc tgc agg tct tgg aat tac ttc cat gcc | 242 |
| Gly Gly Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala | |
| 30 35 40 | |
| tgt gcc tct cag gtc ctg tca ggc tgt ccg gag gag gca gct gca gtg | 290 |
| Cys Ala Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val | |
| 45 50 55 | |
| tgg gaa tca cta cag caa gaa gct cgc cag gcc ccc cgt ccg aat aac | 338 |
| Trp Glu Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn | |
| 60 65 70 75 | |
| ttg cac act ctg tgc ggt gcc ccg gtg cat gtt cgg gag cgc ggc aca | 386 |
| Leu His Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr | |
| 80 85 90 | |
| ggc tcc gaa acc aac cag gag acg ctg cgg gct aca gcg cct gca ctc | 434 |
| Gly Ser Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu | |
| 95 100 105 | |
| ccc atg gcc cct gcg ccc cca ctg ctg gcg gct gct ctg gct ctg gcc | 482 |
| Pro Met Ala Pro Ala Pro Pro Leu Leu Ala Ala Leu Ala Leu Ala | |
| 110 115 120 | |
| tac ctc ctg agg cct ctg gcc tagcttggtg ggttggttag cagcgcccg | 533 |
| Tyr Leu Leu Arg Pro Leu Ala | |
| 125 130 | |
| acctccagcc ctgctctggc ggttggttgtc caggctctgc agagcgcagc agggcttttc | 593 |
| attaaaggta tttatatattg caaaaaaaaa aaaaaaaaa | 631 |

<210> 62
 <211> 722
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..464

<220>
 <221> sig_peptide
 <222> 21..95
 <223> Von Heijne matrix
 score 5.38058532480537
 seq AVTSLLSPTPATA/LA

| | |
|---|-----|
| <400> 62 | |
| ggaagtgagt gatcgaaagc atg gcg tgc gtg gtg ttg gcg ctg agg acc cgg | 53 |
| Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg | |
| -25 -20 -15 | |
| aca gcc gtt aca tcc ttg cta agc ccc act ccg gct aca gct ctt gct | 101 |
| Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala | |
| -10 -5 1 | |
| gtc aga tac gca tcc aag aag tgc ggt ggt agc tcc aaa aac ctc ggt | 149 |
| Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly | |
| 5 10 15 | |
| gga aag tca tca ggc aga cgc caa ggc att aag aaa atg gaa ggt cac | 197 |
| Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His | |
| 20 25 30 | |
| tat gtt cat gct ggg aac atc att gca aca cag cgc cat ttc cgc tgg | 245 |
| Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp | |
| 35 40 45 50 | |

| | |
|--|-----|
| cac cca ggt gcc cat gtg ggt gtt ggg aag aat aaa tgt ctg tat gcc | 293 |
| His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala | |
| 55 60 65 | |
| ctg gaa gag ggg ata gtc cgc tac act aag gag gtc tac gtg cct cat | 341 |
| Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His | |
| 70 75 80 | |
| ccc aga aac acg gag gct gtg gat ctg atc acc agg ctg ccc aag ggt | 389 |
| Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly | |
| 85 90 95 | |
| gct gtg ctc tac aag act ttt gtc cac gtg gtt cct gcc aag cct gag | 437 |
| Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu | |
| 100 105 110 | |
| ggc acc ttc aaa ctg gta gct atg ctt tgaatgtcctg ttgaggccat | 484 |
| Gly Thr Phe Lys Leu Val Ala Met Leu | |
| 115 120 | |
| cggacagaga ctggagccca ggtgacagga gatggtgata ccagaagtca agggttgggg | 544 |
| tggcgacacg gcctcccag gaagaggtct gcttgatggt gactctgcag gagactctga | 604 |
| agtgactgct gggaaaccct ttgggagacc tgacctgggg ccaaaaaataa agtgagccag | 664 |
| cgatcatgaac gcatgctatt tagggacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa | 722 |

<210> 63
 <211> 1442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 178..1050

<220>
 <221> sig_peptide
 <222> 178..279
 <223> Von Heijne matrix
 score 10.0571391689271
 seq FLCLLSALLLLEGG/KK

| | |
|--|-----|
| <400> 63 | |
| agtgcatgtc tggagcgagg agaagctcac gaatcagctg caggtctctg ttttgaaaaa | 60 |
| gcagagatac agaggcagag gaaaagggca ctccctatgtg acctgttctt agagcaagac | 120 |
| aatcaccatc tgaattccag aagccctgtt catggttggg gatattttct cgactgc | 177 |
| atg gaa tca gaa aga agc aaa agg atg gga aat gcc tgc att ccc ctg | 225 |
| Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu | |
| -30 -25 -20 | |
| aaa aga att gct tat ttc cta tgt ctc tta tct gcg ctt ttg ctg act | 273 |
| Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Thr | |
| -15 -10 -5 | |
| gag ggg aag aaa cca gcg aag cca aaa tgc cct gcc gtg tgt act tgt | 321 |
| Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys | |
| 1 5 10 | |
| acc aaa gat aat gct tta tgt gag aat gcc aga tcc att cca cgc acc | 369 |
| Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr | |
| 15 20 25 30 | |
| gtt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act | 417 |
| Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr | |
| 35 40 45 | |
| gaa atc tca gaa ggg agt ttt tta ttc acg cca tcg ctg cag ctc ttg | 465 |
| Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu | |
| 50 55 60 | |

<223> Von Heijne matrix
score 4.30837886795471
seq LMVELLKVFVVEA/AV

<400> 64
gttccggtgg gcgcgcgttg aggctgcggt c atg gag gga gca gga gct gga 52
Met Glu Gly Ala Gly Ala Gly
-45
tcc ggc ttc cgg aag gag ctg gtg agc agg ctg ctg cac ctg cac ttc 100
Ser Gly Phe Arg Lys Glu Leu Val Ser Arg Leu Leu His Leu His Phe
-40 -35 -30
aag gat gac aag acc aaa gtg agc ggg gac gcg ctg cag ctc atg gtg 148
Lys Asp Asp Lys Thr Lys Val Ser Gly Asp Ala Leu Gln Leu Met Val
-25 -20 -15
gag ttg ctg aag gtc ttc gtt gtg gaa gca gca gtc cgc ggc gtg cgg 196
Glu Leu Leu Lys Val Phe Val Val Glu Ala Ala Val Arg Gly Val Arg
-10 -5 1 5
cag gcc cag gca gaa gac gcg ctc cgt gtg gac gtg gac cag ctg gag 244
Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu
10 15 20
aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct 294
Lys Val Leu Pro Gln Leu Leu Asp Phe
25 30
gaggccaccc ccagaggagc ccttgggtcca cagaagcagg ccttgtgttt ccagcggcct 354
ctgataagag gcaggggaagg acctgaagga tttggagttg attcaaaciaa gatctctggg 414
agtctccagc ctgtgcagaa ggggcaggac tgcagtgcac tgcgggcctt ggagtgtcca 474
gtggggacac tgggtgtggga aggggcagca cctggggagt ccttgcctct cctccctggg 534
acaatagtgt gcatgccacc cgggggtccta caggcagggtg ctgggaaagg cctggccagc 594
aggtagcctg tgtgtttgac aaacagcagc tggcagcgct gcctcctgcc cacattcctg 654
ccacccgaca tcaaagctgg cgtgtgacct ttccagccat gcgatattcc ccttgggaaga 714
tgcttcccc ggctataaat ttgttctcac aaagcaacat caataaatca aaactgtctc 774
tctcaaaaaa aaaaaaaaaa a 795

<210> 65
<211> 1236
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 222..920

<220>
<221> sig_peptide
<222> 222..311
<223> Von Heijne matrix
score 4.35083245061594
seq VAHALSLPAESYG/ND

<400> 65
accgaaaatt actgacgagt caatcacctc agatctctca agcagtcacag cctacgcaac 60
agtactccac ctctgcgcct gtgcggggag ggtaaggcgg ggccagcaac ttcctcagct 120
ggagggagag cgcacgggtg agccgccagt tgagaaggac tctgatccgg ctcagctttc 180
caatcagctg cggaaggagc cacgctttcg ggggttgcaa g atg gcg gcc acc agt 236
Met Ala Ala Thr Ser
-30
gga act gat gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg 284
Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala

<220>
 <221> sig_peptide
 <222> 101..160
 <223> Von Heijne matrix
 score 9.32665652007071
 seq LFLCYLLLFTCSG/VE

<400> 66
 ttactcgctg ctgtgcccac ctatcagcag gctccgggct gaagattgct tctcttctct 60
 cctccaaggt ctagtgcagg agcccgcgcg cggcgccacc atg cgg cag aag gcg 115
 Met Arg Gln Lys Ala
 -20
 gta tcg ctt ttc ttg tgc tac ctg ctg ctc ttc act tgc agt ggg gtg 163
 Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val
 -15 -10 -5 1
 gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc ggg 211
 Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly
 5 10 15
 ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca gtc 259
 Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Leu Ala Val
 20 25 30
 gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc aac 307
 Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn
 35 40 45
 tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg ggc 355
 Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly
 50 55 60 65
 tagtggccac gctgcagagc ctcgggggctg gtggcagcag cgtcgtcata ggtaatatg 415
 gtgccctgat gggctacgcc acccacaagt atctcgatag tgaggaggat gaggagtagc 475
 cagcagctcc cagaacctct tcttccttct tggcctaact cttccagtta ggatctagaa 535
 ctttgccctt tttttttttt tttttttttt ttgagatggg ttctcactat attgtccagg 595
 cttagtgca gkggctattc acagatgcga acatagtaca ctgcagcctc caactcctag 655
 cctcaagtga tctcctgtc tcaacctccc aagtaggatt acaagcatgc gccgacgatg 715
 cccaraatcc araactttgt ctatcactct cccaacaac ctatagtgtga aaacagaata 775
 aacttcaccc agaaaaaaaa aaammacaar aaaaaaaaaa aaaaaaaaaa aaaaaaaaaam 835
 aaaaaaaaaa rrraaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 881

<210> 67
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 173..487

<220>
 <221> sig_peptide
 <222> 173..301
 <223> Von Heijne matrix
 score 4.27484469223909
 seq AGSLVATLQSVGA/AG

<400> 67
 agggcagagt aggcgcgtcc ctactggatg gagggggaag taacacccca agaacgctgt 60
 catttcctgg gccaaagtgg gacccggacg gcctcaccat gatgaaacgg gcagctgctg 120
 ctgcagtggg aggagccctg gcagtggggg ctgtgccgtg gtgctcagtg cc atg ggc 178
 Met Gly

```

ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg      226
Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met
-40 -35 -30
tcc gca gca gcc att gcc aac ggg ggt ggt gtt tct gcg ggg agc ctg      274
Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu
-25 -20 -15 -10
gtg gct act ctg cag tcc gtg ggg gca gct gga ctc tcc aca tca tcc      322
Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
-5 1 5
aac atc ctc ctg gcc tct gtt ggg tca gtg ttg ggg gcc tgc ttg ggg      370
Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly
10 15 20
aat tca cct tct tct tct ctc cca gct gaa ccc gag gct aaa gaa gat      418
Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
25 30 35
gag gca aga gaa aat gta ccc caa ggt gaa cct cca aaa ccc cca ctc      466
Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
40 45 50 55
aag tca gag aaa cat gag gaa taaaggtcac atgcagatgc aaaaaaaaaa      517
Lys Ser Glu Lys His Glu Glu
60
aaaaaaa      524

<210> 68
<211> 1472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..1082

<220>
<221> sig_peptide
<222> 210..311
<223> Von Heijne matrix
score 10.0571391689271
seq FLCLLSALLLTEG/KK

<400> 68
acagtacctc acaggtctct tcccccgagc agtgcattgc tggagcgagg agaagctcac      60
gaatcagctg caggtctctg ttttgaaaaa gcagagatac agaggcagag gaaaaggggtg      120
gactcctatg tgacctgttc ttagagcaag acaatcacca tctgaattcc agaagccctg      180
ttcatggttg gggatatttt ctcgactgc atg gaa tca gaa aga agc aaa agg      233
Met Glu Ser Glu Arg Ser Lys Arg
-30
atg gga aat gcc tgc att ccc ctg aaa aga att gct tat ttc cta tgt      281
Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
-25 -20 -15
ctc tta tct gcg ctt ttg ctg act gag ggg aag aaa cca gcg aag cca      329
Leu Leu Ser Ala Leu Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro
-10 -5 1 5
aaa tgc cct gcc gtg tgt act tgt acc aaa gat aat gct tta tgt gag      377
Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu
10 15 20
aat gcc aga tcc att cca cgc acc gtt cct cct gat gtt atc tca tta      425
Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu
25 30 35

```

| | |
|---|------|
| tcc ttt gtg aga tct gtt ttt act gaa atc tca gaa ggg agt ttt tta | 473 |
| Ser Phe Val Arg Ser Val Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu | |
| 40 45 50 | |
| ttc acg cca tcg ctg cag ctc ttg tta ttc aca tcg aac tcc ttt gat | 521 |
| Phe Thr Pro Ser Leu Gln Leu Leu Phe Thr Ser Asn Ser Phe Asp | |
| 55 60 65 70 | |
| gtg atc agt gat gat gct ttt att ggt ctt cca cat cta gag tat tta | 569 |
| Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu | |
| 75 80 85 | |
| ttc ata gaa aac aac aac atc aag tca att tca aga cat act ttc cgg | 617 |
| Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg | |
| 90 95 100 | |
| gga cta aag tca tta att cac ttg agc ctt gca aac aac aat ctc cag | 665 |
| Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln | |
| 105 110 115 | |
| aca ctc cca aaa gat att ttc aaa ggc ctg gat tct tta aca aat gtg | 713 |
| Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val | |
| 120 125 130 | |
| gac ctg agg ggt aat tca ttt aat tgt gac tgt aaa ctg aaa tgg cta | 761 |
| Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu | |
| 135 140 145 150 | |
| gtg gaa tgg ctt ggc cac acc aat gca act gtt gaa gac atc tac tgc | 809 |
| Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys | |
| 155 160 165 | |
| gaa ggc ccc cca gaa tac aag aag cgc aaa atc aat agt ctc tcc tcg | 857 |
| Glu Gly Pro Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser | |
| 170 175 180 | |
| aag gat ttc gat tgc atc att aca gaa ttt gca aag tct caa gac ctg | 905 |
| Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu | |
| 185 190 195 | |
| cct tat caa tca ttg tcc ata gac act ttt tct tat ttg aat gat gag | 953 |
| Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu | |
| 200 205 210 | |
| tat gta gtc atc gct cag cct ttt act gga aaa tgc att ttc ctt gaa | 1001 |
| Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu | |
| 215 220 225 230 | |
| tgg gac cat gtg gaa aag acc ttc cgg aat tat gac aac att aca gtt | 1049 |
| Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Val | |
| 235 240 245 | |
| tta agg gaa ata cac aga ttt aca aac atg tca tagttgactt aagcgcgcatga | 1102 |
| Leu Arg Glu Ile His Arg Phe Thr Asn Met Ser | |
| 250 255 | |
| gacaccaaatt tctgtggctg ccatcagaaa ttttctacag tacatgaccc ggatgaactc | 1162 |
| aatgcatgat gactcttctt atcacacttg caaatgaatg cctttcaaac attgagactg | 1222 |
| ctagaaccaaa gcactaccag tatctccatc cttaactgtc cagtccagtg atgtgggaag | 1282 |
| ttacctttta taagacaaaa ttttaattgtg taactgttct ttgcagtgaa gatgtgtaaa | 1342 |
| taagcgttta atggtatctg ttactccaaa aagaaatatt aatatgtact tttccattta | 1402 |
| tttattcatg tgtacagaaa caactgccaa ataaaatggt tacattttct tacaaaaaaa | 1462 |
| aaaaaaaaa | 1472 |

<210> 69
 <211> 1737
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 172..1449

<220>
 <221> sig_peptide
 <222> 172..255
 <223> Von Heijne matrix
 score 5.94825670923113
 seq XVLLEPFVHQVGG/HS

<400> 69
 aaacaatagg acggaacgc cgaggaaccc ggctgaggcg gcagagcatc ctggccagaa 60
 caagccaagg agccaagacg agagggacac acggacaaac aacagacaga agacgtactg 120
 gccgctggac tccgctgcct ccccatctc cccgccatct gcgcccggag g atg agc 177
 Met Ser
 cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 225
 Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
 -25 -20 -15
 ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 273
 Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
 -10 -5 1 5
 ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag 321
 Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
 10 15 20
 ttc tac gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac 369
 Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr
 25 30 35
 aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg 417
 Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu
 40 45 50
 tgt cta ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att 465
 Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile
 55 60 65 70
 gta gat aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca 513
 Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr
 75 80 85
 aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac 561
 Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp
 90 95 100
 tgg gtg cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta 609
 Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu
 105 110 115
 gaa gaa gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act 657
 Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr
 120 125 130
 gta gag aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct 705
 Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro
 135 140 145 150
 tgg agc atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat 753
 Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn
 155 160 165
 gca aag cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act 801
 Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr
 170 175 180
 tcc cgc tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga 849
 Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg
 185 190 195
 caa cat ggt gat gat gct tca gag gag aag gca gcc aac cag atc cga 897
 Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln Ile Arg
 200 205 210

```

aaa tgt cag cag agc aca tct gca gtc att ggt gtg cgt gtg tgt ggc      945
Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val Cys Gly
215                220                230
atg cag gtg tac caa gca ggc agt ggg cag ctc atg ttc atg aac aag      993
Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met Asn Lys
                235                240                245
tac cat gga cgg aag cta tct atg cag ggc ttc aag gag gca ctt ttc      1041
Tyr His Gly Arg Lys Leu Ser Met Gln Gly Phe Lys Glu Ala Leu Phe
                250                255                260
cag ttc ttc cac aat ggg cgg tac ctg cgc cgt gaa ctc ctg ggc cct      1089
Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu Gly Pro
                265                270                275
gtg ctc aag aag ctg act gag ctc aag gca gtg ttg gag cga cag gag      1137
Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg Gln Glu
                280                285                290
tcc tac cgc ttc tac tca agc tcc ctg ctg gtc att tat gat ggc aag      1185
Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp Gly Lys
295                300                305                310
gag cgg ccc gaa gtg gtc ctg gac tca gat gct gag gat ttg gag gac      1233
Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu Glu Asp
                315                320                325
ctg tca gag gaa tca gct gat gag tct gct ggt gcc tat gcc tac aaa      1281
Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala Tyr Lys
                330                335                340
ccc atc ggc gcc agc tct gta gat gtg cgc atg atc gac ttt gca cac      1329
Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe Ala His
                345                350                355
acc acc tgc agg ctg tat ggc gag gac acc gtg gtg cat gag ggc cag      1377
Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu Gly Gln
                360                365                370
gat gct ggc tat atc ttc ggg ctc cag agc ctg ata gac att gtc aca      1425
Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile Val Thr
375                380                385                390
gag ata agt gag gag agt ggg gag tgagcttgct agctgctcca gtacttgaga      1479
Glu Ile Ser Glu Glu Ser Gly Glu
                395
gcgactctgt gtcccaggca cagctgtgct gcgtcagggg ggaagccagt atggccaggt      1539
ggtggctcct gcagcctgga gctgatgtgc agtggcctct gtgagcccca gcctgagcca      1599
gtcccagctg tgcttgaggt ctttatttat tttaactatt tcttcaacat tccacatttg      1659
atgatgatac ctctttcttc cctgagtgtg tatgtttctaa tacaaatctt tttgtttatt      1719
gaaaaaaaaa aaaaaaaaaa      1737

```

<210> 70

<211> 1637

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..1427

<220>

<221> sig_peptide

<222> 30..77

<223> Von Heijne matrix

score 3.71064775937629

seq YAAAAGVLAGVES/RQ

[illegible][illegible]

| | |
|---|------|
| cat gag gtc cac tac atc ctg ctg gat cct tcc tgc agt ggc tcg ggt | 965 |
| His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly | |
| 285 290 295 | |
| atg ccg agc aga cag ctg gag gag ccc ggg gca ggc aca cct agc ccg | 1013 |
| Met Pro Ser Arg Gln Leu Glu Glu Pro Gly Ala Gly Thr Pro Ser Pro | |
| 300 305 310 | |
| gtg cgt ctg cat gcc ctg gca ggc ttc cag cag cga gcc ctg tgc cac | 1061 |
| Val Arg Leu His Ala Leu Ala Gly Phe Gln Gln Arg Ala Leu Cys His | |
| 315 320 325 | |
| gcg ctc act ttc cct tcc ctg cag cgg ctc gtc tac tcc acg tgc tcc | 1109 |
| Ala Leu Thr Phe Pro Ser Leu Gln Arg Leu Val Tyr Ser Thr Cys Ser | |
| 330 335 340 | |
| ctc tgc cag gag gag aat gaa gac gtg gtg cga gat gcg ctg cag cag | 1157 |
| Leu Cys Gln Glu Glu Asn Glu Asp Val Val Arg Asp Ala Leu Gln Gln | |
| 345 350 355 360 | |
| aac ccg ggc gcc ttc agg cta gct ccc gcc ctg cct gcc tgg ccc cac | 1205 |
| Asn Pro Gly Ala Phe Arg Leu Ala Pro Ala Leu Pro Ala Trp Pro His | |
| 365 370 375 | |
| cga ggc ctg agc acg ttc ccg ggt gcc gag cac tgc ctc cgg gcc tcc | 1253 |
| Arg Gly Leu Ser Thr Phe Pro Gly Ala Glu His Cys Leu Arg Ala Ser | |
| 380 385 390 | |
| cct gag acc aca ctc agc agt ggc ttc ttc gtt gct gta att gaa cgg | 1301 |
| Pro Glu Thr Thr Leu Ser Ser Gly Phe Phe Val Ala Val Ile Glu Arg | |
| 395 400 405 | |
| gtc gag gtg cca agc tca gcc tca cag gcc aaa gca tca gca cca gaa | 1349 |
| Val Glu Val Pro Ser Ser Ala Ser Gln Ala Lys Ala Ser Ala Pro Glu | |
| 410 415 420 | |
| cgc aca ccc agc cca gcc cca aag aga aag aag aga cag caa aga gcc | 1397 |
| Arg Thr Pro Ser Pro Ala Pro Lys Arg Lys Arg Gln Gln Arg Ala | |
| 425 430 435 440 | |
| gca gcc ggt gct tgc aca ccg cct tgc aca tagcagaggc tccgggctga | 1447 |
| Ala Ala Gly Ala Cys Thr Pro Pro Cys Thr | |
| 445 450 | |
| ctccttcctg gtgggaaagg aagatgcctg tcctctccgt ggaggaccct gggccctcac | 1507 |
| cgcaggaagc agtttggtt ttgaaagggtt attgggtccc ttccttgggc tgtgttcttg | 1567 |
| ctggtgagca aagtgttacc tgcaaaaata aaatgcagaa cgtactctac gacaaaaaaa | 1627 |
| aaaaaaaaa | 1637 |

<210> 71

<211> 1636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..1175

<220>

<221> sig_peptide

<222> 30..77

<223> Von Heijne matrix

score 3.71064775937629

seq YAAAAGVLAGVES/RQ

<400> 71

| | | | | | | | | | | | | | | | | | | |
|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cta | atc | gaaa | ag | taa | agg | cg | cg | cg | ga | ac | atg | ggg | ctg | tat | gct | gca | gct | gca |
| Met | Gly | Leu | Tyr | Ala | Ala | Ala | Ala | Ala | Ala | Ala | | | | | | | | |

53

-15

-10

| | |
|---|------|
| ggc gtg ttg gcc gcc gtg gag agc cgc cag gcc tct atc aag ggg ttg | 101 |
| Gly Val Leu Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu | |
| -5 1 5 | |
| gtg tac tcc agc aac ttc cag aac gtg aag cag ctg tac gcg ctg gtg | 149 |
| Val Tyr Ser Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val | |
| 10 15 20 | |
| tgc gaa acg cag cgc tac tcc gcc gtg ctg gat gct gtg atc gcc agc | 197 |
| Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser | |
| 25 30 35 40 | |
| gcc gcc ctc ctc cgt gcg gag aag aag ctg cgg ccg cac ctg gcc aag | 245 |
| Ala Gly Leu Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys | |
| 45 50 55 | |
| gtg cta gtg tat gag ttg ttg ttg gga aag gcc ttt cga ggg ggt ggg | 293 |
| Val Leu Val Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly | |
| 60 65 70 | |
| ggc cga tgg aag gct ctg ttg gcc cgg cac cag gcg agg ctc aag gct | 341 |
| Gly Arg Trp Lys Ala Leu Leu Gly Arg His Gln Ala Arg Leu Lys Ala | |
| 75 80 85 | |
| gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac | 389 |
| Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp | |
| 90 95 100 | |
| ctg ttg gaa gtg gga tcc agg cct ggt cca gcc tcc cag ctg cct cga | 437 |
| Leu Leu Glu Val Gly Ser Arg Pro Gly Pro Ala Ser Gln Leu Pro Arg | |
| 105 110 115 120 | |
| ttt gtg cgt gtg aac act ctc aag acc tgc tcc gat gat gta gtt gat | 485 |
| Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp | |
| 125 130 135 | |
| tat ttc aag aga caa ggt ttc tcc tat cag ggt cgg gct tcc agc ctc | 533 |
| Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu | |
| 140 145 150 | |
| gat gac tta cga gcc ctc aag ggg aag cat ttt ctc ctg gac ccc ttg | 581 |
| Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu | |
| 155 160 165 | |
| atg ccg gag ctg ctg gtg ttt ccc gcc cag aca gat ctg cat gaa cac | 629 |
| Met Pro Glu Leu Leu Val Phe Pro Ala Gln Thr Asp Leu His Glu His | |
| 170 175 180 | |
| cca ctg tac cgg gcc gga cac ctc att ctg cag gac agg gcc agc tgt | 677 |
| Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys | |
| 185 190 195 200 | |
| ctc cca gcc atg ctg ctg gac ccc ccg cca gcc tcc cat gtc atc gat | 725 |
| Leu Pro Ala Met Leu Leu Asp Pro Pro Pro Gly Ser His Val Ile Asp | |
| 205 210 215 | |
| gcc tgt gcc gcc cca gcc aat aag acc agt cac ttg gct gct ctt ctg | 773 |
| Ala Cys Ala Ala Pro Gly Asn Lys Thr Ser His Leu Ala Ala Leu Leu | |
| 220 225 230 | |
| aag aac caa ggg aag atc ttt gcc ttt gac ctg gat gcc aag cgg ctg | 821 |
| Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu | |
| 235 240 245 | |
| gca tcc atg gcc acg ctg ctg gcc cgg gct ggc gtc tct tgc tgt gaa | 869 |
| Ala Ser Met Ala Thr Leu Leu Ala Arg Ala Gly Val Ser Cys Cys Glu | |
| 250 255 260 | |
| ctg gct gag gag gac ttc ctg gcg gtc tcc ccc tcg gat cca cgc tac | 917 |
| Leu Ala Glu Glu Asp Phe Leu Ala Val Ser Pro Ser Asp Pro Arg Tyr | |
| 265 270 275 280 | |
| cat gag gtc cac tac atc ctg ctg gat cct tcc tgc agt ggc tcg ggt | 965 |
| His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly | |
| 285 290 295 | |
| atg ccg agc aga cag ctg gag gag ccc ggg gca ggc aca cct agc ccg | 1013 |


```

Met Pro Ser Arg Gln Leu Glu Glu Pro Gly Ala Gly Thr Pro Ser Pro
          300          305          310
gtg cgt ctg cat gcc ctg gca gct tcc agc agc gag ccc tgt gcc acg      1061
Val Arg Leu His Ala Leu Ala Ala Ser Ser Ser Glu Pro Cys Ala Thr
          315          320          325
cgc tca ctt tcc ctt ccc tgc agc ggc tgc tct act cca cgt gct ccc      1109
Arg Ser Leu Ser Leu Pro Cys Ser Gly Ser Ser Thr Pro Arg Ala Pro
          330          335          340
tct gcc agg agg aga atg aag acg tgg tgc gag atg cgc tgc agc aga      1157
Ser Ala Arg Arg Arg Met Lys Thr Trp Cys Glu Met Arg Cys Ser Arg
          345          350          355          360
acc cgg gcg cct tca ggc tagctcccg cctgcctgcc tggccccacc      1205
Thr Arg Ala Pro Ser Gly
          365
gaggcctgag cacgttcccg ggtgccgagc actgcctccg ggccctccct gagaccacac      1265
tcagcagtgg cttcttcggt gctgtaattg aacgggtcga ggtgccaagc tcagcctcac      1325
aggccaaagc atcagcacca gaacgcacac ccagcccagc cccaaagaga aagaagagac      1385
agcaaagagc cgcagccggt gcttgcacac cgccttgcac atagcagagg ctccgggctg      1445
actccttcct ggtgggaaag gaagatgcct gtccctcccg tggaggaccc tgggccctca      1505
ccgcaggaag cagtttgggt tttgaaaggt tattgggtcc cttccttggg ctgtgttctt      1565
gctggtgagc aaagtgttac ctgcaaaaat aaaatgcaga acgtactcta cgacaaaaaa      1625
aaaaaaaaa a      1636

<210> 72
<211> 1758
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..839

<220>
<221> sig_peptide
<222> 66..173
<223> Von Heijne matrix
      score 4.89555877630516
      seq LLLLRRLNDAALRA/LQ

<400> 72
agaggaggtg gcggtggtgg ccctcgccctg tggcccccggt gctgcttgca ctggaactcg      60
tcgcc atg gag gag ctc cag gag cct ctg aga gga gag ctc cgg ctc tgc      110
      Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys
          -35          -30          -25
ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac      158
Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Arg Leu Asn Asp
          -20          -15          -10
gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg      206
Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
          -5          1          5          10
gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct      254
Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
          15          20          25
ggg tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag      302
Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
          30          35          40
ggc gct ggt ggt agc ttg gac ctt gtg tgc caa cgc ttc ctc agg tct      350
Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser

```

| | | | |
|--|-----|-----|------|
| 45 | 50 | 55 | |
| ggg cct aac agc ctc cac tgc ctg ggc tca ctc agg gag cgc ctc att | | | 398 |
| Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile | | | |
| 60 | 65 | 70 | 75 |
| att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga | | | 446 |
| Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly | | | |
| 80 | 85 | 90 | |
| cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca | | | 494 |
| His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr | | | |
| 95 | 100 | 105 | |
| gga ggc tat tct gaa gga gat gca gta tca cag cca cag atg gca cta | | | 542 |
| Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu | | | |
| 110 | 115 | 120 | |
| gag gag gtg tca gtg tca gat cca ctg gca agc aac caa gga cag tca | | | 590 |
| Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser | | | |
| 125 | 130 | 135 | |
| ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc | | | 638 |
| Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser | | | |
| 140 | 145 | 150 | 155 |
| cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct | | | 686 |
| Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser | | | |
| 160 | 165 | 170 | |
| gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act | | | 734 |
| Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr | | | |
| 175 | 180 | 185 | |
| gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg ccc ccc | | | 782 |
| Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro | | | |
| 190 | 195 | 200 | |
| cct aca agg cct gac caa tca gga ttt aca aga ggg aga aga ttg gga | | | 830 |
| Pro Thr Arg Pro Asp Gln Ser Gly Phe Thr Arg Gly Arg Arg Leu Gly | | | |
| 205 | 210 | 215 | |
| gca aga aga tgaggacatg gacccagat tagaacacaa ttcctcagtt | | | 879 |
| Ala Arg Arg | | | |
| 220 | | | |
| caagaagatt ctgaatcccc aagtcctgaa gatataccag actacctcct gcaatacagg | | | 939 |
| gccatccaca gtgcagaaca gcaacatgcc tatgagcagg actttgagac agattatgct | | | 999 |
| gaataaccgca tcctgcatgc cctgtgtggg actgcaagcc aaaggttcat agagctggga | | | 1059 |
| gcagagatta aaagagttcg gcgaggaact ccagaataca aggtcctgga agacaagata | | | 1119 |
| atccaggaat ataaaaagtt caggaagcag taccgaagtt acagagaaga aaagcgtcgc | | | 1179 |
| tgtgagtacc ttcaccagaa attgtcccac attaaaggtc tcatcctgga gtttgaggaa | | | 1239 |
| aagaacaggg gcagctgaag ttatcaaggg aatttttgag cctctgctta gtgaaacaca | | | 1299 |
| aaggaacaaa gcagctataa actaaataga atgcaactat ctgcttttct tatgctgacc | | | 1359 |
| actggagtcc atggtggcaa gtagagagct gctctaggtt cttgagggtt ggttttcatt | | | 1419 |
| attaattttt aggggtatggg cactgtgcaa agactccata gctgtgccta ggagtctagg | | | 1479 |
| aaaagtgaca gaggcttggc ttttttacct ttagttcagc caagtcattt tcaagtcctg | | | 1539 |
| agaaatgaca tcatcttcag gataaaataa tgaggacatt agacaaacca aactaagtga | | | 1599 |
| atttttagcct ggtagcctct ctaaggaaac agtaataata acttctgata agagttaaaa | | | 1659 |
| gaacttgtag catacctgga tataacggga aagggcctgg gtgttaccca tgtactgaaa | | | 1719 |
| atgaactttt accaacatgg ccaaaaaaaaa aaaaaaaaaa | | | 1758 |

<210> 73

<211> 1647

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 64..903

<220>
 <221> sig_peptide
 <222> 64..162
 <223> Von Heijne matrix
 score 10.6748773272319
 seq LLLLPFLPLLLLA/AP

<400> 73
 agctcaaggg gcctcgagga ctctctgcgt ctctggagac aagggcacta cacgcacttc 60
 aga atg aag agt tgc ggg agc atg ctg ggg ctc tgg ggg cag cgg ctc 108
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu
 -30 -25 -20
 ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg 156
 Pro Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
 -15 -10 -5
 ctt gca gcc ccc gcg ccc cac cgc gcg tcc tac aag ccg gtc atc gtg 204
 Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val
 1 5 10
 gtg cat ggg ctc ttc gac agc tcg tac agc ttc cgc cac ctg ctg gaa 252
 Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
 15 20 25 30
 tac atc aat gag aca cac ccc ggg act gtg gtg aca gtg ctc gat ctc 300
 Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu
 35 40 45
 ttc gat ggg aga gag agc ttg cga ccc ctg tgg gaa cag gtg caa ggg 348
 Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly
 50 55 60
 ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg 396
 Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val
 65 70 75
 cat ctc atc tgc tac tcg cag ggg ggc ctt gtg tgc cgg gct ctg ctt 444
 His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu
 80 85 90
 tct gtc atg gat gat cac aac gtg gat tct ttc atc tcc ctc tcc tct 492
 Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser
 95 100 105 110
 cca cag atg gga cag tat gga gac acg gac tac ttg aag tgg ctg ttc 540
 Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe
 115 120 125
 ccc acc tcc atg cgg tct aac ctc tat cgg atc tgc tat agc ccc ctg 588
 Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu
 130 135 140
 atc aat ggg gaa aga gac cat ccc aat gcc aca gta tgg cgg aag aac 636
 Ile Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn
 145 150 155
 ttt ctg cgt gtg ggc cac ctg gtg ctg att ggg ggc cct gat gat ggt 684
 Phe Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly
 160 165 170
 gtt att act ccc tgg cag tcc agc ttc ttt ggt ttc tat gat gca aat 732
 Val Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn
 175 180 185 190
 gag acc gtc ctg gag atg gag gag caa ctg gtt tat ctg cgg gat tct 780
 Glu Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser
 195 200 205
 ttt ggg ttg aag act cta ttg gcc cgg ggg gcc ata gtg agg tgt cca 828
 Phe Gly Leu Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro
 210 215 220

```

atg gcc ggt atc tcc cac aca gcc tgg cac tcc aac cgt acc ctt tat      876
Met Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr
      225              230              235
gag acc tgc att gaa cct tgg ctc tcc tgaggatata ttcagggggtc      923
Glu Thr Cys Ile Glu Pro Trp Leu Ser
      240              245
cccaggaact cctcgggtcca gagaccaagt ggtggccttg gaaagcagat gtcagggttt      983
ggtgtgcctg tgaccacctc attgctccca tattatcccc catttttagt agagacgggg      1043
ttttagtaga gacttggcct cccagaaccc ccttcctctg ctccctcatg aatgacaatt      1103
ccaggcctcc cctacatcat gtcctctcat ttgggggatt gctccgtgct gtccctttct      1163
ctcaaggccg aagttcggaa gtgagaaacc atgtttttta cttgtggctg ctcttgctgc      1223
tgctgctcct ccgtatctgg ctgtatgggt ggagaaccca cccactgcc accacagggg      1283
tctccttcca ggccactcag gacattttta gcttctctcc tccccatgtt cccttttttc      1343
tctaaagtcc cctgacatca gccctcccaa ctccaaagag ggactaccca tgagagtggg      1403
gttctgaggg tcccctatgg ggacagttcc gttcttgaag tgtcagtgtt ggggaatatc      1463
tgtggcctat gaggcccatc tcaggtttgg ggatccccc gtccttatga tcagtgttgg      1523
agtaccccc tgggagagcc tagtttcttt gagggcccag gccctctttt aactaccttt      1583
gaataggtgt tatccctgta tttatggaaa taaagttcca tttcctcaaa aaaaaaaaaa      1643
aaaaa

```

```

<210> 74
<211> 1646
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 64..585

```

```

<220>
<221> sig_peptide
<222> 64..162
<223> Von Heijne matrix
      score 10.6748773272319
      seq LLLLPFLPLLLLA/AP

```

```

<400> 74
agctcaaggg gcctcgagga ctctctgctg ctctggagac aagggcacta cacgcacttc      60
aga atg aag agt tgc ggg agc atg ctg ggg ctc tgg ggg cag cgg ctc      108
      Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu
            -30              -25              -20
ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg      156
Pro Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
            -15              -10              -5
ctt gca gcc ccc gcg ccc cac cgc gcg tcc tac aag ccg gtc atc gtg      204
Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val
            1              5              10
gtg cat ggg ctc ttc gac agc tgc tac agc ttc cgc cac ctg ctg gaa      252
Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
      15              20              25              30
tac atc aat gag aca cac ccc ggg act gtg gtg aca gtg ctc gat ctc      300
Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu
            35              40              45
ttc gat ggg aga gag agc ttg cga ccc ctg tgg gaa cag gtg caa ggg      348
Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly
            50              55              60
ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg      396
Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val

```

```

        65              70              75
cat ctc atc tgc tac tcg cag ggg ggc ctt gtg tgc cgg gct ctg ctt      444
His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu
      80              85              90
tct gtc atg gat gat cac aac gtg gat tct ttc atc tcc ctc tcc tct      492
Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser
      95              100              105              110
cca cag atg gga cag tat gga gac acg gac tac ttg aag tgg ctg ttc      540
Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe
              115              120              125
ccc acc tcc atg cgg tct aac ctc tat cgg atc tgc tat agc ccc      585
Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro
              130              135              140
tgatcaatgg ggaaagagac catcccaatg ccacagtatg gcggaagaac tttctgcgtg      645
tgggccacct ggtgctgatt gggggccctg atgatggtgt tattactccc tggcagtcca      705
gcttcttttg tttctatgat gcaaatgaga ccgtcctgga gatggaggag caactggttt      765
atctgcggga ttcttttggg ttgaagactc tattggcccg gggggccata gtgaggtgtc      825
caatggcccg tatctccac acagcctggc actccaaccg taccctttat gagacctgca      885
ttgaaccttg gctctcctga ggatatattc aggggtcccc aggaactcct cggtcagag      945
accaagtggg ggccttgaa agcagatgtc aggctttggt gtgcctgtga ccacctcatt      1005
gctcccatat tatccccat ttttagtaga gacgggggtt tagtagagac ttggcctccc      1065
agaaccccc tctctgctc ctccatgaat gacaattcca ggccctcccct acctcatgtc      1125
ctctcatttg ggggattgct ccgtgctgtc ctttctctc aaggccgaag ttcggaagtg      1185
agaaaccatg tttttaactt gtggctgtc ttgtgctgc tgcctcctcg tatctggctg      1245
tatgggtgga gaaccaccc actgccacc acaggggtct ccttcaggc cactcaggac      1305
atttttagct tctctcctcc ccatgttccc tttttctct aaagtcccct gacatcagcc      1365
ctcccaactc ctaagaggga ctacctatga gagtggggtt ctgaggtccc cctatgggga      1425
cagttccgtt cttgaagtgt cagtgttggg gaatatctgt ggcctatgag gcccatctca      1485
ggtttgggga tccccagtc cctatgatca gtgttgaggt acccccctgg gagagcctag      1545
tttctttgag gccccaggcc ctcttttaac tacctttgaa taggtgttat cctgtatatt      1605
atggaaataa agttccattt cctcaaaaaa aaaaaaaaaa a      1646

<210> 75
<211> 1963
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 274..753

<220>
<221> sig_peptide
<222> 274..324
<223> Von Heijne matrix
      score 4.4969823290892
      seq FAAFCYMLSLVLC/AA

<400> 75
cttcttcgat ttgcggacgg ttccctccag cgactctcga cacacgtttt cctgtcttcg      60
ccggagggcc gggctctggg tcgccggagc ctgcgggaat ccagcgctta ttcgctaacc      120
ctcgagtcgc ttcgctagct gtgcgccctc ctgggcacta gcctggagag gagcgtgcag      180
acgcggctcc ttggagggag tgcggtcctc tagggaggca tcgggctcct aggggcttct      240
tggcgtgtgt ggtgggattg gggtcgcgcg gcc atg gcc ttc act ttc gct gcg      294
              Met Ala Phe Thr Phe Ala Ala
              -15
ttc tgc tac atg ctg tct ctg gtg ctg tgc gct cgc ctc atc ttc ttc      342
Phe Cys Tyr Met Leu Ser Leu Val Leu Cys Ala Ala Leu Ile Phe Phe

```

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-------------|-----|-----|-------------|-----|-----|-------------|-----|-----|-------------|------|---------|-------------|-----|-----|-------------|-----|--|------|--|--|--|---|--|--|--|--|--|--|--|--|--|--|---|--|--|--|--|--|--|--|--|--|--|--|
| -10 | | | | | | | | | | | -5 | | | | | | | | | | | 1 | | | | | | | | | | | 5 | | | | | | | | | | | |
| gcc | atc | tgg | cac | ata | att | gcc | ttt | gat | gag | tta | agg | aca | gat | ttt | aag | 390 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala | Ile | Trp | His | Ile | Ile | Ala | Phe | Asp | Glu | Leu | Arg | Thr | Asp | Phe | Lys | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 10 | | | | | | 15 | | | | | | 20 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| agc | ccc | ata | gac | cag | tgc | aat | cct | ggt | cat | gcg | agg | gaa | cgg | ttg | agg | 438 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ser | Pro | Ile | Asp | Gln | Cys | Asn | Pro | Val | His | Ala | Arg | Glu | Arg | Leu | Arg | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 25 | | | | | | 30 | | | | | | 35 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| aac | atc | gag | cgc | atc | tgc | ttc | ctt | ctg | cga | aag | ctg | gtg | ctg | cca | gaa | 486 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asn | Ile | Glu | Arg | Ile | Cys | Phe | Leu | Leu | Arg | Lys | Leu | Val | Leu | Pro | Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 40 | | | | | | 45 | | | | | | 50 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tac | tcc | atc | cat | agc | ctc | ttc | tgc | att | atg | ttc | ctg | tgt | gcg | caa | gag | 534 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Tyr | Ser | Ile | His | Ser | Leu | Phe | Cys | Ile | Met | Phe | Leu | Cys | Ala | Gln | Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 55 | | | | | | 60 | | | | | | 65 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tgg | ctc | acg | ctg | ggg | ctg | aat | gtc | cct | cta | ctt | ttc | tat | cac | ttc | tgg | 582 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Trp | Leu | Thr | Leu | Gly | Leu | Asn | Val | Pro | Leu | Leu | Phe | Tyr | His | Phe | Trp | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 75 | | | | | | 80 | | | | | | 85 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| agg | tat | ttc | cac | tgt | cca | gca | gat | agc | tca | gaa | cta | gcc | tac | gac | cca | 630 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arg | Tyr | Phe | His | Cys | Pro | Ala | Asp | Ser | Ser | Glu | Leu | Ala | Tyr | Asp | Pro | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 90 | | | | | | 95 | | | | | | 100 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ccg | gtg | gtc | atg | aat | ccc | gac | act | ttg | agt | tac | tgt | cag | aag | gag | gcc | 678 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Pro | Val | Val | Met | Asn | Pro | Asp | Thr | Leu | Ser | Tyr | Cys | Gln | Lys | Glu | Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 105 | | | | | | 110 | | | | | | 115 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tgg | tgt | aag | ctg | gcc | ttc | tat | ctc | ctc | tcc | ttc | ttc | tac | tac | ctt | tac | 726 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Trp | Cys | Lys | Leu | Ala | Phe | Tyr | Leu | Leu | Ser | Phe | Phe | Tyr | Tyr | Leu | Tyr | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 120 | | | | | | 125 | | | | | | 130 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tgc | atg | atc | tac | act | tta | gtg | agc | tct | taacgc | aaag | accatgc | caca | | | | 773 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Cys | Met | Ile | Tyr | Thr | Leu | Val | Ser | Ser | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 135 | | | | | | 140 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tcatcagaga | | | ctgagatggg | | | agaggcctga | | | gacggagagg | | | tgcatttctg | | | ctgggtgactg | | | 833 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gaggagggac | | | cagaatgagg | | | atacgtgaga | | | aatagacccg | | | gcaggcagtc | | | agactgaatg | | | 893 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ggagctggaa | | | tcacgcagca | | | gttgggagcc | | | gagttaaccc | | | tgcggtgtctg | | | tgtcacccctg | | | 953 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tttgtcaatc | | | tttggcattc | | | gaattccaca | | | cacgggggtcc | | | tagagccctt | | | ctgagcatca | | | 1013 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gtgggtgtggg | | | ggagtaggtg | | | acgaaacact | | | agacctctcc | | | tgagagagaa | | | ttgctgcttc | | | 1073 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ctgaatccac | | | ttcattgaac | | | agcaccttgc | | | aagttcaaat | | | gagttccttg | | | gagcggaggc | | | 1133 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tggaaggcca | | | caaggtgctt | | | gctaaggaac | | | agaatgaccc | | | agagtcaagg | | | ccaagtctgc | | | 1193 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| agggacctgt | | | tgaaagcctc | | | gagaatgtct | | | tggctgcccc | | | agactcttgt | | | tgccctttctt | | | 1253 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ccaagccatg | | | gccatgccct | | | ttttctcaaa | | | tgggaggggc | | | tggaggggtgt | | | gtgggatttg | | | 1313 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tccttcagctg | | | caaccagcct | | | tgagcctgct | | | gggctatttt | | | cagctgagga | | | ggggtaatat | | | 1373 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| aggaaaaatg | | | cattttttgaa | | | acgttttgcaa | | | catgatcaag | | | gtgttagttc | | | tccaccacac | | | 1433 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| aagttgtatt | | | cttctttttgc | | | cacctcaaac | | | catcacagag | | | tctttaaatg | | | caaatacaatt | | | 1493 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ggtcaatgct | | | agtcaaagct | | | atgttcttac | | | aaaaacccca | | | gacagctcag | | | agctcagaaa | | | 1553 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| atcctgtgga | | | gtggctgctc | | | tgtaccgtgg | | | gcatccggca | | | gccaggaagt | | | gagacaacat | | | 1613 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| aattataact | | | ttgttttatg | | | atgctgcatc | | | atttgtactg | | | tttaggtcga | | | cgtgaggaca | | | 1673 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tcatcttatt | | | tagaattttc | | | cgtttggcat | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```
<210> 76
<211> 1757
<212> DNA
<213> Homo sapiens
```

<220>
 <221> sig_peptide
 <222> 191..274
 <223> Von Heijne matrix
 score 4.02941490119842
 seq GXLLEPFVHQVGG/HS

```

<400> 76
catttttggtg cgagagaaac aataggacgg aaacgccgag gaacccggct gaggcggcag      60
cagagcatcc tggccagaac aagccaagga gccaagacga gagggacaca ctgacaaaaca      120
acagacagaa gacgtactgg ccgctggact ccgctgcctc ccccatctcc ccgccatctg      180
cgccccggagg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc      229
          Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg
                    -25                                -20

gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac      277
Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His
-15          -10          -5          1

tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc      325
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val
          5          10          15

cca agg gaa cat cag ttc tac gag acc ctc cct tct gag atg cgc aaa      373
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys
          20          25          30

ttc act ccc cag tac aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat      421
Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp
          35          40          45

gaa gac agg aac ttg tgt cta ata gca tat cca ttg aaa ggg gac cat      469
Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His
          50          55          60          65

gga att gtg gac att gta gat aat tca gac tgt gaa cca aaa agt aag      517
Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys
          70          75          80

ctc cta agg tgg aca aca aac aaa aaa cat cat gtc tta gaa aca gaa      565
Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu
          85          90          95

aag acc cct aag gac tgg gtg cgt cag cac cgt aaa gag gag aaa atg      613
Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met
          100          105          110

aag agc cat aag tta gaa gaa gaa ttt gag tgg cta aag aaa tct gaa      661
Lys Ser His Lys Leu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu
          115          120          125

gtc ttg tac tac act gta gag aag aag ggg aat ata agt tcc cag ctt      709
Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu
          130          135          140          145

aaa cac tat aac cct tgg agc atg aaa tgt cac cag caa cag tta cag      757
Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln
          150          155          160

aga atg aag gag aat gca aag cat cgg aac cag tac aaa ttt atc tta      805
Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu
          165          170          175

ctg gaa aac ctg act tcc cgc tat gag gtg cct tgt gtc ctt gac ctc      853
Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu
          180          185          190

aag atg ggc aca cga caa cat ggt gat gat gct tca gag gag aag gca      901
Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala
          195          200          205

gcc aac cag atc cga aaa tgt cag cag agc aca tct gca gtc att ggt      949
Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly
  
```

| | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|------|
| 210 | | 215 | | 220 | | 225 | |
| gtg cgt gtg tgt ggc atg cag gtg tac caa gca ggc agt ggg cag ctc | | | | | | | 997 |
| Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu | | | | | | | |
| | 230 | | 235 | | 240 | | |
| atg ttc atg aac aag tac cat gga cgg aag cta tcg gtg cag ggc ttc | | | | | | | 1045 |
| Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe | | | | | | | |
| | 245 | | 250 | | 255 | | |
| aag gag gca ctt ttc cag ttc ttc cac aat ggg cgg tac ctg cgc cgt | | | | | | | 1093 |
| Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg | | | | | | | |
| | 260 | | 265 | | 270 | | |
| gaa ctc ctg ggc cct gtg ctc aag aag ctg act gag ctc aag gca gtg | | | | | | | 1141 |
| Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val | | | | | | | |
| | 275 | | 280 | | 285 | | |
| ttg gag cga cag gag tcc tac cgc ttc tac tca agc tcc ctg ctg gtc | | | | | | | 1189 |
| Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val | | | | | | | |
| | 290 | | 295 | | 300 | | 305 |
| att tat gat ggc aag gag cgg ccc gaa gtg gtc ctg gac tca gat gct | | | | | | | 1237 |
| Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala | | | | | | | |
| | 310 | | 315 | | 320 | | |
| gag gat ttg gag gac ctg tca gag gaa tca gct gat gag tct gct ggt | | | | | | | 1285 |
| Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly | | | | | | | |
| | 325 | | 330 | | 335 | | |
| gcc tat gcc tac aaa ccc atc ggc gcc agc tct gta gat gtg cgc atg | | | | | | | 1333 |
| Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met | | | | | | | |
| | 340 | | 345 | | 350 | | |
| atc gac ttt gca cac acc acc tgc agg ctg tat ggc gag gac acc gtg | | | | | | | 1381 |
| Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val | | | | | | | |
| | 355 | | 360 | | 365 | | |
| gtg cat gag ggc cag gat gct ggc tat atc ttc ggg ctc cag agc ctg | | | | | | | 1429 |
| Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu | | | | | | | |
| | 370 | | 375 | | 380 | | 385 |
| ata gac att gtc aca gag ata agt gag gag agt ggg gag tgagcttgct | | | | | | | 1478 |
| Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly Glu | | | | | | | |
| | 390 | | 395 | | | | |
| agctgctcca gtacttgaga gcgactctgt gtcccaggca cagctgtgct gcgtcaggga | | | | | | | 1538 |
| ggaagccagt atggccagggt ggtggctcct gcagcctgga gctgatgtgc agtggcctct | | | | | | | 1598 |
| gtgagcccca gcctgagcca gtcccagctg tgcttgaggat ctttatattat tttaactatt | | | | | | | 1658 |
| tcttcaacat tccacatttg atgatgatac ctctttcttc cctgagtgtg tatgtttctaa | | | | | | | 1718 |
| tacaaatctt tttgtttatt gtaaaaaaaaa aaaaaaaaaa | | | | | | | 1757 |

<210> 77
 <211> 2027
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..950

<220>
 <221> sig_peptide
 <222> 48..107
 <223> Von Heijne matrix
 score 6.64507667657896
 seq LLPLLSLLVGAWL/KL

<400> 77
 atgcgcagcg gggccgtggg tgtacgcggc gcagcgcggc agtcctg atg gcc cgg 56

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

```

                275                280
aggagaaaaag ccttctaggg tcaactgtcat tccctggcca tgttgcaaac agcgcaattc 1030
caagctcgag agcttcagcc tcaggaaaaga acttcccctt ccctgtctcc catcccctctg 1090
tggcaggcgc ctctcaccag ggcaggagag gactcagcct cctgtgtttt ggagaagggg 1150
cccaatgtgt gttgacgatg gctggggggcc aggtgtttct gttagaggcc aagtattatt 1210
gacacaggat tgcaaacaca caaacaattg gaacagagca ctctgaaagg ccatttttta 1270
agcattttta aatctattct ctcccccttt ctccctggat gattcaggaa gctgacattg 1330
tttcctcaag gcagaatttt cctgggttctg tttcttcagc cagttgctgt ggaaggagaa 1390
tgctttcttt gtggcctcat ctgtggtttc gtgtccctct gaaggaaact agtttcact 1450
gtgtaacagg cagacatgta actattttaa gcacagttca gtccataaag ggtctggggag 1510
aaccagatga tgtactaggt gaagcattgc attgtgggaa tcacaaagca aatagtactc 1570
cagaaagaca aatatcagaa gcttcctatt cttttttttt tttggagaca tttggagaca 1630
gggtctttct ctggtgcca ggctagagt cactgggtgat cacggctcac tctagccttg 1690
aattcctggg cccaagcaat tctcccact cagcctcctg agtagctggg actacaagtg 1750
tgcaccacca tgctgggcta attttttgaa tttttgtagt gatgggatct cgctctgttg 1810
cccagggttg tctcgaactc ctggcctcaa gcgatcctcc cacctcgacc tcccaaagtg 1870
ctgggattac aggtgtgagc cacctcgctt gggccccctt ctccatatgc ctccaaaaac 1930
atgtccctgg agagtagcct gctcccacac tgtcactgga tgtcatgggg ccaataaaat 1990
ctcctgcaat tgtgtatctc aaaaaaaaaa aaaaaaaa 2027

<210> 78
<211> 1880
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 156..512

<220>
<221> sig_peptide
<222> 156..206
<223> Von Heijne matrix
      score 3.55618791452243
      seq WLTAVASLLPSPG/NS

<400> 78
atatacaggt ggcagctctc gtcccctgag agcggggcgaa ggccagggtc ccacactcgc 60
agcgtctgca cggcgctcgg gacctccctc gtccactgct tgagttccag aggtgggtgc 120
ttccctgtcc tgaacttcag agtgcgagat cataa atg ggt tcc ggc tgg ctt 173
                               Met Gly Ser Gly Trp Leu
                               -15

act gca gta gcc tcg ctc ctc ccc agc ccc ggt aac tcc gag cta ccc 221
Thr Ala Val Ala Ser Leu Leu Pro Ser Pro Gly Asn Ser Glu Leu Pro
-10 -5 1 5
gtc cag gcc ctc ggg cgt cgc ggg ggc agg gac tgg gcg cgg aac gag 269
Val Gln Ala Leu Gly Arg Arg Gly Gly Arg Asp Trp Ala Arg Asn Glu
10 15 20
gca ggg agg gac ctg gaa aaa cca ccc aga ttg cat tgc agt ggg cga 317
Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg Leu His Cys Ser Gly Arg
25 30 35
ggc cgc ctg gag gag ccg gtt ccc cct aac cac ctc ccc gtg ggg ctc 365
Gly Arg Leu Glu Glu Pro Val Pro Pro Asn His Leu Pro Val Gly Leu
40 45 50
tcg gtg cgc ggt tcc cag gtg ctc agc tct gct ggg ccc agg agg tgc 413
Ser Val Arg Gly Ser Gln Val Leu Ser Ser Ala Gly Pro Arg Arg Cys
55 60 65
cgc ctc aca ggg acg cgg aac ccc gtg cgt ggc ccc cgc cgg gtg gaa 461
```

```

Arg Leu Thr Gly Thr Arg Asn Pro Val Arg Gly Pro Arg Arg Val Glu
70          75          80          85
cag ata gcg cgg ggc ggt ccg gag gct cgt cgc caa gca ggt gac tct      509
Gln Ile Ala Arg Gly Pro Glu Ala Arg Arg Gln Ala Gly Asp Ser
          90          95          100
tgc tgaaaaagtg gttggaacac ttaaggaaac ccggcccccgc ctgtttctttc      562
Cys
taggtctttg gagtttggat taatcatttg tgtagcccg ttaggataaac cgaagacttt      622
attaaatcag cgcgtttaac aggaattccg cagtagtatac cacattagaa tcttgagtct      682
tggagttgaa catattcaca cagacttgcc ttcttcctgt ttagtttatg ccttggtgtc      742
cgttattgga acgctaagct tgtgggagtt gtttacatcc tactgctcaa ggtcatcgct      802
aaggtgtgat ttttcacaaa aagaatttgc aacctccggc atgaatgact taagggaagt      862
ctaatacccg tttctgattt tttttttttt ttaatttaaa agttaatctt tctgggccgg      922
gcgcggtggc tcacgcctgt aatcccagca ctttgggagg ccgaggcgga tcacgaggtc      982
aggagttcga gaccagcctg accaacaatgg tgaacccccg tctctactaa aaacacaaaa    1042
attagccggg cggggtggcg cgcacctgta atcccagctg ctccgggaggc tgaggcagga    1102
gaatcgcttg aacctgggag gcgggggggt gcagtgagcc gagatctggc cattgcactc    1162
cagcgtgggc aacagagtga gactccatct caaaaaaaaaa ggttaatctt tccaactaga    1222
ttttcaagga tgaggatttt gttgttgttg ttgttgttgt tctcaaatgt attcccaggg    1282
cttggaaacag agcctgacat atactaggca ctcaacaaat atttgttgaa tgattgtaat    1342
gagtaacacc cattttttgca gatctttgtc ttctgagcct agggcatagg tcatcactgc    1402
aggggtgaga ttgtcaaaat gggagcttac aggtaattta agacttaaat gtttaaagag    1462
tatgtgctca ttcttcaaca aacttacttt tgtaaatta aaatggtaaa atgtggtgga    1522
ggggttgga tatatgtaat tcaagacagt tctgaatata aaaatgtttt actgtctatc    1582
accaccatct ataaatctaa ttcactaagg ataactctgt taaggtggct ggaaagaacc    1642
ttgaggagag aggcttattt aagtattggc tcaggaccac acctaaaatt ctcaaaacgt    1702
tgagattctg ttgttttgtt ttttaagcgc agagacccaa gttgaggaac agcctataaa    1762
ataactggcc tgtactctta catacatgaa agccatcaaa gacaaaagact gaagaagaac    1822
ttttgcagat taaaggactt taagagacat gatcctgaac caaaaaaaaaa aaaaaaaaaa    1880

<210> 79
<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..351

<220>
<221> sig_peptide
<222> 67..183
<223> Von Heijne matrix
      score 10.6473524146908
      seq FLCALCSFCPISA/AS

<400> 79
ctgattcttc gaaatgatat aagtcctgag ggcttcagtc ccattcgcgc actcatactt      60
gcaatc atg gac tac agc cgt gtc ttt cag ggt gtg ttc ttc acc ttc      108
      Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe
          -35          -30
aag cat gct ttt gct gat ggt gct tgg gat ctt tca ttt ctc tgt gct      156
Lys His Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala
-25          -20          -15          -10
ctt tgc agt ttc tgc cca atc tca gct gcc tct ggc aga cct tac agg      204
Leu Cys Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg
          -5          1          5
tac ttg gaa ttc tgg aga tta tac ctg tct cct agt tcc atg gaa aat      252

```

| | | | | | | | | | | | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Leu | Glu | Phe | Trp | Arg | Leu | Tyr | Leu | Ser | Pro | Ser | Ser | Met | Glu | Asn | |
| | 10 | | | | | 15 | | | | | 20 | | | | | |
| gga | ggt | caa | aaa | ttc | cac | gaa | act | ttt | ttc | att | gtc | ttt | ttg | ctt | ttg | 300 |
| Gly | Val | Gln | Lys | Phe | His | Glu | Thr | Phe | Phe | Ile | Val | Phe | Leu | Leu | Leu | |
| | 25 | | | | | 30 | | | | | 35 | | | | | |
| ttt | gat | atc | gag | agg | aaa | gga | aaa | agt | tct | gtt | tgt | cca | ttt | tgt | tac | 348 |
| Phe | Asp | Ile | Glu | Arg | Lys | Gly | Lys | Ser | Ser | Val | Cys | Pro | Phe | Cys | Tyr | |
| 40 | | | | | 45 | | | | | 50 | | | | 55 | | |
| aga | taaggaaagt | ggtttcacaa | aggttaagca | acttgttcag | tgttacccag | | | | | | | | | | | 401 |
| Arg | | | | | | | | | | | | | | | | |
| caaagagcag | aatgattttc | aacatttcagt | ttaaaagtcg | gcgggggggca | gtggctcaca | | | | | | | | | | | 461 |
| cctgtaatat | cagcaacttg | ggaggccaag | gtggtacggc | cgcttgaagc | caaggagttc | | | | | | | | | | | 521 |
| aagaccagcc | tggtcaacat | agcaaaacct | tgtctttaca | aaaagtaaaa | aaaaaaaaaa | | | | | | | | | | | 581 |
| aaa | | | | | | | | | | | | | | | | 584 |

<210> 80
 <211> 1351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 259..831

<220>
 <221> sig_peptide
 <222> 259..375
 <223> Von Heijne matrix
 score 5.809301698725
 seq FCVCVIAIGVVQA/LI

| | | | | | | | | | | | | | | | | | |
|-------------|-------------|-------------|-------------|-------------|------------|--|--|--|--|--|--|--|--|--|--|--|-----|
| <400> 80 | | | | | | | | | | | | | | | | | |
| aagctcccg | ccgggctgac | tcaagcggag | gcgcgcggaa | cagtcgccga | ggcgattccc | | | | | | | | | | | | 60 |
| gcccagcagt | tcgacagaag | tgtacagagg | cttctggcaa | cacggattgc | cgtctacctg | | | | | | | | | | | | 120 |
| atgacctttc | tcctcgtgac | agtggcctgg | gcagcacaca | caaggttggt | ccaagttggt | | | | | | | | | | | | 180 |
| gggaaaacag | acgacacact | tgccctgctc | aacctggccg | catcatggct | gtgatgccct | | | | | | | | | | | | 240 |
| ccctccctcc | aggcctgc | atg atg acc | atc acc ttc | ctg cct tac | acg ttt | | | | | | | | | | | | 291 |
| | | Met Met Thr | Ile Thr Phe | Leu Pro Tyr | Thr Phe | | | | | | | | | | | | |
| | | | -35 | | -30 | | | | | | | | | | | | |
| tcg tta atg | gtg acc ttc | cct gat gtg | cct ctg ggc | atc ttc ttg | ttc | | | | | | | | | | | | 339 |
| Ser Leu Met | Val Thr Phe | Pro Asp Val | Pro Leu Gly | Ile Phe Leu | Phe | | | | | | | | | | | | |
| | -25 | | -20 | | -15 | | | | | | | | | | | | |
| tgt gtg tgt | gtg atc gcc | atc ggg gtc | gtg cag gca | ctg att gtg | ggg | | | | | | | | | | | | 387 |
| Cys Val Cys | Val Ile Ala | Ile Gly Val | Val Gln Ala | Leu Ile Val | Gly | | | | | | | | | | | | |
| | -10 | | -5 | | 1 | | | | | | | | | | | | |
| tac gca ttc | cac ttc ccg | cac ctg ctg | agc ccg cag | atc cag cgc | tct | | | | | | | | | | | | 435 |
| Tyr Ala Phe | His Phe Pro | His Leu Leu | Ser Pro Gln | Ile Gln Arg | Ser | | | | | | | | | | | | |
| 5 | | 10 | | 15 | 20 | | | | | | | | | | | | |
| gcc cac agg | gct ctg tac | cga cga cac | gtc ctg ggc | atc gtc ctc | caa | | | | | | | | | | | | 483 |
| Ala His Arg | Ala Leu Tyr | Arg Arg His | Val Leu Gly | Ile Val Leu | Gln | | | | | | | | | | | | |
| | 25 | | 30 | | 35 | | | | | | | | | | | | |
| ggc ccg gcc | ctg tgc ttt | gca gcg gcc | atc ttc tct | ctc ttc ttt | gtc | | | | | | | | | | | | 531 |
| Gly Pro Ala | Leu Cys Phe | Ala Ala Ala | Ile Phe Ser | Leu Phe Phe | Val | | | | | | | | | | | | |
| | 40 | | 45 | | 50 | | | | | | | | | | | | |
| ccc ttg tct | tac ctg ctg | atg gtg act | gtc atc ctc | ctc ccc tat | gtc | | | | | | | | | | | | 579 |
| Pro Leu Ser | Tyr Leu Leu | Met Val Thr | Val Ile Leu | Leu Pro Tyr | Val | | | | | | | | | | | | |
| | 55 | | 60 | | 65 | | | | | | | | | | | | |
| agc aag gtc | acc ggc tgg | tgc aga gac | agg ctc ctg | ggc cac agg | gag | | | | | | | | | | | | 627 |

```

Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu
 70          75          80
ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac gag cca      675
Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro
85          90          95          100
ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac gcc atc      723
Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile
          105          110          115
gtg gcc acg ctt ctc atc ctg gac atc tgc ccc tcc tgc tcc ctt tgg      771
Val Ala Thr Leu Leu Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp
          120          125          130
ctg gct gtt gct tcc ttc cag cgt ctg ctc ctc cgc ggc ctc atc tgc      819
Leu Ala Val Ala Ser Phe Gln Arg Leu Leu Arg Gly Leu Ile Cys
          135          140          145
ctc ttc gtc tgt tagagcgcgc gtctcgtctc agtcgtcacg tttttggttt      871
Leu Phe Val Cys
          150
ttgtgggggtt tttttttttt tttttttttg agacagtcct gctgtgtcgc ccaggctgga      931
gtatagtggc tcaagctcag ctcaactgcaa cctccgcctc ccaggttcaa gcaattctcc      991
tgctcagcc tccaagtag ttgggattac aagcaccac caccatgccc agctaacttt      1051
ttgcattttt aatagagatg aggtttcacc aagttggcca ggctgggtctt gaactcctga      1111
cctcagggtga tctgccacc tcggcctccc aaagtgtcgg gattacaggt gtaagccacc      1171
gtgcccggcc atcgtaatgt ttgaatttgc ttttttacat cttccatcct tttggagtgt      1231
cttgttccct cgtcatagtt cagcactgtg accaccttgg ggtagacac tatggtttta      1291
tatcctgtac ttgatattct cgagtccaag tctcctgatg ctctcaaaaa aaaaaaaaaa      1351

<210> 81
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..377

<220>
<221> sig_peptide
<222> 111..233
<223> Von Heijne matrix
      score 5.26415334394122
      seq LWFLAQIPSRVAG/SL

<400> 81
aaaccgaaac cagcgctcca aacaattggg acccgggatc ttatgccagt gaggctgtgc      60
tgcggtctgag cgggcctccc atccctctta aaagagttag gcatttagcc atg cct      116
                                     Met Pro
                                     -40
ccc acc cgg gac cct ttc cag cag cct aca tta gat aac gat gat tcc      164
Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp Asp Ser
          -35          -30          -25
tac tta gga gaa ctg cgg gct tcc aag gta ctg tgg ttt ctt gcg cag      212
Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu Ala Gln
          -20          -15          -10
att ccc agt agg gtc gcc ggt agt ctt ctt tct gtc tgt gtg atg agc      260
Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val Met Ser
          -5          1          5
aga gat ggt aac ata aag gac tct ggt gaa gac act cag tcg ggt acc      308
Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser Gly Thr

```

| | | | | |
|--|-----|----|----|--|
| 10 | 15 | 20 | 25 | |
| agg gaa gtc tgt ttt ctg cct gcc tcc cta tct cca tat tca agt cgg | 356 | | | |
| Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser Ser Arg | | | | |
| 30 35 40 | | | | |
| cta acg ttt cag agg cgt ttt tgagcagagg aaagtagagt tctagtctag | 407 | | | |
| Leu Thr Phe Gln Arg Arg Phe | | | | |
| 45 | | | | |
| aggaacaagg ggctctggca gctcaaatca attaaccaag atccaattcc ctggagaatt | 467 | | | |
| tttaaccct cccactccac ccatcacttg cctggctaac atcagacact ggatcaaccc | 527 | | | |
| taaaaaggag tccatccaca gcatccaagg atccatagtg tcccctcaca ctgcagccac | 587 | | | |
| caatggaggc tactcccgaa agaaagatgg tggcttcttc tccacctagt gttgacagat | 647 | | | |
| ccctgaacta attatagtga aacatactgc ggcccacttc cattaatatag atttgtgcaa | 707 | | | |
| aaaaaaaaaaa aaa | 720 | | | |

<210> 82
 <211> 1029
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 223..432

<220>
 <221> sig_peptide
 <222> 223..336
 <223> Von Heijne matrix
 score 4.17665217008018
 seq LVNVLFFFFTPLMT/LV

| | |
|---|-----|
| <400> 82 | |
| gtttttgtat tggaagcagt tgtttggcct tgctgagcaa acgtctatgc cttctccatt | 60 |
| acatccaaag gagaatagcc ccatgtgaag aatggaatca gtagatgttt ggtcgctgta | 120 |
| ccatatccac tcctaggata caacaagagc aagcccaatt ctcttggtgg tgtgggcagt | 180 |
| cggcttgcac cacgtaccta tctcagctct ttttggaagc tt atg tcc tcc cca | 234 |
| Met Ser Ser Pro | |
| -35 | |
| caa ctt cca gct ttc tta tgg gac aag ggt aca ctc acc act gcc ata | 282 |
| Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile | |
| -30 -25 -20 | |
| tct aat cct gct tgc ctg gta aat gtt ctc ttc ttc ttt aca ccc ctg | 330 |
| Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe Phe Thr Pro Leu | |
| -15 -10 -5 | |
| atg act ctg gtc act cta ctc atc ctg gtc tgg aaa gta acc aaa gac | 378 |
| Met Thr Leu Val Thr Leu Ile Leu Val Trp Lys Val Thr Lys Asp | |
| 1 5 10 | |
| aaa agc aac aag aac aga gag aca cac cca aga aag gag gca aca tgg | 426 |
| Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp | |
| 15 20 25 30 | |
| ctg cca taaagatctg gatctcttgg tggggactcc actgaggtga agacctgatt | 482 |
| Leu Pro | |
| gtacaagaga ggcacggcca ctggagctgt ctcagagccc agagccaggg gagccagagc | 542 |
| tgcttttagcc accctgttcc tccattgccat gatgtccccc caggcctcat ttccttcctc | 602 |
| tgccaccatc cctcttataa tgcactcctc ctgcggttct ttggtctgtc ccagcttctg | 662 |
| agtttgaatg tctttttttt tttttttttt tttttgkga tcttcaagac tgaaatagta | 722 |
| aatggctctt gatttctgca ctaacagagg aaagaaacaa gtacatggaa aagtaaaaat | 782 |
| tgattacaaa gcctaaattt tcctctataa attgggcatg tgctgactgt gggatattga | 842 |
| aattattggg agctcacagc atctcaagtt atataatgaa gctattcttg aagctcattt | 902 |

ccagaagatc cttaaaatga aatggctcac tctctgctga attaatattgg agcaagttaa 962
ctcctttttc aaatgaaatc caaattaaaag aggcagtttt ttttgaaaaa ccaaaaaaaa 1022
aaaaaaa 1029

<210> 83
<211> 1788
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 769..1272

<220>
<221> sig_peptide
<222> 769..843
<223> Von Heijne matrix
score 5.65786415517206
seq AAHLLVVILPANA/AL

<400> 83
ttgggcagaa aaattcaagc aggagattgt atttcttttg gagttgtacg atttccttta 60
ttatttgaac tgcagtaaag aaagctggga tgggctcctc tagggatact tccagatccc 120
tgggcgggttg tagccctggc tcctctttta atggatttgg tttcaaagac gatcatctcc 180
gtcttctcgg atgtcatagt gccactgac atctccagct cctggccacc ctgggctttc 240
tccacttttg cctctatgtt ttgcttctcc accgtcttag ccacgatac tacctctctg 300
tcatgtgatg tgacccttgt ttttgaacca ggagtggccc tgaggctcct taaaaaagag 360
ctgatcttac tggcttttct ttgtaaagct cctgtgctag atgcagattg gttcttcccc 420
agttcctgag ttgttctcga ctcttttttg gtggagctgt gggaggagct cttgcgagag 480
gagccatgtc gcttgccctc tacgttgctg tacccttttt cttttttgtc atctctcgtg 540
tttttatggc cagatgcgga ccggtgggaa gacgctttct gattcttgtc ccccgctctc 600
ctgcgggtgac tttaacctgc cttgcggtga tgagaacttt tcctactggg atgtctgtcc 660
ttcttttctc ttcttttctt gttttcattc cagacttcag cactgggctg ggaaactttc 720
tggtttccat ctctttcact catgtagcct tcgctttgca aggtggag atg agg ggt 777
Met Arg Gly
-25
ccc act gct ggt cct tca gtt ctt tct gct gca cac ttg ctg gtc gta 825
Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu Leu Val Val
-20 -15 -10
ata ctg cct gca aac gcc gca ctc aag ctg ctg tct tgg gag aga ctg 873
Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp Glu Arg Leu
-5 1 5 10
gcg gcc ccc gcc atc gag gtg gaa gta cct tcc aag gag gtg ctt gca 921
Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu Val Leu Ala
15 20 25
gca ccc acc aag gcc aag cta ata ccc tct gag gat atg ttg gca gca 969
Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met Leu Ala Ala
30 35 40
cct gcc atg gac ttg ctg gat tca ttt tct cct gga ttt ttg ata gct 1017
Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe Leu Ile Ala
45 50 55
gct ccc gcc agc gct gtg atc act tgg cct ggg cct gca gat ttg gtt 1065
Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala Asp Leu Val
60 65 70
gtt gct atg ctc ata gca cct gtt gca gga ctc att gct gcc cct gct 1113
Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala
75 80 85 90
att gcc aca tct gtt cta ggt cct gtt gct gtt cct gcc act gcc atg 1161

```

Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala Thr Ala Met
          95                      100                      105
cca cct gct gtc ctt gct gct cct cct tca gca gcc cct gga gtg ctc      1209
Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro Gly Val Leu
          110                      115                      120
gtg gat gga gaa gcc gca cta gcc gtt ccg tgg gag gca tgt tgg att      1257
Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala Cys Trp Ile
          125                      130                      135
ccc tct ccc cca gca taagcagaag aggtggctgc agatacatca caaggcttgt      1312
Pro Ser Pro Pro Ala
          140
agagcccagt ctcaactctga tcccccttctc tgtggagctc tgcagcctat accaagggga      1372
agagaaacag atgagattga gatgactgaa agggagatca gaactttcta ctccctctctt      1432
atcctggagt taattcaagg gcttataatt agaagaacct gggtcgggtg tggaggctca      1492
cgctgtaat cccaacactt tgggaggcca aggagggcag atcgcttgag gccaggagtt      1552
caagaccagc cttgccaaca tagcaaaacc ccgactctac taaaaataca aaaaattagc      1612
tggacaggat ggcgcagccc tgtaatccca gctactcagt aggctgaggt aggagtatcg      1672
cttgaactcg gatggcggag gctgcagtga gccaaagactg cgccactcca ctgcactcca      1732
gcctgggcaa cagagtgaga cactgttttaa aaaaaagaaa gaaaaaaaaa aaaaaa      1788

<210> 84
<211> 805
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..527

<220>
<221> sig_peptide
<222> 30..74
<223> Von Heijne matrix
      score 8.68924532952647
      seq PLLIICLLPAIEG/KN

<400> 84
actggggcac agtaggagga acccagaag atg ctg cct ctc ctg atc atc tgt      53
                        Met Leu Pro Leu Leu Ile Ile Cys
                        -15                      -10
ctc ctg cct gcc att gaa ggg aag aac tgc ctc cgc tgc tgg cca gaa      101
Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
          -5                      1                      5
ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca      149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
          10                      15                      20                      25
ggg cca ccc aca gaa ctt tct caa aat cgt gac cat ttg gaa gaa gaa      197
Gly Pro Pro Thr Glu Leu Ser Gln Asn Arg Asp His Leu Glu Glu Glu
          30                      35                      40
aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg tta cga      245
Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr Leu Arg
          45                      50                      55
gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag aat ctc      293
Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys Asn Leu
          60                      65                      70
ttt act gag agg ctg aat aag ata tct gat ggg ctg aag gag aag gac      341
Phe Thr Glu Arg Leu Asn Lys Ile Ser Asp Gly Leu Lys Glu Lys Asp
          75                      80                      85

```



```

ata cag tcc aca ctg aag gtc acc agc tgt gct gac tgc agg act cac      389
Ile Gln Ser Thr Leu Lys Val Thr Ser Cys Ala Asp Cys Arg Thr His
90                      95                      100                      105
ttc ctc tcc tgc aat gac ccc act ttc tgc cca gcc agg aac cgg cgg      437
Phe Leu Ser Cys Asn Asp Pro Thr Phe Cys Pro Ala Arg Asn Arg Arg
110                      115                      120
acc tcc ctg tgg gct gtg agt ctc agc agt gct cta ctc ctg gcc ata      485
Thr Ser Leu Trp Ala Val Ser Leu Ser Ser Ala Leu Leu Leu Ala Ile
125                      130                      135
gct gga gat gtt tct ttt act ggc aaa gga aga agg agg cag      527
Ala Gly Asp Val Ser Phe Thr Gly Lys Gly Arg Arg Arg Gln
140                      145                      150
taaagcagga acagggcagc ccgcatgtct tccagaagtg aacagaggcc gcagctacca      587
ccgtcacaaa gttcactcat ctctgggtcc cggtagcccc atccccccat accctccatc      647
ctgggtcctg gggcccaaaa gctctgaggc ctaggagact gcgctgtctc gtggtttgcc      707
tactctaca cctttgtaaa gagtctcttc attaaaaccc ctcttcataa aaaaaaaaaa      767
aaaaaaaaaa aaaaaaaaaa aataaaaaaa aaaaaaaa      805

<210> 85
<211> 814
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..506

<220>
<221> sig_peptide
<222> 39..83
<223> Von Heijne matrix
      score 5.91494342964539
      seq ILMLTFIICGLLT/RV

<400> 85
attcctcagg acacagagct tcctctctcc caggagcc atg aat atc ctg atg ctg      56
                        Met Asn Ile Leu Met Leu
                        -15                      -10
acc ttc att atc tgt ggg ttg cta act cgg gtg acc aaa ggt agc ttt      104
Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg Val Thr Lys Gly Ser Phe
                        -5                      1                      5
gaa ccc caa aaa tgt tgg aag aat aat gta gga cat tgc aga aga cga      152
Glu Pro Gln Lys Cys Trp Lys Asn Asn Val Gly His Cys Arg Arg Arg
10                      15                      20
tgt tta gat act gaa agg tac ata ctt ctt tgt agg aac aag cta tca      200
Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu Cys Arg Asn Lys Leu Ser
25                      30                      35
tgc tgc att tct ata ata tca cat gaa tat act cga cga cca gca ttt      248
Cys Cys Ile Ser Ile Ile Ser His Glu Tyr Thr Arg Arg Pro Ala Phe
40                      45                      50                      55
cct gtg att cac cta gag gat ata aca ttg gat tat agt gat gtg gac      296
Pro Val Ile His Leu Glu Asp Ile Thr Leu Asp Tyr Ser Asp Val Asp
60                      65                      70
tct ttt act ggt tcc cca gta tct atg ttg aat gat ctg ata aca ttt      344
Ser Phe Thr Gly Ser Pro Val Ser Met Leu Asn Asp Leu Ile Thr Phe
75                      80                      85
gac aca act aaa ttt gga gaa acc atg aca cct gag acc aat act cct      392
Asp Thr Thr Lys Phe Gly Glu Thr Met Thr Pro Glu Thr Asn Thr Pro

```

| | | | |
|---|-----|-----|-----|
| 90 | 95 | 100 | |
| gag act act atg cca cca tcc gag gcc act act ccc gag act act atg | | | 440 |
| Glu Thr Thr Met Pro Pro Ser Glu Ala Thr Thr Pro Glu Thr Thr Met | | | |
| 105 | 110 | 115 | |
| cca cca tct gag act gct act tcc gag act atg cca cca cct tct cag | | | 488 |
| Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr Met Pro Pro Pro Ser Gln | | | |
| 120 | 125 | 130 | 135 |
| aca gct ctt act cat aat taattaacat ttacttctgg tatggaacaa | | | 536 |
| Thr Ala Leu Thr His Asn | | | |
| 140 | | | |
| ctagaaatac tgctggaaat aatatccaaa gagctgattc taccaatcca atttcaccag | | | 596 |
| gaaaattcca tcagggattg gatgaccatg gggatggaca taattgctac taccaacaca | | | 656 |
| acagccaaga gattgacctt acaattagaa atgtgtagac agaaatgtat agaagatata | | | 716 |
| aggattctct taattggact taaattcttt atctgtcttc ctccgatgta ctcaaatata | | | 776 |
| tgagctaatt tttgtcttaa gtgaaaaaaaa aaaaaaaaaa | | | 814 |
| | | | |
| <210> 86 | | | |
| <211> 598 | | | |
| <212> DNA | | | |
| <213> Homo sapiens | | | |
| | | | |
| <220> | | | |
| <221> CDS | | | |
| <222> 115..429 | | | |
| | | | |
| <220> | | | |
| <221> sig_peptide | | | |
| <222> 115..210 | | | |
| <223> Von Heijne matrix | | | |
| score 8.2583062681354 | | | |
| seq LVAAMVLLSVVFC/LY | | | |
| | | | |
| <400> 86 | | | |
| attctaccag ctctggctga gcttgagctt ccaaaagtga gctgagctgt tcaaccttgg | | | 60 |
| atcttaatta ctcttagcag ggataattag gtccctcttt ctcagattac aggc atg | | | 117 |
| | | | Met |
| gca aag atg ttt gat ctc agg acg aag atc atg atc ggc atc gaa agc | | | 165 |
| Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu Ser | | | |
| -30 | -25 | -20 | |
| agc tta ctg gtt gcc gcg atg gtg ctc cta agt gtt gtg ttc tgt ctt | | | 213 |
| Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys Leu | | | |
| -15 | -10 | -5 | 1 |
| tac ttc aaa gta gct aag gca cta aaa gct gca aag gac cct gat gct | | | 261 |
| Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp Ala | | | |
| 5 | 10 | 15 | |
| gtg gct gta aaa aat cac aac cca gac aag gtg tgt tgg gcc acg aac | | | 309 |
| Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr Asn | | | |
| 20 | 25 | 30 | |
| agc cag gcc aaa gcc acc acc atg gag tct tgt cca tct ctc cag tgc | | | 357 |
| Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln Cys | | | |
| 35 | 40 | 45 | |
| tgt gaa ggt tgt aga atg cat gcc agt tct gat tcc ctg cca cct tgc | | | 405 |
| Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro Cys | | | |
| 50 | 55 | 60 | 65 |
| tgt tgt gac ata aat gag gcc ctc tgacttggga aagctgggca caaaaatctt | | | 459 |
| Cys Cys Asp Ile Asn Glu Gly Leu | | | |
| 70 | | | |
| catgagcaat atttctttct taatagaatg ttttattatt caagtcaagt tctagagtgt | | | 519 |

ttacatacta ttatataatg tacagtgtta ttttctgtac ttctgaataa atgtgcaata 579
 ttgcaaaaaa aaaaaaaa 598

<210> 87
 <211> 699
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 332..574

<220>
 <221> sig_peptide
 <222> 332..412
 <223> Von Heijne matrix
 score 7.96491294552426
 seq ILGLFCCLPLAIP/AV

<400> 87
 aatccccctgt ggttggtgat caaggaagag catagtgcc aacctaggtg ccctcctggg 60
 aatggtccag gagggcagga gtaggaggag gagtggtaga gtagagggga aatgatgaga 120
 gcagaaagga gagtctcgct ctgtcaccca ggctggagtg cagtggcagg atcttggtc 180
 acttcaacct ccacctcccg agttctgcct cagcctccca agtagctggg attacaggtc 240
 cagtcactcc acgcttcgag agtccaatta acaagagcaa gttctggtag aaagaagggtg 300
 actttattcc agagctcagg tgtttgaact g atg tct gat gag gat gaa tcc 352
 Met Ser Asp Glu Asp Glu Ser
 -25
 agc gac tac ctc tgc ctg tcc atc ctg ggc ctc ttc tgt tgc ctt ccc 400
 Ser Asp Tyr Leu Cys Leu Ser Ile Leu Gly Leu Phe Cys Cys Leu Pro
 -20 -15 -10 -5
 cta gcc atc cca gcc gtg atc ttt tct tgc ctg aca aag aac tac aat 448
 Leu Ala Ile Pro Ala Val Ile Phe Ser Cys Leu Thr Lys Asn Tyr Asn
 1 5 10
 aaa tcc agt gac tat gag ctg gca gcc aag acc tcc aaa caa gcc tac 496
 Lys Ser Ser Asp Tyr Glu Leu Ala Ala Lys Thr Ser Lys Gln Ala Tyr
 15 20 25
 tac tgg gcc atc gcg agc atc act gtg gga atc tta ggt acc atc ttg 544
 Tyr Trp Ala Ile Ala Ser Ile Thr Val Gly Ile Leu Gly Thr Ile Leu
 30 35 40
 tac acc tac ctg ata tac tta ctt aga ttg taaactgctt cccagctctt 594
 Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg Leu
 45 50
 gaacaaacca ccaaataat accacagtgc aattttaaaaa aaaaaaaaaa aaaaaaaaaa 654
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaaa 699

<210> 88
 <211> 905
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..417

<220>
 <221> sig_peptide
 <222> 133..213

<223> Von Heijne matrix
score 11.106948594338
seq LTSLILVTLISA/FV

<400> 88
atttccaggg agctgaggag ctgagggcag agctagcttt tggttatttg ggatgttatt 60
gccagtttcc tcccagggcc attgttacca cctgatcatt tgagtttttag tttctctagc 120
agatgctgac ta atg act gac cag gat cga atc atc aat tta gtt gtt ggc 171
Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly
-25 -20 -15
agc tta aca tcc tta ttg att cta gta acg ctg ata agt gct ttt gtt 219
Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val
-10 -5 1
ttc cct caa cta cct cca aaa ccg ttg aat ata ttc ttt gct gtc tgc 267
Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys
5 10 15
atc tct ttg agt agt att act gcc tgc ata atc tac tgg tat cga caa 315
Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln
20 25 30
gga gac tta gaa ccg aaa ttt aga aag cta att tac tat atc ata ttt 363
Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe
35 40 45 50
tct atc atc atg ttg tgt ata tgt gca aac ctg tac ttc cat gat gtg 411
Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val
55 60 65
gga agg tgaggctgcc aaggagaagt acttaccagg actcttcaaa atgatacatt 467
Gly Arg
aggacagtga gtaatttttg gataaggtat gctgaagaat ctctgcaga agtctgatac 527
atgatttttca tggttaattgt aaatgttaat tccctcttgc aaggagagaca tctcctagat 587
cactttgctt tttctttaag gagctgatgt tgcacctaaa cattccaacc cttaaagcta 647
aaacagcaca aaaaaatttc acttttgaaa tgaaattttt ataattgtat ggcaaaaggc 707
tatgtaaaaa caaatcttgc atcttaagac aaatattctt ttatttctgt taaactgaat 767
atacaattgt tccctaggca accaactttt gcttataact acaatttaat ttcacgttga 827
caaaacacag tgaaaagaca acttttgtgaa gatctaatta caataataaa taaaataatt 887
tacaaaaaaa aaaaaaaa 905

<210> 89
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 113..364

<220>
<221> sig_peptide
<222> 113..172
<223> Von Heijne matrix
score 4.37180298395146
seq SLLLSLP HQGLT/FS

<400> 89
ttttttacat ggtgttccca cagctgggag gacacccaca tggtcggcgt gcaggatatt 60
tcgctggacc ctgaaaaagc caccacgacc tgtgggccat gatgctaccc ca atg gct 118
Met Ala
-20
gct gct gct gtt cct tct ctt ctt ctt tct ctt cct cct cac cag ggg 166

<220>
 <221> sig_peptide
 <222> 185..253
 <223> Von Heijne matrix
 score 9.49395175807817
 seq SLLFICFFGESFC/IC

<400> 92
 atatttttgct gactggcaag gttatatgaa gtgctttttat tgaagcacca ttttaactaa 60
 tagctcctgg tatttttctgc ttcccttctgt aggggaattta gttattttat tttattattt 120
 agctaattta gctatttttaa aatagctaaa ttttagctac ttttttttca attgacaaag 180
 aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
 -20 -15 -10
 tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277
 Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
 -5 1 5
 aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa ggt 325
 Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly
 10 15 20
 tgt tta tat ctc att tat aat tta tta caa gct gtc ttc ttc gtc tta 373
 Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu
 25 30 35 40
 ttt gtt ttg tct gtg cat tac ctg tgg aag aaa tgg aag aaa cac caa 421
 Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln
 45 50 55
 aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469
 Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu
 60 65 70
 gaa agc cca ttg atc aac aac att gac caa aca ctc cac aga gtg gca 517
 Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala
 75 80 85
 acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565
 Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His
 90 95 100
 cct tcc tct aag aaa att aag cac tgc aaa tta aag aag aag agt aaa 613
 Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys
 105 110 115 120
 gaa gaa gga gcc aga aga tac taaataaatg catatgcaaa tgtagcttag 664
 Glu Glu Gly Ala Arg Arg Tyr
 125
 tcaattatag atatcacaaa agaaatctat catctaagga ttaaaaaattg ttcttttgaa 724
 aaaaaaaaaa aaa 737

<210> 93
 <211> 728
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 53..646

<220>
 <221> sig_peptide
 <222> 53..91
 <223> Von Heijne matrix
 score 4.95353272042967

seq MLLGRLTSQLLRA/VP

<400> 93

```

aatttgagcc gcgtcgagct cccctgggac ctgtggccgc cgcccacaga cc atg ctc      58
                                     Met Leu

ctg ggg cgc ctg act tcc cag ctg ttg agg gcc gtt cct tgg gca ggc      106
Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp Ala Gly
-10 -5 1 5
ggc cgc ccg cct tgg ccc gtc tct gga gtg ctg ggc agc cgg gtc tgc      154
Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg Val Cys
10 15 20
ggg ccc ctt tac agc aca tcg ccg gcc ggc cca ggt agg gcg gcc tct      202
Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser
25 30 35
ctc cct cgc aag ggg gcc cag ctg gag ctg gag gag atg gtc ccc agg      250
Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val Pro Arg
40 45 50
aag atg tcc gtc agc ccc ctg gag agc tgg ctc acg gcc cgc tgc ttc      298
Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe
55 60 65
ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa      346
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln
70 75 80 85
tcc tac cag tgt ccg ccc agc cag ata ggg gaa ggg gcc gag cag ggg      394
Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly
90 95 100
gat gaa ggc gtc gcg gat gcg cct caa att cag tgc aaa aac gtg ctg      442
Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu
105 110 115
aag atc cgc cgg cgg aag atg aac cac aag tac cgg aag ctg gtg      490
Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val
120 125 130
aag aag acg cgg ttc ctg cgg agg aag gtc cag gag gga cgc ctg aga      538
Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg
135 140 145
cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag      586
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys
150 155 160 165
gcg ggg cta aag gaa gcc ccc gaa ggc tgg cag acc ccc aag atc tac      634
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr
170 175 180
ctg cgg ggc aaa tgagtctggc gccgcccttc ccgccggtg ctgctgtgat      686
Leu Arg Gly Lys
185
ccgtagtaat aaattctcag aggacccaaa aaaaaaaaaa aa      728

```

<210> 94

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..510

<220>

<221> sig_peptide

<222> 247..318

<223> Von Heijne matrix
score 5.20026065148038
seq FCALEVVLPS CDC/RS

<400> 94
atcataactca ccatggctca caaactgcct gtttgaaact cccttcagtt ctgagaggat 60
gggaacattc tttaagcggg tcgtcttggc acgagacata aggcagttca acatcaagcc 120
cttgccctga acagttccaa atgccaagaa ctggcgaatt actactttgg tttcaatggg 180
tggtccaaaa ggatcatcaa gcttcaggag ctttctgacc ttgaagaaag ggaaaatgaa 240
gatagc atg gtg cca ctt ccg aag caa agc ctg aag ttc ttc tgt gct 288
Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala
-20 -15
tta gaa gtg gtg ttg cca tcc tgt gat tgc agg agt cct ggc att ggc 336
Leu Glu Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly
-10 -5 1 5
ttg gtg gag gag cct atg gat aag gtg gag gaa gga cca tta tca ttc 384
Leu Val Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe
10 15 20
ctt atg aaa agg aag aca gcc cag aag ctt gct att cag aag gct ttg 432
Leu Met Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu
25 30 35
tca gat gca ttc cag aaa ctg ttg att gtt gtt cta ggt aag act gtc 480
Ser Asp Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val
40 45 50
ttg atc atc ctt gaa gta ctt cag ttt cag taagcaaata aactcatttt 530
Leu Ile Ile Leu Glu Val Leu Gln Phe Gln
55 60
gaaaagttaa ttgaataaaa atattgatat ctaaagcaaa aaaaaaaaaa aa 582

<210> 95
<211> 1913
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..592

<220>
<221> sig_peptide
<222> 143..277
<223> Von Heijne matrix
score 5.94057630118762
seq VLVDLAILGQAYA/FA

<400> 95
atttttttgt gcctaagatg cccagtgcgt tgctgggttt ttctgctgtc ctggggtctt 60
ggacatgagg ccagaccttg tgaccttggt ggcagtgggc agtggttga tgtgaggtcc 120
cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc 172
Met Val Leu Met Trp Thr Ser Gly Asp Ala
-45 -40
ttc aag acg gcc tac ttc ctg ctg aag ggt gcc cct ctg cag ttc tcc 220
Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser
-35 -30 -25 -20
gtg tgc ggc ctg ctg cag gtg ctg gtg gac ctg gcc atc ctg ggg cag 268
Val Cys Gly Leu Leu Gln Val Leu Val Asp Leu Ala Ile Leu Gly Gln
-15 -10 -5
gcc tac gcc ttc gcc cca ccc cca gaa gcc ggc gcc cca cgc cgt gca 316


```

<400> 96
aggtgggtcc ccccggcacc cccagacctg cc atg gcg acc gcg agt cct agc      53
                               Met Ala Thr Ala Ser Pro Ser
                               -15
gtc ttt cta ctc atg gtc aac ggg cag gtg gag agc gcc cag ttt cca      101
Val Phe Leu Leu Met Val Asn Gly Gln Val Glu Ser Ala Gln Phe Pro
-10 -5 1
gag tat gat gac ttc tac tgc aag tac tgc ttt gtg tac ggc cag gac      149
Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr Cys Phe Val Tyr Gly Gln Asp
5 10 15 20
tgg gcc ccc aca gcg ggt ctg gag gag ggg atc tca cag atc aca tcc      197
Trp Ala Pro Thr Ala Gly Leu Glu Glu Gly Ile Ser Gln Ile Thr Ser
25 30 35
aag agc caa gat gtg cgg caa gca ctg gtg tgg aac ttc ccc att gat      245
Lys Ser Gln Asp Val Arg Gln Ala Leu Val Trp Asn Phe Pro Ile Asp
40 45 50
gtc acc ttt aaa agc acc aac ccc tac ggc tgg cca cag atc gtg ctc      293
Val Thr Phe Lys Ser Thr Asn Pro Tyr Gly Trp Pro Gln Ile Val Leu
55 60 65
agc gtg tat gga cca gat gtg ttc ggg aac gat gtg gtt cga ggc tat      341
Ser Val Tyr Gly Pro Asp Val Phe Gly Asn Asp Val Val Arg Gly Tyr
70 75 80
ggg gcc gtg cac gtg ccc ttc tca cct ggc cgg cac aaa agg acc atc      389
Gly Ala Val His Val Pro Phe Ser Pro Gly Arg His Lys Arg Thr Ile
85 90 95 100
ccc atg ttt gtc cca gaa tct acg tct aaa ctg cag aag ttt aca aga      437
Pro Met Phe Val Pro Glu Ser Thr Ser Lys Leu Gln Lys Phe Thr Arg
105 110 115
tct gca agc tgc tcc acc cac tgaggacaaa tagaaacagg tcccctggga      488
Ser Ala Ser Cys Ser Thr His
120
gtgctgagtc acgggggtcc cttcagccct gttccagcag cagaaggccg ggcgatttta      548
ccctgtgccc tgtgaaaaat ctttgtgtct gagggggcag aggaaaaact cttgtcagat      608
gggaaaaatg ctcatgacat aatgtgacat taaaagggtgg gaaacaaaaa aaaaaaaaaa      668
aa                                                                 670

```

```

<210> 97
<211> 939
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 1..336

```

```

<220>
<221> sig_peptide
<222> 1..81
<223> Von Heijne matrix
      score 3.68137078794859
      seq AHLCSDSLPEQQ/QD

```

```

<400> 97
act tcc gaa gag aga acc gcc atg aag aga gaa ggg ggt gcc gcc cac      48
Thr Ser Glu Glu Arg Thr Ala Met Lys Arg Glu Gly Ala Ala His
-25 -20 -15
ctc tgc tcc gac agc ctc ccg gag tcc cag cag caa gac ggc aac cac      96

```

```

Leu Cys Ser Asp Ser Leu Pro Glu Ser Gln Gln Gln Asp Gly Asn His
-10 -5 1 5
gca ccc aac ttc tcc agc cac ggc tca tgc cgc cgt cgc cag cgg scc 144
Ala Pro Asn Phe Ser Ser His Gly Ser Cys Arg Arg Arg Gln Arg Xaa
10 15 20
gac atg aca agg cgc tgc atg ccc gct agg cca ggt ttc ccc tca tcc 192
Asp Met Thr Arg Arg Cys Met Pro Ala Arg Pro Gly Phe Pro Ser Ser
25 30 35
cca gcc ccg ggg tgc tgc ccc ccg cgc tgc cat ctg aga ccc ggt agt 240
Pro Ala Pro Gly Ser Ser Pro Pro Arg Cys His Leu Arg Pro Gly Ser
40 45 50
acc gcc cat gct gca gcg gga aag aga aca gag agt cct ggg gac agg 288
Thr Ala His Ala Ala Ala Gly Lys Arg Thr Glu Ser Pro Gly Asp Arg
55 60 65
tac cgt gca gag ggc ttg aga agg ggc cgg gtc gcg ggg gca agg gta 336
Tyr Arg Ala Glu Gly Leu Arg Arg Gly Arg Val Ala Gly Ala Arg Val
70 75 80 85
tgaggggagg gctgcagacc gccgctcttc cagttcccg cctcctccgc gagctcaggc 396
gttggcattt cggggcctgg caaatccccg cccgcctcc gcgcaggggc tactgggagt 456
tggagtttgc ttctctgtag ttgggcagct gctcttggtc tagtgaccac cagcctggac 516
agctacggag aaccgcctt aggtagaaag aaagtgattt ttttcctttg caagagtttg 576
acccgggacc ctaactgctt aatgcatatt tagatcgttt tctgtacggt gtcagttcta 636
ctgatcctag tggtttagta atataaacct tttctatggt gtgggtgaaa ttatgtaacc 696
tgtgatgagg gaatcccttc cacgaattac tttgtagtcc agcgtgcacg ctagttcata 756
cttaaaagaa cttgcagatt tggaatgtga cgtgttttct ctttcagtaa cttcacgcct 816
ctccaagagg ctaatttttt tgtaaagatt ttgtgggagc tatgtaatga gatggggagt 876
ttcatctaata gacatcctct gacaataaaa aatgtttaa ttccccaaaa aaaaaaaaaa 936
aaa 939

<210> 98
<211> 661
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 174..443

<220>
<221> sig_peptide
<222> 174..269
<223> Von Heijne matrix
score 4.13107367257584
seq SSLAFCQVGFLTA/QP

<400> 98
aaaaaggaac tttcagtgat aatgaacaaa actcaggagc tatgtggatg acaggagcac 60
ctagatgacc gactttaccc acttcaaagt ctaccttgac cctagcactc tctccaccct 120
gcatcctcac ctcagaccat cagttgggta ggccaacagc tcaccatcaa ttc atg 176
Met
ccc tgc cta gac caa cag ctc act gtt cat gcc cta ccc tgc cct gcc 224
Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro Ala
-30 -25 -20
cag ccc tcc tct ctg gcc ttc tgc caa gtg ggg ttc tta aca gca cag 272
Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala Gln
-15 -10 -5 1
cct tca cct ccg aga agg cgc aat ggg aaa gac aga tac acg ttg gtt 320
Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu Val

```

| | | | | |
|--|----|----|----|-----|
| | 5 | 10 | 15 | |
| ctg caa cac cag gaa tgc cag gat gat tta gcc acc tcc tca ctt gtc | | | | 368 |
| Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu Val | | | | |
| | 20 | 25 | 30 | |
| tac ctt tcc ctc ccc tgc ttc aaa gac ttg ggt cga tcg aag cac caa | | | | 416 |
| Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His Gln | | | | |
| | 35 | 40 | 45 | |
| agc atc act gtt gct gac act aac aag tagtgccaag ggattgcctt | | | | 463 |
| Ser Ile Thr Val Ala Asp Thr Asn Lys | | | | |
| 50 | 55 | | | |
| taaggaagat caggagcgga acatctggtg gcaaagaaaa tcttttctaag agccccattc | | | | 523 |
| tagtgaccac cttcaacctc ctcatagcag gagagtttg gagtagggga cttaggatgt | | | | 583 |
| tttgttcttt taatcaattc agaaaatatg tatgtttgaa ataaaaataa aaatacttga | | | | 643 |
| gccaaaaaaa aaaaaaaa | | | | 661 |

<210> 99
 <211> 647
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 282..521
 <220>
 <221> sig_peptide
 <222> 282..386
 <223> Von Heijne matrix
 score 3.64439944832387
 seq LEPGLSSSAACNG/KE

| | |
|---|---------------------|
| <400> 99 | |
| acttgctgt caccgttacc gtagcgactg ggcttctgga ctgtatatcc tagctgcctt | 60 |
| gtcaacatct tcgagcatcg gcagctccgg aggccggggg aactggcagg taggaaacta | 120 |
| tgtgaaagaa tctctgatg tcataatttc cgggtgtcac cggaacattt gatcatcatt | 180 |
| cctttggcaa ttccagcctt ctgtggaaag gccagtagaa agcattgatt tattcacctc | 240 |
| tacaggaatc agactcagcc tcttttggtt ttcagtgaag t atg cct ttt caa ttt | 296 |
| | Met Pro Phe Gln Phe |
| | -35 |
| gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att | 344 |
| Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile | |
| -30 -25 -20 -15 | |
| gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag | 392 |
| Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu | |
| -10 -5 1 | |
| atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg | 440 |
| Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu | |
| 5 10 15 | |
| aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca | 488 |
| Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro | |
| 20 25 30 | |
| cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcttttg | 541 |
| Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys | |
| 35 40 45 | |
| tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct ggtaaacaaa | 601 |
| taaaagtggg ggcaccttta gatgatgaca aaaaaaaaaa aaaaaa | 647 |

<210> 100

<211> 1006
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 251..643

<220>
 <221> sig_peptide
 <222> 251..295
 <223> Von Heijne matrix
 score 3.74215118492367
 seq LLMFTQLLLCGFL/YV

<400> 100
 aggaagccag agggctggaa atacagcagc ctttgaagta ccctctgtta atttggatgg 60
 atctcagtgt gcccgttcg agacctctcc accaacacct tctgatcttg cgatttgc 120
 ttcttgactt taattagtat ctaggaaagt ctaaactttg gacctacctc tttttttgat 180
 actcattttt gtacttttgc tctctgggat tggtttctta aagaatctgg atccttttta 240
 atatgtcaaaa atg agt ctg ctg atg ttt aca caa cta ctg ctc tgt gga 289
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly
 -15 -10 -5
 ttt tta tat gtt cgg gtt gat gga tcg cgt ctt cgc cag gag gac ttt 337
 Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe
 1 5 10
 ccc ccg cgg att gtg gag cat cct tcc gat gtc atc gtc tct aag ggc 385
 Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly
 15 20 25 30
 gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc 433
 Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr
 35 40 45
 att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat 481
 Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp
 50 55 60
 ccc cgg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg 529
 Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu
 65 70 75
 cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt 577
 Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val
 80 85 90
 tgt gtt gcg agg aac tat ctt ggt gaa gca gtg agt cga aat gcg tct 625
 Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser
 95 100 105 110
 ctg gaa gtg gca tgt aag tgaacataat gaacctcatg tgcacattta 673
 Leu Glu Val Ala Cys Lys
 115
 cttttattta tttcaagtaa gttttgatgt gttcccatag acgctgaaac ctaaagaatc 733
 aatcaacaca ctgcataatt ttacttggtc ttcttcagag aagtctggtc aagatagtat 793
 caagccaggg tggtttagta agtttgttta tatgaaatca agatgaccaa tatgttatta 853
 taagaaagca ggccgggctc ggtggctcac gcctgtaatc ccagcacttt gggaggcgga 913
 ggccggcgga tcacgaggtc aggagatcga gaccatcctg ggtagcacgg tggggccccg 973
 tctctacaaa aaatacaaaa aaaaaaaaaa aaa 1006

<210> 101
 <211> 1059
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 179..475

<220>
 <221> sig_peptide
 <222> 179..295
 <223> Von Heijne matrix
 score 4.14109371250204
 seq PSLIAGLFVGCLA/GY

<400> 101
 gtttttccag gagggagcgg cctttgctca ggcgagacg gctgggcgcc gagtgggaca 60
 gcgctggtgc ggagactgct tccggactcc aggtaccgcg cttggcggca gctggcccca 120
 gacttctgtc ttttcagctg cagtgaaggc tcggggctgc agaattgcaa ccttgcca 178
 atg gac ctg atc ggt ttt ggt tat gca gcc ctc gtg aca ttt gga agc 226
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 att ttt gga tat aag cgg aga ggt ggt gtt ccg tct ttg att gct ggt 274
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 ctt ttt gtt gga tgt ttg gcc ggc tat gga gct tac cgt gtc tcc aat 322
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 gac aaa cga gat gta aaa gtg tca ctg ttt aca gct ttc ttc ctg gct 370
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 acc ata atg ggt gtg aga ttt aag agg tcc aag aaa ata atg cct gct 418
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 ggt ttg gtt gca ggt tta agc ctc atg atg atc ctg aga ctt gtc ttg 466
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 ttg ctg ctc tgagcatctg gaggaacaga aaactaagtt catgtcatcc 515
 Leu Leu Leu
 60
 tgctgtaatg ggcagagcat attttttttg tattttaaag ataaacttca atatggaatg 575
 ctagaaacac aaatagcact gtcacctcta atatgaacat tagtttgagg tagttttttt 635
 ctaaagcaaa aatttttaact gtttttcta tgtcaagcac tattttcatt aaaagtgtct 695
 aatgaatcat gatatactct tccatttggt gtgtctatatt tttatatatt tggatatttt 755
 tgaaaattcc aaatactcat gtctcaagta agcttaaact acaacttgtc acataaagga 815
 agtcttaagt ggagttcaca gaatgataat gtatctatatt gtcatttggt ttatatttga 875
 aattattaga aattatgctt tttccatttt aattgtattg ctgccagtgc tatttttttc 935
 tttaaaaaat tttattctta gcacactggt atgtcctaac tgaatgtatt cagtattcaa 995
 ataaaagaca ttttgggtcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1055
 aaaa 1059

<210> 102
 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..327

<220>

<221> sig_peptide
 <222> 34..162
 <223> Von Heijne matrix
 score 5.69273078757386
 seq LGDALLFLRPAGS/CA

<400> 102
 agagacctat ggggttcgcc tgaagccccc gga atg tgt gag aca ctt ctt act 54
 Met Cys Glu Thr Leu Leu Thr
 -40
 agt aaa tgg gct tca gta tcc ccc atc cct gca ctc ctg cag gaa ggt 102
 Ser Lys Trp Ala Ser Val Ser Pro Ile Pro Ala Leu Leu Gln Glu Gly
 -35 -30 -25
 gag aat cgg gac agt cgc agg ctg gga gac gct ctg ctt ttc ctg cgt 150
 Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg
 -20 -15 -10 -5
 cct gct ggg agc tgc gcg ctc cag gta tcc tgg cct gcc gcc cta gcc 198
 Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala
 1 5 10
 ggc cca agg agc cac aca gga cag ttg acc caa cac ttc tgc cac ctg 246
 Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu
 15 20 25
 aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca 294
 Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser
 30 35 40
 ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg 347
 Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr
 45 50 55
 gcatcctgaa aacggccttc cttgtgtgta cattatttgc aacaagcaac aagtttataa 407
 gcactttgggt aaaattgcat gtgaggggta aaatattaaa gtcagtgcgt caacttgaaa 467
 taaatgatga gttattgatt actgctaaag aaaaaaaaaa aaaaaaa 514

<210> 103
 <211> 1158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 303..953

<220>
 <221> sig_peptide
 <222> 303..359
 <223> Von Heijne matrix
 score 5.47911600153114
 seq LCCSGCVPSLCCS/SY

<400> 103
 aaaaacttcc gccgccgcgt ccgccgcctc cggaactaaa cggggtgagg tcacattcgg 60
 ttatctctaa cgttggaaaa cgatggagct aacacccatt atggagatta accacttttc 120
 atcaggtttt taacttaagt cgtgaggaat acaacggtga acacaagatt cattttattt 180
 tcatcaccat gggacgtatc ctgttgttga gttctctggg tcagacctct gaagacttct 240
 cagatggatc ctagtctctg ggcttgccct gaaattactc gctgctcagg gagagagttg 300
 aa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt gtc ccc tgc 347
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser
 -15 -10 -5
 ctc tgt tgt tcc agc tat gtc ccc tct gtt gct cca act gca gct cat 395

| | | | | | | | | | | | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|-----|-----|-----|------------|------------|-----|-----|-----|-----|------|
| Leu | Cys | Cys | Ser | Ser | Tyr | Val | Pro | Ser | Val | Ala | Pro | Thr | Ala | Ala | His | |
| | | | | 1 | | | | 5 | | | | | 10 | | | |
| tct | ggt | aga | ggt | cct | cat | tca | gct | ggg | cac | tgt | ggc | cag | agg | gtg | ttg | 443 |
| Ser | Val | Arg | Val | Pro | His | Ser | Ala | Gly | His | Cys | Gly | Gln | Arg | Val | Leu | |
| | | 15 | | | | | 20 | | | | | 25 | | | | |
| gcc | tgc | tcc | ctt | cct | caa | gta | ttc | tta | aag | cca | tgg | att | ttt | gtg | gag | 491 |
| Ala | Cys | Ser | Leu | Pro | Gln | Val | Phe | Leu | Lys | Pro | Trp | Ile | Phe | Val | Glu | |
| | | 30 | | | | 35 | | | | | 40 | | | | | |
| cat | ttt | tct | tcc | tgg | ctc | tcc | ctt | gag | tta | ttt | tcc | ttt | ctt | cgc | tat | 539 |
| His | Phe | Ser | Ser | Trp | Leu | Ser | Leu | Glu | Leu | Phe | Ser | Phe | Leu | Arg | Tyr | |
| | | | | 50 | | | | | | 55 | | | | | 60 | |
| ctt | ggg | act | ctt | ctt | tgt | gct | tgc | gga | cat | cgg | ttg | aga | gaa | gga | cga | 587 |
| Leu | Gly | Thr | Leu | Leu | Cys | Ala | Cys | Gly | His | Arg | Leu | Arg | Glu | Gly | Arg | |
| | | | | 65 | | | | 70 | | | | | | 75 | | |
| ctt | ctt | cct | tgt | ctc | ctt | ggg | gtt | ggc | tcg | tgg | ttg | ctc | ttc | aac | aac | 635 |
| Leu | Leu | Pro | Cys | Leu | Leu | Gly | Val | Gly | Ser | Trp | Leu | Leu | Phe | Asn | Asn | |
| | | | 80 | | | | | 85 | | | | | 90 | | | |
| tgg | act | gga | ggc | tct | tgg | ttt | tct | ctt | cat | ctt | caa | caa | gtc | agt | ctc | 683 |
| Trp | Thr | Gly | Gly | Ser | Trp | Phe | Ser | Leu | His | Leu | Gln | Gln | Val | Ser | Leu | |
| | | 95 | | | | | 100 | | | | | 105 | | | | |
| tct | caa | ggg | tct | cac | ggt | gca | gca | ttc | tta | cca | gag | gcc | att | ggg | cct | 731 |
| Ser | Gln | Gly | Ser | His | Val | Ala | Ala | Phe | Leu | Pro | Glu | Ala | Ile | Gly | Pro | |
| | | 110 | | | | 115 | | | | | 120 | | | | | |
| gga | ggt | cca | ggt | cca | gtg | tct | gga | gag | tcc | acc | tca | gct | cag | caa | tct | 779 |
| Gly | Val | Pro | Val | Pro | Val | Ser | Gly | Glu | Ser | Thr | Ser | Ala | Gln | Gln | Ser | |
| | | | | | 130 | | | | | 135 | | | | | 140 | |
| cat | gcc | ggg | tgg | caa | ttg | tca | gca | gaa | gcc | gat | gcc | tgc | cca | tca | gtt | 827 |
| His | Ala | Gly | Trp | Gln | Leu | Ser | Ala | Glu | Ala | Asp | Ala | Cys | Pro | Ser | Val | |
| | | | | 145 | | | | | 150 | | | | | | 155 | |
| ctt | tac | tct | gag | gtg | tta | gag | tgg | aat | aaa | aat | ata | aat | act | tat | act | 875 |
| Leu | Tyr | Ser | Glu | Val | Leu | Glu | Trp | Asn | Lys | Asn | Ile | Asn | Thr | Tyr | Thr | |
| | | | | 160 | | | | 165 | | | | | | 170 | | |
| agt | ttt | cat | gac | ttc | tgc | tta | ata | ttg | ggg | att | ttt | ktt | gtt | ttg | ttt | 923 |
| Ser | Phe | His | Asp | Phe | Cys | Leu | Ile | Leu | Gly | Ile | Phe | Xaa | Val | Leu | Phe | |
| | | 175 | | | | 180 | | | | | 185 | | | | | |
| tgt | ttt | ggc | ggg | gat | agg | ctt | acc | tta | cat | taaaccaggc | cttagccttt | | | | | 973 |
| Cys | Phe | Gly | Gly | Asp | Arg | Leu | Thr | Leu | His | | | | | | | |
| | | 190 | | | | 195 | | | | | | | | | | |
| ctgtggccttt | ggtatggcaa | agcctcatat | tactctctag | tctgggttcag | caggacagtc | | | | | | | | | | | 1033 |
| aggccacac | ctggggctgt | ttgttttcta | cgtttacctc | aacataaggt | accttatcat | | | | | | | | | | | 1093 |
| tgtagcctt | catctcctga | tccaaaataa | aataaaatgc | cacaggtcaa | aaaaaaaaaa | | | | | | | | | | | 1153 |
| aaaaa | | | | | | | | | | | | | | | | 1158 |

<210> 104
 <211> 1563
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 97..645

<220>
 <221> sig_peptide
 <222> 97..156
 <223> Von Heijne matrix
 score 8.42885652997473
 seq AVVGCLLVPPAEA/NK

<220>
 <221> misc_feature
 <222> 972
 <223> n=a, g, c or t

```

<400> 104
aatagaagct aggagagggc ggggacaact ggggtcttttg cggtgcagc gggctttag 60
gtgtccggct ttgctggccc agcaagcctg ataagc atg aag ctc tta tct ttg 114
                                     Met Lys Leu Leu Ser Leu
                                     -20 -15
gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag 162
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                                     -10 -5 1
agt tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac 210
Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                                     5 10 15
atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac 258
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                                     20 25 30
tgc ctg cac gtg gtg gag ccc atg cca gtg cct gcc cat gac gtg gag 306
Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu
35 40 45 50
gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc 354
Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr
                                     55 60 65
acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg 402
Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu
70 75 80
ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag 450
Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys
85 90 95
ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat 498
Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp
100 105 110
gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca 546
Ala Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
115 120 125 130
aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg 594
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu
135 140 145
cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc 642
Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu
150 155 160
agc tagatgggct ggtgtggttg ggtcaaggcc ccaacacccat ggctgccagc 695
Ser
ttccaggctg gacaaagcag ggggtactt ctcccttccc tcggttccag tcttcccttt 755
aaaagcctgt ggcatttttc ctcccttctcc ctaacttttag aaatgttgta cttggctatt 815
ttgattaggg aagaggggatg tgggtctctga tctctgttgt cttcttgggt ctttgggggt 875
gaagggaggg ggaaggcagg cccasaaggg aatggagaca ttcgaggcgg cctcaggagt 935
ggatgcgac ttgtctctcc tkggcctccc actcttngcc gccttccagc tctgagtctt 995
gggaatgttg ttacccttgg aagataaagy ctgggtcttc aggaactcag tgtctgggag 1055
gaaagcatgg cccagcattc agcatgtgtt cttttctgca gtgggttctta tcaccacctc 1115
cctcccagcc ccagcgctc agccccagcc ccagctccag ccctgaggac agctctgatg 1175
ggagagctgg gccccctgag cccactgggt cttcaggggt cactggaagc tgggtgttcgc 1235
tgtcccctgt gcacttctcg cactggggca tggagtgccc atgcatactc tgctgccggt 1295
cccctcacct gcacttgagg ggtctgggca gtccctcctc tcccagtggt ccacagtcac 1355
tgagccagac ggtcgggttg aacatgagac tcgaggctga gcgtggatct gaacaccaca 1415

```

```

ccccctgtac ttgggttgcc tcttgtccct gaacttcggt gtaccagtgc atggagagaa 1475
aattttgtcc tcttgtctta gagttgtgtg taaatcaagg aagccatcat taaattgttt 1535
tatttctctc taaaaaaaaa aaaaaaaaaa 1563

```

```

<210> 105
<211> 1621
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 80..820

```

```

<220>
<221> sig_peptide
<222> 80..118
<223> Von Heijne matrix
      score 5.76690322882439
      seq MLVLRSA LTRALA/SR

```

```

<400> 105
acctttccac tcgggaaacc ttcagaggag tctcagaaag gacacggctg gctgcttttc 60
tcagegcgca agccgcgcc atg ctc gtc ctc aga agc gcc ctg act cgg gcg 112
               Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
               -10                               -5

ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg 160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
      1           5           10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac 208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
15           20           25           30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac 256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
      35           40           45

gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta 304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
      50           55           60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat 352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
      65           70           75
aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag 400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys
      80           85           90
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa 448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys
      95           100          105          110
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa 496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys
      115          120          125

cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct 544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro
      130          135          140
ggg gga cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct 592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala
      145          150          155
cat gtc aat cta ggc tac aca aaa cta gtt gga gtg ttc cac aca gag 640
His Val Asn Leu Gly Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu
      160          165          170

```

[illegible]

```
<210> 106
<211> 557
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> sig_peptide
<222> 77..217
<223> Von Heijne matrix
score 4.57105404339594
seq FLYLTNLNOSCIFA/NY
```

| | | | | | | | | | | | | | | | | |
|--------|-------|--------|-------|--------|-------|--------|-------|-------|--------|-------|--------|-------|-----|-----|-----|-----|
| Gly | Arg | Tyr | Thr | Arg | Glu | Ile | Gln | Arg | Leu | Thr | Ser | Pro | Ala | Ala | Trp | |
| 15 | | | | | 20 | | | | | 25 | | | | | | |
| ccc | acc | aga | gac | aag | aac | agg | atg | ata | agc | aat | gga | atg | gca | ttg | aac | 352 |
| Pro | Thr | Arg | Asp | Lys | Asn | Arg | Met | Ile | Ser | Asn | Gly | Met | Ala | Leu | Asn | |
| 30 | | | | 35 | | | | | 40 | | | | | 45 | | |
| tct | cct | gct | gaa | gga | ctt | gca | ttt | caa | tgt | aga | ttc | tgagg | ctg | ggg | | 398 |
| Ser | Pro | Ala | Glu | Gly | Leu | Ala | Phe | Gln | Cys | Arg | Phe | | | | | |
| | | | 50 | | | | | | 55 | | | | | | | |
| tgaaa | acttc | tctgt | cac | ctt | ttact | acagc | attct | caccc | atttat | atatt | ctttcc | ccctt | | | | 458 |
| ctacat | ctct | attact | gttg | cactat | gtta | tgcatt | acac | catgg | caaaa | ttaat | caatt | | | | | 518 |
| aataca | ataa | aagct | taatt | ttaaaa | aaaaa | aaaaa | aaaaa | | | | | | | | | 557 |

<210> 107
 <211> 600
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 139..513

<220>
 <221> sig_peptide
 <222> 139..201
 <223> Von Heijne matrix
 score 5.86857787719223
 seq IVMGVQVVGRAFA/RA

| | | | | | | | | | | | | | | | | | |
|------------|-------------|-------------|------------|------------|-------------|---------|---------|-----|-----|-----|-----|-----|--|--|--|-----|--|
| <400> 107 | | | | | | | | | | | | | | | | | |
| gaggcaatgc | gcatgcccag | cgcgcgtatcg | cgcacgctct | ctgcggcttt | cttgacctc | | | | | | | | | | | 60 | |
| tgacccgccg | accacgcttg | atccccggcc | gcggggccag | gaagtcggag | tttgagcccc | | | | | | | | | | | 120 | |
| ggaggcagag | cggctgcc | atg gcc | aag tac | ctg gcc | cag atc | att gtg | atg | | | | | | | | | 171 | |
| | | Met | Ala | Lys | Tyr | Leu | Ala | Gln | Ile | Ile | Val | Met | | | | | |
| | | -20 | | | | | | -15 | | | | | | | | | |
| ggc gtg | cag gtg | gtg ggc | agg gcc | ttt gca | cgg gcc | ttg cgg | cag gag | | | | | | | | | 219 | |
| Gly Val | Gln Val | Val Gly | Arg Ala | Phe Ala | Arg Ala | Leu Arg | Gln Glu | | | | | | | | | | |
| -10 | | -5 | | 1 | | 5 | | | | | | | | | | | |
| ttt gca | gcc agc | cgg gcc | gca gct | gat gcc | cga gga | cgc gct | gga cac | | | | | | | | | 267 | |
| Phe Ala | Ala Ser | Arg Ala | Ala Ala | Ala Asp | Ala Arg | Gly Arg | Ala Gly | His | | | | | | | | | |
| | 10 | | | 15 | | 20 | | | | | | | | | | | |
| cgg tct | gca gcc | gct tcc | aac ctc | tcc ggc | ctc agc | ctc cag | gag gca | | | | | | | | | 315 | |
| Arg Ser | Ala Ala | Ala Ser | Asn Leu | Ser Gly | Leu Ser | Leu Gln | Glu Ala | | | | | | | | | | |
| | 25 | | 30 | | 35 | | | | | | | | | | | | |
| cag cag | att ctc | aac gtg | tcc aag | ctg agc | cct gag | gag gtc | cag aag | | | | | | | | | 363 | |
| Gln Gln | Ile Leu | Asn Val | Ser Lys | Leu Ser | Pro Glu | Glu Val | Gln Lys | | | | | | | | | | |
| 40 | | 45 | | 50 | | | | | | | | | | | | | |
| aac tat | gaa cac | tta ttt | aag gtg | aat gat | aaa tcc | gtg ggt | ggc tcc | | | | | | | | | 411 | |
| Asn Tyr | Glu His | Leu Phe | Lys Val | Asn Asp | Lys Ser | Val Gly | Gly Ser | | | | | | | | | | |
| 55 | | 60 | | 65 | | 70 | | | | | | | | | | | |
| ttc tac | ctg cag | tca aag | gtg gtc | cgc gca | aag gag | cgc ctg | gat gag | | | | | | | | | 459 | |
| Phe Tyr | Leu Gln | Ser Lys | Val Val | Arg Ala | Lys Glu | Arg Leu | Asp Glu | | | | | | | | | | |
| | 75 | | 80 | | 85 | | | | | | | | | | | | |
| gaa ctc | aaa atc | cag gcc | cag gag | gac aga | gaa aaa | ggg cag | atg ccc | | | | | | | | | 507 | |
| Glu Leu | Lys Ile | Gln Ala | Gln Glu | Asp Arg | Glu Lys | Gly Gln | Met Pro | | | | | | | | | | |
| | 90 | | 95 | | 100 | | | | | | | | | | | | |
| cat acg | tgactgctcg | gctcccccg | cccacccgc | cgcttcta | attttagcttg | | | | | | | | | | | 563 | |
| His Thr | | | | | | | | | | | | | | | | | |
| gtaataa | aatt tctttt | ctac aaaaaa | aaaaa | | | | | | | | | | | | | 600 | |

<210> 108
 <211> 1129
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..986

<220>
 <221> sig_peptide
 <222> 81..134
 <223> Von Heijne matrix
 score 5.03543461931947
 seq ITLLGLAVNVVTT/LV

```

<400> 108
acagcgcggc gggcgtctcg ctgctcgagc cgccgctgca gctctactgg acctggctgc      60
tccagtggat cccgctctgg atg gcc ccc aac tcc atc acc ctg ctg ggg ctc      113
                Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu
                -15                      -10

gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg      161
Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr
                -5                      1                      5

gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga      209
Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly
10                15                20                25
ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga      257
Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg
                30                35                40

aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt      305
Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys
                45                50                55

gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct      353
Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala
60                65                70

cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg      401
Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly
75                80                85

atg ttt gtg ttt tat tgc gct cat tgg cag act tat gtt tca ggc atg      449
Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met
90                95                100                105

ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg      497
Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val
110                115                120

att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat      545
Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr
125                130                135

acg ggc acc agt gtc ttg tca cct gga ctc cac ata gga cta att att      593
Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile
140                145                150

ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa      641
Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu
155                160                165

aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa      689
Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys
170                175                180                185

```

| | |
|---|------|
| gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt gaa cta tat | 737 |
| Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser Glu Leu Tyr | |
| 190 195 200 | |
| ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt tta gac cag | 785 |
| Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln | |
| 205 210 215 | |
| tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg atg gca atg | 833 |
| Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met | |
| 220 225 230 | |
| gtg att tct tca ttt gat atg gtg ata tac ttt agt gct ttg tgc ctg | 881 |
| Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu | |
| 235 240 245 | |
| caa att tca aga cac ctt cat cta aat ata ttc aag act gca tgt cat | 929 |
| Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr Ala Cys His | |
| 250 255 260 265 | |
| caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt cat cag aat | 977 |
| Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser His Gln Asn | |
| 270 275 280 | |
| aac atg gat tgaagagact tccgaacact tgctatctct tgctgctgct | 1026 |
| Asn Met Asp | |
| gtttcatgga aggagatatt aaacatttgt ttaattttta tttaagtgtt atacctattt | 1086 |
| cagcaaataa aatatttcat tgcttgaaaa aaaaaaaaaa aaa | 1129 |

<210> 109
 <211> 778
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 266..586

<220>
 <221> sig_peptide
 <222> 266..307
 <223> Von Heijne matrix
 score 4.534746808071
 seq ILVTVPGVCPAQC/CW

| | |
|---|-----|
| <400> 109 | |
| tagatgtag aattggtatt tgttcttgct ttttggttgc gatggagtta tataactaagt | 60 |
| tacttatact aaggcattag tagtctcata tctgaggagc aattgtattt ttagttcagc | 120 |
| taaattaatg cctcttttta aatactaact tgtactactt ttgtggctgt gaatggtatc | 180 |
| ttttattgaa ctgaggcagc ttttaaaaga cttgcctgat catttagagc actcccattg | 240 |
| aggttaaatt agacttgaat ctgta atg att ctc gta act gtt cct ggt gtg | 292 |
| Met Ile Leu Val Thr Val Pro Gly Val | |
| -10 | |
| tgt cca gca caa tgt tgc tgg gca gag cag agg ggc aga ggc tca ggt | 340 |
| Cys Pro Ala Gln Cys Cys Trp Ala Glu Gln Arg Gly Arg Gly Ser Gly | |
| -5 1 5 10 | |
| atg tac ttc att gac aag tgg gca agg cca tcc tgg gta cca cat tgg | 388 |
| Met Tyr Phe Ile Asp Lys Trp Ala Arg Pro Ser Trp Val Pro His Trp | |
| 15 20 25 | |
| ctt aat gat ctc ttc att gtg aag tcc ggc tac ctc gtt tgc ata aga | 436 |
| Leu Asn Asp Leu Phe Ile Val Lys Ser Gly Tyr Leu Val Cys Ile Arg | |
| 30 35 40 | |
| act aca gta atc agg caa ggc att gtc aga att ggg agg aat aaa atc | 484 |
| Thr Thr Val Ile Arg Gln Gly Ile Val Arg Ile Gly Arg Asn Lys Ile | |

```

      45              50              55
agt gag tct gga agg agt gct ctg tat aca att gca aag aac aaa atg      532
Ser Glu Ser Gly Arg Ser Ala Leu Tyr Thr Ile Ala Lys Asn Lys Met
60              65              70              75
gtc atc ttt aag gta cct gat tgc atg cac tta aat gca gat tat ttt      580
Val Ile Phe Lys Val Pro Asp Cys Met His Leu Asn Ala Asp Tyr Phe
      80              85              90
gga gtt tgaaaaggga ctattaatga aatctttctt ttccctcctt tctctttttc      636
Gly Val
ccttccccgc cactgattca gtgagctgga gattggatca cagccgaagg agtaaagggtg      696
ctgcaatgat gttagctgtg gccactgtgg atttttcgca agaacattaa taaactaaaa      756
acttcaaaaa aaaaaaaaaa aa      778

```

```

<210> 110
<211> 1301
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 59..745

```

```

<220>
<221> sig_peptide
<222> 59..160
<223> Von Heijne matrix
      score 5.94384548075359
      seq LGAAALALLLANT/DV

```

```

<400> 110
attcaaaacc aggctgaaga ttggaaggaa gttggccagc ctcggtctgca ggacagaa      58
atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30              -25              -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Leu Ala
      -15              -10              -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1              5              10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15              20              25              30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
      35              40              45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
      50              55              60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
      65              70              75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
      80              85              90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
95              100              105              110

```



```

agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
      115                      120                      125

aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
      130                      135                      140

gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga aag cag      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
      145                      150                      155

ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aaa gta aac      682
Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
      160                      165                      170

cta ctt tct gtt ctg gaa gct gct aag atg atc aaa cca cag act ttg      730
Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
      175                      180                      185                      190

gcc tca gag aaa aaa tgattgtgtg aaactgccca gctcagggat aaccagggac      785
Ala Ser Glu Lys Lys
      195

attcacctgt gttcatggga tgtattgttt ccactcgtgt ccctaaggag tgagaaaccc      845
atttatactc tactctcagt atggattatt aatgtatttt aatattctgt ttagggccac      905
taaggcaaaa tagcccaaaa acaagactga caaaaatctg aaaaaactaat gaggattatt      965
aagctaaaaac ctgggaaata ggaggtttaa aattgactgc caggctgggt gcagtggctc     1025
acacctgtaa tcccagcact ttgggaggcc aaggtgagca agtcacttga ggtcggggagt     1085
tcgagaccag cctgagcaac atggcgaaac cccgtctcta ctaaaaatac aaaaatcacc     1145
cgggtgtggt ggcaggcacc tgtagtccca gctaccgggg aggctgaggc aggagaaatca     1205
cttgaacctg ggaggtggag gttgcggtga gctgagatca caccactgta ttccagcctg     1265
ggtgactgag actctaacta aaaaaaaaaa aaaaaa                                1301

<210> 111
<211> 1300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..676

<220>
<221> sig_peptide
<222> 59..160
<223> Von Heijne matrix
      score 5.94384548075359
      seq LGAAALALLLANT/DV

<400> 111
attcaaaacc aggctgaaga ttggaaggaa gttggccagc ctcggctgca ggacagaa      58
atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30                      -25                      -20

att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Leu Ala
      -15                      -10                      -5

aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1                      5                      10

ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
      15                      20                      25                      30

```

```

aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
                               35                               40                               45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
                               50                               55                               60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
                               65                               70                               75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
                               80                               85                               90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
                               95                               100                               105                               110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
                               115                               120                               125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
                               130                               135                               140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
                               145                               150                               155
gca ttc ttc ttg agc acc gag aaa aag aat ttg gag aca aag      676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
                               160                               165                               170
taaacctact ttctgttctg gaagctgcta agatgatcaa accacagact ttggcctcag      736
agaaaaaatg attgtgtgaa actgccagc tcagggataa ccagggacat tcacctgtgt      796
tcattgggatg tattgtttcc actcgtgtcc ctaaggagtg agaaacccat ttatactcta      856
ctctcagtat ggattattaa tgtatttttaa tattctgttt aggcccacta aggcaaaata      916
gccccaaaac aagactgaca aaaatctgaa aaactaatga ggattattaa gctaaaacct      976
gggaaatagg aggttttaaaa ttgactgcca ggctgggtgc agtggctcac acctgtaac      1036
ccagcacttt gggaggccaa ggtgagcaag tcacttgagg tcgggagttc gagaccagcc      1096
tgagcaacat ggcgaaaccc cgtctctact aaaaatacaa aaatcaccgg ggtgtggtgg      1156
caggcacctg tagtcccagc taccggggag gctgaggcag gagaatcact tgaacctggg      1216
aggtggaggt tgcggtgagc tgagatcaca ccactgtatt ccagcctggg tgactgagac      1276
tctaactaaa aaaaaaaaaa aaaa      1300

```

<210> 112

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..278

<220>

<221> sig_peptide

<222> 15..146

<223> Von Heijne matrix

score 12.2610572403264

seq PLFLLLLLLGSVTA/DI

<400> 112

```

gagaggagag gaga atg gcg gcg gaa ggc tgg att tgg cgt tgg ggc tgg
Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp

```

50


```

acacagaaca agggagggaa gaaaagctca gccttaaaca tagcaagggtg aaacctttgt 120
cctggggaat agtctggccc gctccttgga accacactca gactca atg gac tct 175
                                     Met Asp Ser
                                     -30
gcc tca aat ccc acc aac ctt gtc agc acc tcc caa agg cac cgg ccc 223
Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg His Arg Pro
                                     -25 -20 -15
ttg ctt tca tcc tgt ggc ctc cca cca agc act gcc tca gct gtg cgc 271
Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser Ala Val Arg
                                     -10 -5 1
agg cta tgc tcc agg gga gtg tta aaa gga tca aat gaa aga agg gat 319
Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu Arg Arg Asp
5 10 15
atg gaa tca ttt tgg aaa cta aat cgt tcc cca ggg tcg gac cga tac 367
Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser Asp Arg Tyr
20 25 30 35
ctg gag agc cgc gat gcc tct cga ctg agt ggc cgg gac ccc tcc tca 415
Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp Pro Ser Ser
40 45 50
tgg aca gtc gag gat gtg atg cag ttt gtc cgg gaa gct gat cct cag 463
Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala Asp Pro Gln
55 60 65
ctt gga ccc cac gct gac ctg ttt cgc aaa cac gag atc gat ggc aag 511
Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile Asp Gly Lys
70 75 80
gcc ctg ctg ctg ctg cgc agt gac atg atg atg aag tac atg ggc ctg 559
Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr Met Gly Leu
85 90 95
aag ctg ggg cct gca ctc aag ctc tcc tac cac att gac cgg ctg aag 607
Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp Arg Leu Lys
100 105 110 115
cag ggc aag ttc tgaaccagga gaggcagcct agacaaccaa gtggcagcag 659
Gln Gly Lys Phe
gtgggggcat tcttctagga atgaggggca tcagcccacc ccaggcacct cagtgggggtt 719
ccggggccacc tcaggactcc aagaggctgt gtggagccac cactcctagc cacagctgcc 779
atgataagtc cttccatgaa ggactgagga gggagagtgg ggggccaggg ctggtgctgc 839
tcttccctca gctctgccgg ggctctaagg tccctctatt tatttctcaa ccctggctgg 899
cctctcacca ggagtttagg ctgaatgcct tccacgtgat ggaggaaaag gccaactctg 959
tctgtgtcct gctgtggcac cccatcgccc cacagctcgt accttctcac cagattcccc 1019
tgaatccaaa ctsgtgggtgc aaacctctac cttttttaca aaaagatctt attgttaatt 1079
tattgtttct ggcacttggg caaacctgt agttaatact cctcccmac actagacact 1139
gggtttcagg aggagggaga ctgccctgct ttggtcccca gagaggccct ctgcagatag 1199
gcgtggcccc tcttcagagg acactaccct agggcacttt ctctttgagg tggagagacc 1259
cataaagcct tgaccacatc actccatatg gggaggagaa ggatccctgt caccttctcc 1319
tctcttcacg gggccctttt gcagccctag gcctcatctg tgggaaggga gtccctggct 1379
tatactgccc ccaccacagc tccttgccct ggccagaact gctgtcgaag aaaatcaggc 1439
cggaaggcca agaaggcgct aagggggatg ggagggcagg ttttccaggc tggagtgggt 1499
tccaccact cgctgtcca caggcttcct tgtaagcaag tcagcagcac agctactcac 1559
gctgccatct ggacttattt tatgtcaatc tgtttataaa taaaaaccaa tataggtaaa 1619
aaaaaaaaa aaaaaa 1634

```

<210> 114
 <211> 693
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 223..417

<220>

<221> sig_peptide

<222> 223..270

<223> Von Heijne matrix

score 4.19788230215007

seq LACVRESTSVAWA/CK

<400> 114

| | | | | | | |
|------------|------------|------------|------------|-----------------|------------|-----|
| ttagggggcc | tgtaacccag | cacgtgcatc | gggggctgtc | ccgggggtca | ggggagggag | 60 |
| gccagcgggc | mgtgtcgggg | tccgccccga | ccccatccac | gaccccgact | cctatccgat | 120 |
| cctatccccg | gccccgctcg | ggcctttccc | cttgccgcct | ggctcggtcg | gctcgacgag | 180 |
| cagtaagttc | gtagccgccc | tccgaagccg | ggcgtgcatg | gg atg gca | gag ttg | 234 |
| | | | | Met Ala Glu Leu | | |

-15

| | | | | | | | | |
|---------|---------|---------|---------|---------|----------|---------|---------|-----|
| gcg tgc | gtg cgt | gag tcc | acc agt | gtg gca | tggt gca | tgt aag | gtg cgc | 282 |
| Ala Cys | Val Arg | Glu Ser | Thr Ser | Val Ala | Trp Ala | Cys Lys | Val Arg | |

-10

-5

1

| | | | | | | | | |
|---------|---------|---------|---------|---------|---------|---------|---------|-----|
| gga ggg | act gca | cct tct | cca tca | ggg gca | gaa ggc | cac gtc | atg ctg | 330 |
| Gly Gly | Thr Ala | Pro Ser | Pro Ser | Gly Ala | Glu Gly | His Val | Met Leu | |

5

10

15

20

| | | | | | | | | |
|---------|---------|---------|---------|---------|---------|---------|---------|-----|
| aac aag | agc cga | gaa gta | gaa tcg | cca gtg | tca agc | cgt cca | cgt tgt | 378 |
| Asn Lys | Ser Arg | Glu Val | Glu Ser | Pro Val | Ser Ser | Arg Pro | Arg Cys | |

25

30

35

| | | | | | | | | |
|---------|---------|---------|---------|---------|---------|-----------|--------|-----|
| ggg atg | ccc act | ggt ccc | cca gga | tca ctc | aag acc | ctg tgact | ttgtgg | 427 |
| Gly Met | Pro Thr | Val Pro | Pro Gly | Ser Leu | Lys Thr | Leu | | |

40

45

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| tcactgatga | gtggaccaag | tgaagtccac | aagatggctg | ctgtggctcc | aggcatcacg | 487 |
| tccacatgca | aatccatcca | gaggcaggaa | ctgggaatag | gcttggaggt | ggccaggaca | 547 |
| gcaagtgggc | tgtctgtata | aacctcccct | ccacttggga | aggaaaatca | ccccccaagt | 607 |
| cgattttctg | tccatcttat | tgatcagaga | gcgttataaa | ttcaccatt | aaataatctg | 667 |
| gacaagggga | aaaaaaaaaa | aaaaaa | | | | 693 |

<210> 115

<211> 784

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 166..732

<220>

<221> sig_peptide

<222> 166..237

<223> Von Heijne matrix

score 6.60662787180923

seq KMHLLVLSGAWG/MQ

<400> 115

| | | | | | | |
|------------|------------|------------|------------|-----------------|-------------|-----|
| attattgggt | gggggaaacc | cacgagggga | cgcggccgag | gagggctcgt | gtccaccg | 60 |
| gggcgtggga | gtgaggtacc | agattcagcc | catttggccc | cgacgcctct | gttctcgga | 120 |
| tccgggtgct | gcggattgag | gtcccgggtc | ctaacggact | gcaag atg | gag gaa ggc | 177 |
| | | | | Met Glu Glu Gly | | |

| | | | | | | | | |
|---------|---------|---------|---------|---------|---------|---------|---------|-----|
| ggg aac | cta gga | ggc ctg | att aag | atg gtc | cat cta | ctg gtc | ttg tca | 225 |
| Gly Asn | Leu Gly | Gly Leu | Ile Lys | Met Val | His Leu | Leu Val | Leu Ser | |

-20

-15

-10

-5

```

ggg gcc tgg ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg      273
Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu
      1      5      10
ctt ttc cga agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa      321
Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys
      15      20      25
ctc ttc ccc ttc tac ttc cac atc tcc atg ggc tgt gsc ttc atc aac      369
Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Xaa Phe Ile Asn
      30      35      40
ctc tgc atc ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg      417
Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp
      45      50      55      60
gag gcc agc cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act      465
Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr
      65      70      75
gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc      513
Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala
      80      85      90
ctg caa acc gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc      561
Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly
      95      100      105
agc cac cag ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc      609
Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro
      110      115      120
aag tac agt gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc      657
Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser
      125      130      135      140
tct ctt tgc aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct      705
Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
      145      150      155
ggc ctt gcc ctg gaa ata agg agc ctc tagcatgggc cctgcatgct      752
Gly Leu Ala Leu Glu Ile Arg Ser Leu
      160      165
aataaatgct tctccaaaaa aaaaaaaaaa aa      784

```

```

<210> 116
<211> 804
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 75..623

```

```

<220>
<221> sig_peptide
<222> 75..215
<223> Von Heijne matrix
      score 8.34104221735598
      seq RLLLPCLVRMALC/AP

```

```

<400> 116
agtacggtgg ccgacgggag tcagacgctg gggatgaatg aaggtgctgg gtgcaggatc      60
aacaaacagt aata atg act gaa tgt aca agt ctt cag ttt gtc agc cct      110
      Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro
      -45      -40
ttt gct ttt gag gca atg cag aag gtg gat gtt gtt tgc ctg gca tct      158
Phe Ala Phe Glu Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser

```

| | | | | |
|---|-----|-----|-----|-----|
| -35 | -30 | -25 | -20 | |
| tta agt gat cca gaa tta aga ctt ctt ctg ccc tgt ttg gta cgg atg | | | | 206 |
| Leu Ser Asp Pro Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met | | | | |
| | -15 | -10 | -5 | |
| gca ctt tgt gca cct gct gac cag agc caa agc tgg gct cag gat aag | | | | 254 |
| Ala Leu Cys Ala Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys | | | | |
| | 1 | 5 | 10 | |
| aaa ctc atc ctt cgc ctt ctt tct gga gtg gaa gct gtc aac tcc att | | | | 302 |
| Lys Leu Ile Leu Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile | | | | |
| | 15 | 20 | 25 | |
| gtt gca ttg ttg tcc gtg gac ttt cat gct tta gaa caa gat gcc agc | | | | 350 |
| Val Ala Leu Leu Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser | | | | |
| | 30 | 35 | 40 | 45 |
| aaa gaa cag cag ctt aga ccg agt ctt gcc ctg ttg ccc agg ctg gag | | | | 398 |
| Lys Glu Gln Gln Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu | | | | |
| | 50 | 55 | 60 | |
| tgc ggt ggc gtg atc tcg gct cac tgc aac ctc cac ctc ctg ggt tca | | | | 446 |
| Cys Gly Gly Val Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser | | | | |
| | 65 | 70 | 75 | |
| agt gat tct tct gcc tca gtc tcc cga gta gat ggg act aca ggc acg | | | | 494 |
| Ser Asp Ser Ser Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr | | | | |
| | 80 | 85 | 90 | |
| cgc cac cat gcc cgg ctt ttt tgt att att agt aga gac gag gtt tca | | | | 542 |
| Arg His His Ala Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser | | | | |
| | 95 | 100 | 105 | |
| cca tat tgg cca ggc tgg tct cga act ccc aac ctt gtg atc cac ctg | | | | 590 |
| Pro Tyr Trp Pro Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu | | | | |
| | 110 | 115 | 120 | 125 |
| cct cag cct ccc aaa gta ctg gga tta ccg gcg tgagccactg tgcctggcct | | | | 643 |
| Pro Gln Pro Pro Lys Val Leu Gly Leu Pro Ala | | | | |
| | 130 | 135 | | |
| atgtggtgga gtatttatta tacgtaggat gtgaatccct gaaatacaca ggcaaactaa | | | | 703 |
| atagcatttc agaagtaaca gaacatttta gaacacttta tacatccttt tatagcttat | | | | 763 |
| ttcaataaaaa gataattttt atacaaaaaa aaaaaaaaaa a | | | | 804 |

<210> 117
 <211> 484
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..335

<220>
 <221> sig_peptide
 <222> 30..71
 <223> Von Heijne matrix
 score 4.49063834776683
 seq FLTALLWRGRIPG/RQ

| | | | | |
|---|-----|-----|-----|-----|
| <400> 117 | | | | |
| gcagagtctt gagcagcgcg gcaggcacc atg ttc ctg act gcg ctc ctc tgg | | | | 53 |
| | Met | Phe | Leu | Thr |
| | | | | Ala |
| | | | | Leu |
| | | | | Leu |
| | | | | Trp |
| | | | | -10 |
| cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg ccg | | | | 101 |
| Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg Pro | | | | |
| | -5 | 1 | 5 | 10 |

```

cgg ttc gtg tgc ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag      149
Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu
              15              20              25
atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg      197
Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg
              30              35              40
gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc gag      245
Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe Glu
              45              50              55
gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga ttc att      293
Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg Phe Ile
              60              65              70
gcg gac cag ctc gac cat ctc aat gtc acc aag aaa tgg tcc      335
Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser
              75              80              85
taatcctgag tcgtcaccct tggattttat ggatcacgga gctgaccatc tttacctggt      395
cctggaactg aaaaactgta gcttgtgtga aaatgagcct ttggaccagt ctttattaaa      455
acaaacaaac acaaaaaaaaa aaaaaaaaaa      484

```

<210> 118
 <211> 985
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..752

<220>
 <221> sig_peptide
 <222> 21..107
 <223> Von Heijne matrix
 score 3.61056351168286
 seq FPLYLLNFLGLWS/WI

```

<400> 118
gttttttttcc cttctgagca atg gag ctt acc atc ttt atc ctg aga ctg gcc      53
              Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala
              -25              -20
att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg ggc ttg      101
Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu
              -15              -10              -5
tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc      149
Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe
              1              5              10
act gtg ata tac aac gaa cag atg gca agc aag aag cgg gag ctc ttc      197
Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe
              15              20              25              30
agt aac ctg cag gag ttt gcg ggc ccc tcc ggg aaa ctc tcc ctg ctg      245
Ser Asn Leu Gln Glu Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu
              35              40              45
gaa gtg ggc tgt ggc acg ggg gcc aac ttc aag ttc tac cca cct ggg      293
Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly
              50              55              60
tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg      341
Cys Arg Val Thr Cys Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu
              65              70              75
atc aag agc att gca gag aac cga cac ctg cag ttt gag cgc ttt gtg      389

```


| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|------------|------------|-----|-----|-----|-----|-----|-----|--|
| Ile | Lys | Ser | Ile | Ala | Glu | Asn | Arg | His | Leu | Gln | Phe | Glu | Arg | Phe | Val | | |
| 80 | | | | | | 85 | | | | 90 | | | | | | | |
| gta | gct | gcc | ggg | gag | aac | atg | cac | cag | gtg | gct | gat | ggc | tct | gtg | gat | 437 | |
| Val | Ala | Ala | Gly | Glu | Asn | Met | His | Gln | Val | Ala | Asp | Gly | Ser | Val | Asp | | |
| 95 | | | | | 100 | | | | | 105 | | | | | 110 | | |
| gtg | gtg | gtc | tgc | acc | ctg | gtg | ctg | tgc | tct | gtg | aag | aac | cag | gag | cgg | 485 | |
| Val | Val | Val | Cys | Thr | Leu | Val | Leu | Cys | Ser | Val | Lys | Asn | Gln | Glu | Arg | | |
| | | | | 115 | | | | | 120 | | | | | 125 | | | |
| att | ctc | cgc | gag | gtg | tgc | aga | gtg | ctg | aga | ccg | gga | ggg | gct | ttc | tat | 533 | |
| Ile | Leu | Arg | Glu | Val | Cys | Arg | Val | Leu | Arg | Pro | Gly | Gly | Ala | Phe | Tyr | | |
| | | | 130 | | | | | 135 | | | | | 140 | | | | |
| ttc | atg | gag | cat | gtg | gca | gct | gag | tgt | tcg | act | tgg | aat | tac | ttc | tgg | 581 | |
| Phe | Met | Glu | His | Val | Ala | Ala | Glu | Cys | Ser | Thr | Trp | Asn | Tyr | Phe | Trp | | |
| | | | 145 | | | | | 150 | | | | 155 | | | | | |
| caa | caa | gtc | ctg | gat | cct | gcc | tgg | cac | ctt | ctg | ttt | gat | ggg | tgc | aac | 629 | |
| Gln | Gln | Val | Leu | Asp | Pro | Ala | Trp | His | Leu | Leu | Phe | Asp | Gly | Cys | Asn | | |
| | | | 160 | | | | 165 | | | | 170 | | | | | | |
| ctg | acc | aga | gag | agc | tgg | aag | gcc | ctg | gag | cgg | gcc | agc | ttc | tct | aag | 677 | |
| Leu | Thr | Arg | Glu | Ser | Trp | Lys | Ala | Leu | Glu | Arg | Ala | Ser | Phe | Ser | Lys | | |
| | | | | | 180 | | | | 185 | | | | | 190 | | | |
| ctg | aag | ctg | cag | cac | atc | cag | gcc | cca | ctg | tcc | tgg | gag | ttg | gtg | cgc | 725 | |
| Leu | Lys | Leu | Gln | His | Ile | Gln | Ala | Pro | Leu | Ser | Trp | Glu | Leu | Val | Arg | | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| cct | cat | atc | tat | gga | tat | gct | gtg | aaa | tagtgtgagc | tggcagttaa | | | | | | 772 | |
| Pro | His | Ile | Tyr | Gly | Tyr | Ala | Val | Lys | | | | | | | | | |
| | | | 210 | | | | 215 | | | | | | | | | | |
| gagctgaatg | gctcaaagaa | tttaaagctt | cagttttaca | tttaaaatgc | taggtgggtg | | | | | | | | | | | 832 | |
| cctgtaatcc | caggtacttg | gaaggctgag | gcaggagaat | ctcttgaacc | cagaaggcga | | | | | | | | | | | 892 | |
| aggttgcaat | gaaccgagat | catgccattg | tactctagcc | tgggtgacaa | gagcaagact | | | | | | | | | | | 952 | |
| ccgtctcaaa | aaaaaataaa | aaaaaaaaaa | aaa | | | | | | | | | | | | | 985 | |

<210> 119
 <211> 839
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..715

<220>
 <221> sig_peptide
 <222> 185..253
 <223> Von Heijne matrix
 score 9.49395175807817
 seq SLLFICFFGESFC/IC

| | | | | | | | | | | | | | | | | | |
|--------------|-------------|-------------|-------------|-------------|-------------|--|--|--|--|--|--|--|--|--|--|-----|--|
| <400> 119 | | | | | | | | | | | | | | | | | |
| atattttgct | gactggcaag | gttatatgaa | gtgcttttat | tgaagcacca | ttttaactaa | | | | | | | | | | | 60 | |
| cagctcctgg | tattttctgc | ttcccttcgt | aggggaattta | gttattttat | tttattat | | | | | | | | | | | 120 | |
| agctaattta | gctattttta | aatagctaaa | ttttagctac | ttttttttca | attgacaaag | | | | | | | | | | | 180 | |
| aagg atg tct | aat caa aga | cta ccg ctg | att ttt tct | ctg ttg ttt | atc | | | | | | | | | | | 229 | |
| | Met Ser Asn | Gln Arg Leu | Pro Leu Ile | Phe Ser Leu | Leu Phe Ile | | | | | | | | | | | | |
| | | -20 | | -15 | | | | | | | | | | | | | |
| tgc ttc ttc | ggg gag agt | ttc tgc att | tgt gat gga | act gtc tgg | aca | | | | | | | | | | | 277 | |
| Cys Phe Phe | Gly Glu Ser | Phe Cys Ile | Cys Asp Gly | Thr Val Trp | Thr | | | | | | | | | | | | |
| | -5 | | 1 | | 5 | | | | | | | | | | | | |
| aag gtt gga | tgg gag att | ctt cca gaa | gaa gta cat | tat tgg aaa | gtt | | | | | | | | | | | 325 | |

```

Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val
 10          15          20
aag ggt tct cca tct cac tgc ctg cct tat ctt ctg gat aaa cta tgc      373
Lys Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys
25          30          35          40
tgc gac ttt gct aac atg gat ata ttt cag ggt tgt tta tat ctc att      421
Cys Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile
          45          50          55
tat aat tta tta caa gct gtc ttc ttc gtc tta ttt gtt ttg tct gtg      469
Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val
          60          65          70
cat tac ctg tgg aag aaa tgg aag aaa cac caa aaa aag ctg aaa aag      517
His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys
          75          80          85
caa gcc tcc tta gaa aaa cct ggt aat gat cta gaa agc cca ttg atc      565
Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile
          90          95          100
aac aac att gac caa aca ctc cac aga gtg gca acc aca gca tca gtg      613
Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val
          105          110          115          120
ata tac aag atc tgg gag cac agg tct cac cat cct tcc tct aag aaa      661
Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys
          125          130          135
att aag cac tgc aaa tta aag aag aag agt aaa gaa gaa gga gcc aga      709
Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg
          140          145          150
aga tac taaataaatg catatgcaaa tgtagcttac tcaattatag atatcacaaa      765
Arg Tyr
agaaatctat catctaagga ttaaaaattg ttctttggaa acctttataa aaaaaaaaga      825
aaaaaaaaaa aaaa      839

<210> 120
<211> 583
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..527

<220>
<221> sig_peptide
<222> 54..116
<223> Von Heijne matrix
      score 6.80928714315144
      seq ALXSLNLAPPTVA/AP

<400> 120
aacgtcatct aggagcaccg agcagcttgg ctaaaagtaa ggggtgctgtg ctg atg      56
                                   Met
gcc ctg tgc gca ctg acc cgc gct ctg ccs tct ctg aac ctg gcg ccc      104
Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala Pro
-20          -15          -10          -5
ccg acc gtc gcc gcc cct gcc ccg agt ctg ttc ccc gcc gcc cag atg      152
Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln Met
          1          5          10
atg aac aat gcc ctc ctc caa cag ccc tct gcc ttg atg ttg ctc ccc      200
Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu Pro

```

```

      15      20      25
tgc cgc cca gtt ctt act tct gtg gcc ctt aat gcc aac ttt gtg tcc      248
Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser
      30      35      40
tgg aag agt cgt acc aag tac acc att aca cca gtg aag atg agg aag      296
Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys
      45      50      55      60
tct ggg ggc cga gac cac aca ggt gct gga aac gtg cgt aga aca gta      344
Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr Val
      65      70      75
ggc cga gta tcc aac gtt gat cat aac aaa cgg gtc att ggc aag gca      392
Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys Ala
      80      85      90
ggg cgc aac cgc tgg ctg ggc aag agg cct aac agt ggg cgg tgg cac      440
Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp His
      95      100      105
cgc aag ggg ggc tgg gct ggc cga aag att cgg cca cta ccc ccc atg      488
Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro Met
      110      115      120
aag agt tac gtg aag ctg cct tct gct tct gcc caa agc tgatatccct      537
Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
      125      130      135
gtactctaataaaaatgcccc cccccctcaaaaaaaaaa aaaaaa      583

<210> 121
<211> 1024
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 129..686

<220>
<221> sig_peptide
<222> 129..185
<223> Von Heijne matrix
      score 6.45239823575329
      seq SVFLLMVNGQVES/AQ

<400> 121
cttcgcgaag gtgtcgctgc caagaaacgt gtcctgcgcg ctacgccgtc tgtttctagg      60
gcaacgccgg cgtctcttag caaccgcgcg cggcctagggt ggggtcccccc ggcaccccca      120
gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac      170
      Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn
      -15      -10
ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc      218
Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys
      -5      1      5      10
aag tac tgc ttt gtg tac ggc cag gac tgg gcc ccc aca gcg ggt ctg      266
Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu
      15      20      25
gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa      314
Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln
      30      35      40
gca ctg gtg tgg aac ttc ccc att gat gtc acc ttt aaa agc acc aac      362
Ala Leu Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn
      45      50      55

```

```

ccc tac ggc tgg cca cag atc gtg ctc agc gtg tat gga cca gat gtg      410
Pro Tyr Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val
60          65          70          75
ttc ggg aac gat gtg gtt cga ggc tat ggg gcc gtg cac gtg ccc ttc      458
Phe Gly Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe
80          85          90
tca cct ggc cgg cac aaa agg acc atc ccc atg ttt gtc cca gaa tct      506
Ser Pro Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser
95          100          105
acg tct aaa ctg cag aag ttt aca agc tgg ttc atg ggg cgg cgg ccc      554
Thr Ser Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro
110          115          120
gag tac aca gac ccc aag gtg gtg gct cag ggt gaa gcc cgg gaa gct      602
Glu Tyr Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala
125          130          135
atc aca gct ccc cgg aaa gct gtc ttc tct gtc cat ggc ctc acc tca      650
Ile Thr Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser
140          145          150          155
ccc agg gca ctg gcc ttg gtc cac atc aag ggg acc tgaagcttcc      696
Pro Arg Ala Leu Ala Leu Val His Ile Lys Gly Thr
160          165
ctgaagcctc tagcctgtgg tgtgcacgta caagcctcag gccccatttg tccagcctgt      756
cagcagctgg gaaatactaa gtcaccctct tctggttatg ttttaattttc caatttttct      816
caacattact gaaatgtcta aatgtggaaa agttgacatc attttacagt gaacaccaca      876
taccaccac ctagatttta ccattaccaa tttcctgttc cgtacttgta tattcacata      936
tatccaacta ttcattccctg cttcaatcca tcctattttt attgcatttc aaaataaact      996
gtgaaatcag gaaaaaaaaa aaaaaaaaaa      1024

```

```

<210> 122
<211> 760
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 165..614

```

```

<220>
<221> sig_peptide
<222> 165..305
<223> Von Heijne matrix
      score 5.10820788278539
      seq ALGLALCSTKALS/VG

```

```

<400> 122
aatttccgat gccaggcacc ctcaaggcac agaggctggg gctcatgttg ggggcacttg      60
gcctctccag gcctcgaagg cttctcctgg gctgatgcga gctggggaac gggagggacg      120
gacgtgggag cgagaacgtc acactggagg cagctgggtgg cacg atg ggg gac aga      176
                               Met Gly Asp Arg
                               -45
gtg aaa ggt agc aag tca aga gcc ttc gtg tca cca tgg cca cac acc      224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr
-40          -35          -30
ccg atg gct tcc ggc ttg agg gac ccc tgg ctg cag ccc aca gcc ctg      272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu
-25          -20          -15
ggc ctt gca ctg tgc tct acg aag gcc ctg tcc gtg ggc tct gcc cct      320
Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val Gly Ser Ala Pro

```

| | | | | |
|---|---------------------|-----------------|-----------------|-----|
| -10 | -5 | 1 | 5 | |
| ttg ccc ccg cga aat tcc aac acc atg gcg gcg gct gcc ctg gct gcc | | | | 368 |
| Leu Pro Pro Arg | Asn Ser Asn Thr Met | Ala Ala Ala Ala | Leu Ala Ala | |
| | 10 | 15 | 20 | |
| ccc agc ctg ggc ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc | | | | 416 |
| Pro Ser Leu Gly | Phe Asp Gly Val | Ile Gly Val Leu | Val Ala Asp Thr | |
| | 25 | 30 | 35 | |
| agc ctc acg gac atg cac gtg gtg gat gta gag ctg agc gga ccc cgg | | | | 464 |
| Ser Leu Thr Asp | Met His Val Val | Asp Val Glu Leu | Ser Gly Pro Arg | |
| | 40 | 45 | 50 | |
| ggc ccc acg ggc cga agc ttt gct gtg cac acc cgc aga gag aac cct | | | | 512 |
| Gly Pro Thr Gly | Arg Ser Phe Ala | Val His Thr Arg | Arg Glu Asn Pro | |
| | 55 | 60 | 65 | |
| gcc gag cca ggc gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg | | | | 560 |
| Ala Glu Pro Gly | Ala Val Thr Gly | Ser Ala Thr Val | Thr Ala Phe Trp | |
| | 70 | 75 | 80 | 85 |
| cgg agc ctc ctg gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat | | | | 608 |
| Arg Ser Leu Leu | Ala Cys Cys Gln | Leu Pro Ser Arg | Pro Gly Ile His | |
| | 90 | 95 | 100 | |
| ctc tgc tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc | | | | 664 |
| Leu Cys | | | | |
| accaccatcc caccctgcc ctgcccact tcccagggt ctcccttctg actcagtaaa | | | | 724 |
| gatcaccgct gcctccctca aaaaaaaaaa aaaaaa | | | | 760 |

<210> 123
 <211> 594
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 192..476

<220>
 <221> sig_peptide
 <222> 192..326
 <223> Von Heijne matrix
 score 6.60884760057354
 seq FILLLLLSGPAEM/SA

| | |
|---|-----|
| <400> 123 | |
| actttttattg aaaaagacta cagcaaata tactgaggtg aatgaagaca gtgaaatgaa | 60 |
| ggagaaggca ggtcctcttt atgttttcgc agctggttca aggggttttg gggtttctat | 120 |
| ctaggttaaa gattgcgtaa tacacagctg gagccataga cattaatgca tgtttatcac | 180 |
| acgcaacaac g atg ctg cat cat gtg att aca gct ggg cct gtg ctg ctt | 230 |
| Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu | |
| -45 -40 -35 | |
| cta cac ctc cct cgc cct gac act tcc acc agg ttg ctc ctc acc tcc | 278 |
| Leu His Leu Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser | |
| -30 -25 -20 | |
| gtc tct gct ttt atc ctc tta ctg ctc ctt tca gga cca gca gaa atg | 326 |
| Val Ser Ala Phe Ile Leu Leu Leu Leu Ser Gly Pro Ala Glu Met | |
| -15 -10 -5 | |
| tca gct tcc cag gaa tcc ttc cct gga tct ctg cag caa gaa ata gct | 374 |
| Ser Ala Ser Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala | |
| 1 5 10 15 | |
| tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct | 422 |
| Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser | |

| | | | | |
|---|----|----|----|-----|
| | 20 | 25 | 30 | |
| acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta | | | | 470 |
| Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val | | | | |
| | 35 | 40 | 45 | |
| aac ctt tgaaggtatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct | | | | 526 |
| Asn Leu | | | | |
| | 50 | | | |
| gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaactt gaaaaaaaaa | | | | 586 |
| aaaaaaaa | | | | 594 |

<210> 124
 <211> 559
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..297

<220>
 <221> sig_peptide
 <222> 16..93
 <223> Von Heijne matrix
 score 6.65836819891491
 seq FCGSACLLAVIRA/FF

| | |
|--|-------------|
| <400> 124 | |
| ttacacaggg gataa atg gca gca atc gag att gaa gtc aag cct aac cag | 51 |
| Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln | |
| | -25 -20 -15 |
| ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt | 99 |
| Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe | |
| | -10 -5 1 |
| ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg | 147 |
| Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu | |
| | 5 10 15 |
| ggc ggc atg ggc cct gtg gtc ttt tcg tac aga ggg ctt cct ctt tgg | 195 |
| Gly Gly Met Gly Pro Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp | |
| | 20 25 30 |
| ctc ttt gcc tgg ttg ttt oca aga tgt act gtg cct ctt act ttc ggt | 243 |
| Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly | |
| | 35 40 45 50 |
| ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc | 291 |
| Phe Glu Asn Met Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro | |
| | 55 60 65 |
| agc act tagggaggcc gagggcgggag gatggcttga ggtccgtagt tgagaccagc | 347 |
| Ser Thr | |
| ctggccaaca tgggtgaagcc tgggtctctac aaaaaaataa taacaaaaaat tagccgggtg | 407 |
| tgggtggctcg tgcctgtggt ccagctgct ccggtggctg aggcgggagg atctcttgag | 467 |
| cttaggcttt tgagctatca tggcgccagt gcaactccagc gtgggcaaca gagcgagacc | 527 |
| ctgtctctca aaaacaaaaa aaaaaaaaaa aa | 559 |

<210> 125
 <211> 744
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 216..635

<220>
 <221> sig_peptide
 <222> 216..335
 <223> Von Heijne matrix
 score 4.38054120608596
 seq ITLVSAAPGKVIC/EM

<400> 125
 gcttcgtcac aagggtgcga tgaaagtcag tgagcaaadc gcggaccacc ggggctgcca 60
 gctcgccctga ctcccggcct cttgcgctcc taggggcgga gaagggtgcg ggctcttcgc 120
 cctttgtgtc ctccctcttt cactaacttc tggactttcc agctcttccg aagttcgttc 180
 ttgcgcaaag cccaaaggct ggaaaaccgt ccacg atg acc agc atg act cag 233
 Met Thr Ser Met Thr Gln
 -40 -35
 tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag 281
 Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu
 -30 -25 -20
 aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg 329
 Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val
 -15 -10 -5
 att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act 377
 Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr
 1 5 10
 ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg 425
 Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met
 15 20 25 30
 gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg 473
 Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met
 35 40 45
 aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att 521
 Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile
 50 55 60
 aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg 569
 Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val
 65 70 75
 gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac 617
 Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His
 80 85 90
 aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaaagaaac 665
 Thr Lys His Leu Gly Asn
 95 100
 ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg aaataaacta 725
 gcaaaaaaaaa aaaaaaaaaa 744

<210> 126
 <211> 824
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 164..280

<220>
 <221> sig_peptide

<222> 164..268
 <223> Von Heijne matrix
 score 5.73290676305402
 seq TLPLCPVTSPVWG/WS

<400> 126
 tgtgttcaat cgtgtgaatg gccggcgggc cccctccacg tccccatcct tgcagggggac 60
 ccaggagacc tacacagtgg cccacgagga gaatgtccgc tttgtgtccg aaggtagcga 120
 gcggggccag aggggtgcggc ataggctgct ggggtcgcaaa acc atg gac ccg gga 175
 Met Asp Pro Gly
 -35
 tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc 223
 Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe
 -30 -25 -20
 ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg 271
 Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp
 -15 -10 -5 1
 agt cca ggg tgaccatcag gccctgggtg ggcgatggggg tgcctggggac 320
 Ser Pro Gly
 ctgggtcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat 380
 ggtggcccag ccggtgaggg cgggccaagg cctgtgcagt acgtggagag gacccccaat 440
 ccccggtctgc agaactttgt gccattttac ctgacgaggt ggtgggcgca gcagttcctg 500
 gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc 560
 tgctgccagg agagaagcat ggcgccctgc ccacccactg cgcctggctg ggtgccggcc 620
 acacctgaag tgccagcatt tggacttttg cacctttttt tcccttggcc cggctgtccc 680
 aaccaagctg ccatggccaa gggccgaacc cgtctgacct cagccctgct cactgtgccc 740
 agggaccagc gaccagcccc tggggctggc agggaggagc tccaggctaa taaagtggag 800
 aaactgtcaa aaaaaaaaaa aaaa 824

<210> 127
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..301

<220>
 <221> sig_peptide
 <222> 68..190
 <223> Von Heijne matrix
 score 4.68908216483476
 seq AYLLYILLTGALQ/FG

<400> 127
 acatccggtg tggctgacgg gtcctccaag agtttggggc gcggaccgga gtaccttgcg 60
 tgcagtt atg tcg gcg tcg gta gtg tct gtc att tcg cgg ttc tta gaa 109
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu
 -40 -35 -30
 gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac 157
 Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr
 -25 -20 -15
 ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc 205
 Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu
 -10 -5 1 5
 ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct 253
 Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser

| | | | | |
|---|----|----|----|-----|
| | 10 | 15 | 20 | |
| tgt gtg ggg agt ttc atc cta gcg ggt tca ctc ttt gaa ttt cct gga | | | | 301 |
| Cys Val Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly | | | | |
| | 25 | 30 | 35 | |
| taagagttct ggagatggca gcttattgga cacatggatt ttcttcagat ttgcacttac | | | | 361 |
| tgctagctct gctttttatg caggagaaaa gccagagtt cactgtgtgt cagaacaact | | | | 421 |
| ttctaacaaa catttattaa tccagcctct gcctttcatt aaatgtaacc ttttgccttc | | | | 481 |
| caaattaaag aactccatgc cactcctcaa aaaaaaaaaa aaaaa | | | | 526 |

<210> 128
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 179..427

<220>
 <221> sig_peptide
 <222> 179..298
 <223> Von Heijne matrix
 score 7.72883276007822
 seq CLVVVTMATLSLA/RP

| | |
|--|-----|
| <400> 128 | |
| aagcgaagag atgggtctgc actttggagg agccggacac tgttgacttt cctgatgtga | 60 |
| aatctaccca ggaacaaaac accagtgact gcagcagcag cggcagcgcc tcggttccctg | 120 |
| agcccaccgc aggctgaagg cattgcgcgt agtccatgcc cgtagaggaa gtgtgcag | 178 |
| atg gga tta acg tcc aca tgg aga tat gga aga gga ccg ggg att ggt | 226 |
| Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly | |
| -40 -35 -30 -25 | |
| acc gta acc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc | 274 |
| Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val | |
| -20 -15 -10 | |
| acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag | 322 |
| Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu | |
| -5 1 5 | |
| gat acc aca tta gag cca gaa gat gcc atc tca tcc gga gat gat gag | 370 |
| Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu | |
| 10 15 20 | |
| gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac | 418 |
| Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn | |
| 25 30 35 40 | |
| aag agt aag taactgcccg gctccgatgg tccccgagag aggagcatgg | 467 |
| Lys Ser Lys | |
| agggaagttc tgcctgtcac ctgtcttctt gtgcactctt ctgcgccatg ctgtgtcccg | 527 |
| cggcccttgc ctttccccgc tgtgtctact ttctgtactt tcaaacctga gaataaacca | 587 |
| gtgttgctgc acataaaaaa aaaaaaaaaa a | 618 |

<210> 129
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..297

<220>
 <221> sig_peptide
 <222> 22..66
 <223> Von Heijne matrix
 score 4.68058603039206
 seq VLAGSLLGPTSRS/AA

<400> 129
 actgcggggac ccactgcgga t atg gct gtc ttg gct gga tcc ctg ttg ggc 51
 Met Ala Val Leu Ala Gly Ser Leu Leu Gly
 -15 -10
 ccc acg agt agg tcg gca gcg ttg ctg ggt ggc agg tgg ctc cag ccc 99
 Pro Thr Ser Arg Ser Ala Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro
 -5 1 5 10
 cgg gcc tgg ctg ggg ttc cca gac gcc tgg ggc ctc ccc acc ccg cag 147
 Arg Ala Trp Leu Gly Phe Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln
 15 20 25
 cag gcc cgg ggc aag gct cgc ggg aat gag tat cag ccg agc aat atc 195
 Gln Ala Arg Gly Lys Ala Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile
 30 35 40
 aaa cgc aag aac aag cac ggc tgg gtc cgg cgc ctg agc acg ccg gcc 243
 Lys Arg Lys Asn Lys His Gly Trp Val Arg Arg Leu Ser Thr Pro Ala
 45 50 55
 ggc gtg cag gtc atc ctt cgc cga atg ctc aag ggc cgc aag tcg ctg 291
 Gly Val Gln Val Ile Leu Arg Arg Met Leu Lys Gly Arg Lys Ser Leu
 60 65 70 75
 agc cat tgaggatcgc gacgcagtcg gcggggaccc tcatggaagc atcgccctcg 347
 Ser His
 cctcggacct tgccctggcgc tatttttgca gggagctggg gagcaggaac gcctcggacc 407
 tgagtgtctt ccatattgtg ggtttgaagt ctggatggga gccttgccaa gtcccttttt 467
 aggtttttta attaggaagc atttcgaacc tgcgcaacag accaaagaac agtacaaaga 527
 acatccgtgt acccagtacc ctgactaccg actacctaca acccgctccct gcccctcct 587
 gagttctttt gaagctgata tcaggcatcg gattattttt tctgtaaata tttcagaatg 647
 tatctctcca agatgagagc tcattaaaag ataattacaa agcttatcac atccaaaaga 707
 attatcaata attttgaaat attattaaac gtgtataataa tgttcaaagt tcaaaaaaaaa 767
 aaaaaaaaa 776

<210> 130
 <211> 998
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 9..845

<220>
 <221> sig_peptide
 <222> 9..134
 <223> Von Heijne matrix
 score 6.13963522287438
 seq RSLALAAAPSSNG/SP

<400> 130
 aacgaaag atg gcg gcg ccc gta agg cgg acg ctg tta ggg gtg gcg ggg 50
 Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly
 -40 -35 -30

```

ggg tgg cgg cgg ttc gag agg ctc tgg gcc ggc agt cta agc tct cgc      98
Gly Trp Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg
-25 -20 -15
agc ctg gct ctt gca gcc gca ccc tca agc aac gga tcc cca tgg cgc      146
Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg
-10 -5 1
ttg ttg ggc gcg ttg tgc ctg cag cgg cca cct gta gtc tcc aag ccg      194
Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys Pro
5 10 15 20
ttg acc cca ttg cag gaa gag atg gcg tct cta ctg cag cag att gag      242
Leu Thr Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu
25 30 35
ata gag aga agc ctg tat tca gac cac gag ctt cgt gct ctg gat gaa      290
Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu
40 45 50
aac cag cga ctg gca aag aag aaa gct gac ctt cat gat gaa gaa gat      338
Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp
55 60 65
gaa cag gat ata ttg ctg gcg caa gat ttg gaa gat atg tgg gag cag      386
Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln
70 75 80
aaa ttt cta cag ttc aaa ctt gga gct cgc ata aca gaa gct gat gaa      434
Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu
85 90 95 100
aag aat gac cga aca tcc ctg aac agg aac cta gac agg aac ctt gtc      482
Lys Asn Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val
105 110 115
ctg tta gtc aga gag aag ttt gga gac cag gat gtt tgg ata ctg ccc      530
Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro
120 125 130
cag gca gag tgg cag cct ggg gag acc ctt cga gga aca gct gaa cga      578
Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg
135 140 145
acc ctg gcc aca ctc tca gaa aac aac atg gaa gcc aag ttc cta gga      626
Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly
150 155 160
aat gca ccc tgt ggg cac tac aca ttc aag ttc ccc cag gca atg cgg      674
Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg
165 170 175 180
aca gag agt aac ctc gga gcc aag gtg ttc ttc ttc aaa gca ctg cta      722
Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu Leu
185 190 195
tta act gga gac ttt tcc cag gct ggg aat aag ggc cat cat gtg tgg      770
Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp
200 205 210
gtc att aag gat gag ctg ggt gac tat ttg aaa cca aaa tac ctg gcc      818
Val Ile Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala
215 220 225
caa gtt agg agg ttt gtt tca gac ctc tgatgggccc agctgcctgt      865
Gln Val Arg Arg Phe Val Ser Asp Leu
230 235
ggacggtgct cagacaagtc tgggattaga gcctcaagga cattgtgtga ttgcctcaca      925
tttgcaggta atatcaagca gcaaactaaa ttctgagaaa taaacgagtc tattaccaa
985
aaaaaaaaa aaa      998

```

```

<210> 131
<211> 779
<212> DNA

```

<213> Homo sapiens

<220>

<221> CDS

<222> 27..578

<220>

<221> sig_peptide

<222> 27..119

<223> Von Heijne matrix

score 4.50637135496675

seq TALMVGAASILLEG/RP

<400> 131

```
atctttctgg actggccctg cagagg atg gca tgc acc act act gcc ccc gcc      53
                               Met Ala Cys Thr Thr Thr Ala Pro Ala
                               -30                               -25
cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct      101
Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
      -20                               -15                               -10
gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga      149
Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
      -5                               1                               5                               10
gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt      197
Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
                               15                               20                               25
ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg      245
Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
                               30                               35                               40
tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca      293
Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
                               45                               50                               55
gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct      341
Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
      60                               65                               70
gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tcg      389
Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
      75                               80                               85                               90
tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt      437
Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
                               95                               100                               105
ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag      485
Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
                               110                               115                               120
cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct      533
Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
                               125                               130                               135
act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg      578
Thr Val Asp His Leu Ser Thr Leu Gly Cys Asn Met Arg Glu Leu
      140                               145                               150
tgaacttctg tcttgtttga gccatggttt cattctcttt ttcagccatg tagcctgtgc      638
tgtaactcag taccacatta gcaactagtg aaagtcaatg tgggtaaatt tgtcattctt      698
caggttagaa catttcttcc ttttattctt gtgttttttg ctaaataaac tgggaaatta      758
tagtaaaaaa aaaaaaaaaa a
```

<210> 132

<211> 1025

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 408..710

<220>

<221> sig_peptide

<222> 408..533

<223> Von Heijne matrix

score 5.66440183652506

seq QLCFHLSWLYSWA/SQ

<400> 132

```
atggtttgtt gtgagttcca tgcctcttgg gatcagtcac tgtggccatg catgtttggc 60
cacatgatta atccagtctg ggtcatgacc ttttcttcat ccaaaacaag gtgatgggaa 120
gacaaaaaca atagctacta caaacaatag gagtttataa ttatgtgctg atgtattcga 180
agatgtgttg acagtcgtga gtgtgtatcc taggaaaggc gagctggact ctgtctccat 240
ggtggctctc accccagggg cctaggaaca gcctgtcacc acacaattac ttttataacc 300
ctggagatga aaatctcctt gtcctcaaaa tacttccaga agaacaacca gatgggaagg 360
accttggttg ggactctttc cagttcactt ggggcagagg gaattta atg gct cac 416
Met Ala His
```

-40

```
gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga 464
Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly
```

-35

-30

-25

```
ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg 512
Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu
```

-20

-15

-10

```
agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt 560
Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val
```

-5

1

5

```
att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt 608
Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val
```

10

15

20

25

```
ctc att ggt cca gac gag gaa ggt atc cag cct caa gtc atc att gtg 656
Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val
```

30

35

40

```
gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac 704
Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His
```

45

50

55

```
aga gac tgagagttgg tgctgggtgt tgtgggtggca gatgatatta cctgaagaag 760
Arg Asp
```

```
ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt 820
ccctgggtgtc ttcattttcc tccgtctccc tgctgtccct taccctctgc ccaatctcat 880
tactcctggt ctggggaggt gccttctgag gatactccac tgggggtacc tgagcctgga 940
ttagaggggca gggggaggat attgcctagc caaagtgggt gttcaataaa gaaccatttg 1000
gagatggcaa aaaaaaaaaa aaaaaa 1025
```

<210> 133

<211> 607

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..501

<220>
 <221> sig_peptide
 <222> 247..306
 <223> Von Heijne matrix
 score 6.43040298500966
 seq LLLVTLVASTVPG/NS

<400> 133
 tggtacaaat attccctatg atctctcctt taaatattct tatcaggata ttggaaattc 60
 ttgattttca caactctgct tcagtggcat atgttttagct ttttgtcttc tgaattaatt 120
 gggcttctga tgggtccctag aggtatcagc tactcagtca gaaaacatac atggggaaga 180
 aactgaagtt catgccacaa actgtagcag ctttgggaaca gaagggacca gacaacctca 240
 aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt 288
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val
 -20 -15 -10
 gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca 336
 Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala
 -5 1 5 10
 cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta 384
 His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val
 15 20 25
 ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat 432
 Phe Gln Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn
 30 35 40
 gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat 480
 Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn
 45 50 55
 tgt tct cac ggg cag gcc ttt tgaaccaccc tggtacagaa caccaaccct 531
 Cys Ser His Gly Gln Ala Phe
 60 65
 ggtgcttttag gctgtctgtg ccatttctag gcaatgaacg agtagttact gtaccaaccc 591
 aaaaaaaaaa aaaaaa 607

<210> 134
 <211> 774
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 333..602

<220>
 <221> sig_peptide
 <222> 333..416
 <223> Von Heijne matrix
 score 4.79986448293481
 seq VPALPLLSSLICMA/MV

<400> 134
 ctcttcagtc cggggccttg ttgaacggac tcaccaggaa acgtgacttt cgtgtccgac 60
 ctctgctgta tcaggattcg attcttgggtg ttaaacaaga caacgctgaa ggctcgggtgc 120
 agcagccctg caaagggtttt tccagcgcctc ttgggaggtg ggctgtgccc tgcctggccc 180
 acctggccca cctggcccac cattacctga agggaagcat gaacagcctt tgacgtggga 240
 gtggcgactg ctgagaggga actgtctgta cacaagcaat gtacgcttat gggacctgag 300
 tggagcccca acccagcag ggcgtgktct tc atg gct ttt cct ggc caa tct 353
 Met Ala Phe Pro Gly Gln Ser
 -25

| | |
|---|-----|
| gat acc aag atg cag tgg cca gaa gta cct gca ctt cca ctc ctg tca | 401 |
| Asp Thr Lys Met Gln Trp Pro Glu Val Pro Ala Leu Pro Leu Leu Ser | |
| -20 -15 -10 | |
| agt ctc tgc atg gct atg gtg agg aag agc tct gca ctg ggc aag gaa | 449 |
| Ser Leu Cys Met Ala Met Val Arg Lys Ser Ser Ala Leu Gly Lys Glu | |
| -5 1 5 10 | |
| gtt ggc cgt cga gtg aag gaa atg gtg atg ctg gtg gcc cct ttc cgg | 497 |
| Val Gly Arg Arg Val Lys Glu Met Val Met Leu Val Ala Pro Phe Arg | |
| 15 20 25 | |
| cag tca agt tcc cta tca agg aca ttc agt tct cgg aaa gtg gtg aag | 545 |
| Gln Ser Ser Ser Leu Ser Arg Thr Phe Ser Ser Arg Lys Val Val Lys | |
| 30 35 40 | |
| gca cat gct tcc ctg cat ggt gcc cgc ctc tct cca ctc tct aga aat | 593 |
| Ala His Ala Ser Leu His Gly Ala Arg Leu Ser Pro Leu Ser Arg Asn | |
| 45 50 55 | |
| att aga ggc taggctgctg ctgtatgtca gggctagtcc ctcttctatg | 642 |
| Ile Arg Gly | |
| 60 | |
| aatccagaat aactctgaag aagccgagta acaggcatga agtgaagaga aatcgctgta | 702 |
| acaggaagac agcaaagcag atgctaata ccaactatt taacgaactg gaaccaacaa | 762 |
| aaaaaaaaaa aa | 774 |

<210> 135
 <211> 611
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 110..376

<220>
 <221> sig_peptide
 <222> 110..208
 <223> Von Heijne matrix
 score 3.64796206065748
 seq LVPHSPLPGALSS/AP

<220>
 <221> misc_feature
 <222> 347
 <223> n=a, g, c or t

| | |
|---|-----|
| <400> 135 | |
| tcttgtcaac actgcccact cagcgaggaa gcagccgcga cgcccacact tctgttgga | 60 |
| gcctgcgcag agccagaggc ctcagaagcc acaggaacat ggcctaggc atg gct cag | 118 |
| Met Ala Gln | |
| cca gca gcc ccc tcc ctg acg cgg ccc ttc ctg gca gag gcc ccg aca | 166 |
| Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu Ala Pro Thr | |
| -30 -25 -20 -15 | |
| gca ctg gtc cca cac agc ccc ctg cct ggg gcc ctg tca agc gcc cct | 214 |
| Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser Ser Ala Pro | |
| -10 -5 1 | |
| ggc ccg aag cag ccc ccg acg gca agc aca ggc ccg gag ctg ctg ctg | 262 |
| Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu Leu Leu Leu | |
| 5 10 15 | |
| ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg | 310 |
| Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala Pro Ala Arg | |

```

      20              25              30
gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc ctc      358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu
35              40              45              50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctgggggactt      406
Ile Pro Gly Gln Cys Pro
      55
ctcagcgcca gccattggc gcctgcgttg cccgcatcca ggccctgcgg caggccctgt      466
gctagcgtgt tcgcaccagg aacgcagggtg ctgggctgtc ggggaggcct caggccacct      526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa      586
atgaattact gttcaaaaaa aaaaa      611

```

<210> 136
 <211> 925
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..417

<220>
 <221> sig_peptide
 <222> 22..66
 <223> Von Heijne matrix
 score 5.47092708754574
 seq RVLCPAAGAVRA/LR

```

<400> 136
agtcgaggag tcaaggcagc a atg aat cgt gtc ttg tgt gcc ccg gcg gcc      51
                        Met Asn Arg Val Leu Cys Ala Pro Ala Ala
                        -15                        -10
ggg gcc gtc cgg gcg ctg agg ctc ata ggc tgg gct tcc cga agc ctt      99
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu
-5              1              5              10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa      147
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu
      15              20              25
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac      195
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn
      30              35              40
cct cac cgc tgg tcg gtg ggc cat acc atg gga aag gga cat cag cgg      243
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg
      45              50              55
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc      291
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile
60              65              70              75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga      339
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg
      80              85              90
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct      387
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro
      95              100              105
gag act cca gct gcc tac aga gcg aga act tgacggggtg cccgctgggg      437
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
      110              115
ctggcaggaa gggagccgac agccgccctt cggatttgat gtcacgtttg cccgtgactg      497
tcctggctat gcgtgcgtcc tcagcactga aggacttggc tgggtggatgg ggcacttggc      557

```


<220>
 <221> CDS
 <222> 107..1618

<220>
 <221> sig_peptide
 <222> 107..178
 <223> Von Heijne matrix
 score 6.19650168602189
 seq LGLYSLVLSGALA/YA

<400> 138
 agagctcagc cggtcgcacg gacggacagt tggaagccgg accccagagc ctgaggtggg 60
 cagtgtgccca gggtccttg cggcctcctc aagccctgtc caggct atg ggc atc 115
 Met Gly Ile
 aag aca gca ttg ccg gcg gct gag ctg ggc ctc tac tct ctg gtg ctg 163
 Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser Leu Val Leu
 -20 -15 -10
 agt ggg gcc ctg gcc tat gct ggc cgg ggc ctc ctt gag gct tca caa 211
 Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu Ala Ser Gln
 -5 1 5 10
 gat ggg gcc cac agg aag gcc ttc cgg gag tct gtg cga cct ggc tgg 259
 Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg Pro Gly Trp
 15 20 25
 gag tac att ggc cgg aag atg gat gtg gct gac ttc gag tgg gtg atg 307
 Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu Trp Val Met
 30 35 40
 tgg ttc acc tcc ttt cgc aac gtc atc atc ttt gcc ctc tcc gga cat 355
 Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu Ser Gly His
 45 50 55
 gtg ctg ttt gct aaa ctc tgc acg atg gtt gcc cca aag ctc cgc tcc 403
 Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys Leu Arg Ser
 60 65 70 75
 tgg atg tat gct gtg tac ggg gcc ttg gct gtg atg ggc aca atg ggc 451
 Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly Thr Met Gly
 80 85 90
 cct tgg tac ctg ctg ctg ctg ctt ggt cac tgt gtg ggc ctc tat gtg 499
 Pro Trp Tyr Leu Leu Leu Leu Gly His Cys Val Gly Leu Tyr Val
 95 100 105
 gcc tcg ctt ttg ggc cag ccc tgg ctc tgt ctt ggc ctt ggc ttg gcc 547
 Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu Gly Leu Ala
 110 115 120
 agc ctg gcc tcc ttc aag atg gac ccc cta atc tct tgg cag agc ggg 595
 Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp Gln Ser Gly
 125 130 135
 ttt gta aca ggc act ttt gat ctt caa gag gtg ctg ttt cat ggg ggc 643
 Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe His Gly Gly
 140 145 150 155
 agc agc ttc aca gtg ctg cgt tgc acc agc ttt gca ctg gag agc tgt 691
 Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu Glu Ser Cys
 160 165 170
 gcc cac cct gac cgc cac tac tcc tta gct gac ctg ctc aag tac agc 739
 Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu Lys Tyr Ser
 175 180 185
 ttc tac ctg ccc ttc ttc ttc ttc ggg ccc atc atg acc ttt gat cgc 787
 Phe Tyr Leu Pro Phe Phe Phe Phe Gly Pro Ile Met Thr Phe Asp Arg
 190 195 200
 ttc cat gct cag gtg agc cag gtg gag cca gtg aga cgc gag ggt gag 835

| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|-------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|------|--|
| Phe | His | Ala | Gln | Val | Ser | Gln | Val | Glu | Pro | Val | Arg | Arg | Glu | Gly | Glu | | |
| 205 | | | | | | 210 | | | | | 215 | | | | | | |
| ctg | tgg | cac | atc | cga | gcc | cag | gca | ggc | cta | agc | gtg | gtg | gcc | atc | atg | 883 | |
| Leu | Trp | His | Ile | Arg | Ala | Gln | Ala | Gly | Leu | Ser | Val | Val | Ala | Ile | Met | | |
| 220 | | | | | 225 | | | | | 230 | | | | | 235 | | |
| gcc | gtc | gac | atc | ttc | ttt | cac | ttc | ttc | tac | atc | ctc | act | atc | ccc | agc | 931 | |
| Ala | Val | Asp | Ile | Phe | Phe | His | Phe | Phe | Tyr | Ile | Leu | Thr | Ile | Pro | Ser | | |
| | | | | 240 | | | | | 245 | | | | | 250 | | | |
| gac | ctc | aag | ttc | gcc | aac | cgc | ctc | cca | gac | att | gcc | ctc | gct | ggc | cta | 979 | |
| Asp | Leu | Lys | Phe | Ala | Asn | Arg | Leu | Pro | Asp | Ile | Ala | Leu | Ala | Gly | Leu | | |
| | | | 255 | | | | | 260 | | | | | 265 | | | | |
| gcc | tat | tca | aac | ctg | gtg | tat | gac | tgg | gtg | aag | gcg | gcc | gtc | ctc | ttt | 1027 | |
| Ala | Tyr | Ser | Asn | Leu | Val | Tyr | Asp | Trp | Val | Lys | Ala | Ala | Val | Leu | Phe | | |
| | | | 270 | | | | 275 | | | | | | 280 | | | | |
| ggt | ggt | gtc | aac | act | gtg | gca | tgc | ctc | gac | cac | ctg | gac | cca | ccc | cag | 1075 | |
| Gly | Val | Val | Asn | Thr | Val | Ala | Cys | Leu | Asp | His | Leu | Asp | Pro | Pro | Gln | | |
| | | | 285 | | | 290 | | | | | 295 | | | | | | |
| cct | ccc | aag | tgc | atc | acc | gca | ctc | tac | gtc | ttt | gcg | gaa | acg | cac | ttt | 1123 | |
| Pro | Pro | Lys | Cys | Ile | Thr | Ala | Leu | Tyr | Val | Phe | Ala | Glu | Thr | His | Phe | | |
| | | | | | 305 | | | | | 310 | | | | | 315 | | |
| gac | cgt | ggc | atc | aac | gac | tgg | ctt | tgc | aaa | tat | gtg | tat | aac | cac | att | 1171 | |
| Asp | Arg | Gly | Ile | Asn | Asp | Trp | Leu | Cys | Lys | Tyr | Val | Tyr | Asn | His | Ile | | |
| | | | | 320 | | | | | 325 | | | | | 330 | | | |
| ggt | ggg | gag | cat | tcc | gct | gtg | atc | cca | gag | ctg | gca | gcc | aca | gtg | gcc | 1219 | |
| Gly | Gly | Glu | His | Ser | Ala | Val | Ile | Pro | Glu | Leu | Ala | Ala | Thr | Val | Ala | | |
| | | | 335 | | | | | 340 | | | | | 345 | | | | |
| aca | ttt | gcc | atc | acc | aca | ctg | tgg | ctt | ggg | cct | tgt | gac | att | gtc | tac | 1267 | |
| Thr | Phe | Ala | Ile | Thr | Thr | Leu | Trp | Leu | Gly | Pro | Cys | Asp | Ile | Val | Tyr | | |
| | | | 350 | | | | 355 | | | | | 360 | | | | | |
| ctg | tgg | tca | ttc | ctt | aac | tgc | ttt | ggc | ctc | aac | ttt | gag | ctc | tgg | atg | 1315 | |
| Leu | Trp | Ser | Phe | Leu | Asn | Cys | Phe | Gly | Leu | Asn | Phe | Glu | Leu | Trp | Met | | |
| | | | 365 | | | 370 | | | | 375 | | | | | | | |
| caa | aaa | ctg | gca | gag | tgg | ggg | ccc | cta | gca | cga | att | gag | gcc | tct | ctg | 1363 | |
| Gln | Lys | Leu | Ala | Glu | Trp | Gly | Pro | Leu | Ala | Arg | Ile | Glu | Ala | Ser | Leu | | |
| | | | | | 385 | | | | 390 | | | | | | 395 | | |
| tca | gtg | cag | atg | tcc | cgt | agg | gtc | cgg | gcc | ctg | ttt | gga | gcc | atg | aac | 1411 | |
| Ser | Val | Gln | Met | Ser | Arg | Arg | Val | Arg | Ala | Leu | Phe | Gly | Ala | Met | Asn | | |
| | | | | 400 | | | | | 405 | | | | | 410 | | | |
| ttc | tgg | gcc | atc | atc | atg | tac | aac | ctt | gtg | agc | ctg | aac | agc | ctc | aaa | 1459 | |
| Phe | Trp | Ala | Ile | Ile | Met | Tyr | Asn | Leu | Val | Ser | Leu | Asn | Ser | Leu | Lys | | |
| | | | 415 | | | | | 420 | | | | | 425 | | | | |
| ttc | aca | gag | ctg | gtt | gcc | cgg | cgc | ctg | cta | ctc | aca | ggg | ttc | ccc | cag | 1507 | |
| Phe | Thr | Glu | Leu | Val | Ala | Arg | Arg | Leu | Leu | Leu | Thr | Gly | Phe | Pro | Gln | | |
| | | | 430 | | | | 435 | | | | | 440 | | | | | |
| acc | acg | ctg | tcc | atc | ctg | ttt | gtc | acc | tac | tgt | ggc | gtc | cag | ctg | gta | 1555 | |
| Thr | Thr | Leu | Ser | Ile | Leu | Phe | Val | Thr | Tyr | Cys | Gly | Val | Gln | Leu | Val | | |
| | | | 445 | | | 450 | | | | | 455 | | | | | | |
| aag | gag | cgt | gag | cga | acc | ttg | gca | ctg | gag | gag | gag | cag | aag | cag | gac | 1603 | |
| Lys | Glu | Arg | Glu | Arg | Thr | Leu | Ala | Leu | Glu | Glu | Glu | Gln | Lys | Gln | Asp | | |
| | | | 460 | | 465 | | | | 470 | | | | | 475 | | | |
| aaa | gag | aag | ccg | gag | taggagggag | cgggtagagg | gatgggctct | gctcagctat | | | | | | | | 1658 | |
| Lys | Glu | Lys | Pro | Glu | | | | | | | | | | | | | |
| | | | | 480 | | | | | | | | | | | | | |
| tcttgggcca | gatggggcct | gaccgataga | ataaaaagact | tttctacaac | aaaaaaaaaa | | | | | | | | | | | 1718 | |
| aaaaaaaa | | | | | | | | | | | | | | | | 1725 | |

<210> 139

<211> 1474

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..471

<220>
<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
score 5.809301698725
seq FCVCVIAIGVVQA/LI

```

<400> 139
tacacgtttt cgtta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc      51
              Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe
              -25              -20              -15
ttg ttc tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att      99
Leu Phe Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile
              -10              -5              1
gta ggg tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag      147
Val Gly Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln
              5              10              15
cgc tct gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc      195
Arg Ser Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val
              20              25              30
ctc caa ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc      243
Leu Gln Gly Pro Ala Leu Cys Phe Ala Ala Ile Phe Ser Leu Phe
              35              40              45              50
ttt gtc ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc      291
Phe Val Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro
              55              60              65
tat gtc agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac      339
Tyr Val Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His
              70              75              80
agg gag ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac      387
Arg Glu Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His
              85              90              95
gag cca ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac      435
Glu Pro Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr
              100              105              110
gcc atc gtg gcc acg ctt ctc atc ctg gac atc tgg tgaggacccc      481
Ala Ile Val Ala Thr Leu Leu Ile Leu Asp Ile Trp
              115              120              125
gcgtcacctg cccagctat caggtggcca atgtgtcttg agtccttggc gtctcatcct      541
ggaaacccca gaaaggcaca ggggtcttgg ctccaccctc ctctggatgc cttagagtttt      601
gtgtgagggtc agggcagccc ccacttcagg gaggacaacc ttcccgcgcg cccctccctt      661
cccagcggccc cctcccttcc cagaggctcc caccccaagc acagccgagg atgggggtgcc      721
aggggtgaggt cagcaccagc agccaactgc tctcctcact cctctcagag gggctcagca      781
gccatgggta tccccctgcc ccaggcctca cccctgcccc aacaccagcc cctcctagtc      841
cctagtccct cccattccct ccggtccct cccagtgcc cccatcgctt cgcagccct      901
tctgetccct ttggctggct gttgcttcc tccagcgtct gctcctccgc ggccctcatct      961
gcctcttcgt ctgtagagc gcgcgtctcg tctcagtcgt cacgtttttg gtttttgtgg      1021
ggtttttttt tttttttttt tttgagacag tctgtctgtg tcgcccaggc tggagtatag      1081
tggctcaagc tcagctcact gcaacctcg cctcccaggt tcaagcaatt ctctgcctc      1141
agcctcccaa gtagttggga ttacaagcac ccaccacat gccagctaa ctttttgcac      1201
ttttaataga gatgagggtt caccaagttg gccaggctgg tcttgaactc ctgacctcag      1261

```

```

gtgatctgcc cacctcggcc tcccaaagtg ctgggattac aggtgtaagc caccgtgccc 1321
ggccatcgta atgtttgaat ttgctttttt acatcttcca tccttttgga gtgtcttggt 1381
ccctcgcat agttcagcac tgtgaccacc ttggggtagt acactatggg tttatatcct 1441
gtacttgata ttctccaaaa aaaaaaaaaa aaa 1474

```

```

<210> 140
<211> 653
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 222..374

```

```

<220>
<221> sig_peptide
<222> 222..299
<223> Von Heijne matrix
      score 4.28353322771141
      seq ILFKFSLCPYAAA/LS

```

```

<400> 140
taataatggtt gttaaattat tgccttctca tctgcgtgtc tcttatgttc tgcttaaaga 60
gattgtcagt ttgttcaagc tcttttttagt tggtgctcct ccagtgccta gctttgagct 120
ttgtacacgg tagttattga gttgagtaac atagtttggt ctgagtcatt tgtccacat 180
gcttgaagac ttggcttaac ctagtagata ataggaaaga a atg gaa atg ctc ttt 236
                                         Met Glu Met Leu Phe
                                         -25
gat gaa aga gcc cct ctc tta ttc atc ctt ttt aaa ttt tct ttg tgc 284
Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe Lys Phe Ser Leu Cys
-20 -15 -10
cca tat gca gca gct ctc agc aaa cct ata ttt ggc agt gtg gcc tgt 332
Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe Gly Ser Val Ala Cys
-5 1 5 10
atg act aaa gaa atc ctg gcc agg cac ggt ggc tca cgc ctg 374
Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly Ser Arg Leu
15 20 25
taatcccagc actttgggag gccgaggcgg gtggattacg aggtcaggag attgagacca 434
tcctggctaa catggcgaaa ccccatctct acgaaaaata caaaaaaaaaa aattagccgg 494
gcatcatggc gggcgctgt agtcttagct actcaggagg ctgaggcagg agaatggcgt 554
gaacccggga ggcggagctt gcagtgagcc gagattgcgc cactgcactc cagcctgggg 614
caacagagca agactccgtc tcaaaaaaaaa aaaaaaaaaa 653

```

```

<210> 141
<211> 1490
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 59..274

```

```

<220>
<221> sig_peptide
<222> 59..127
<223> Von Heijne matrix
      score 7.37647149292058
      seq LGLCSLLVGAEAA/PS

```

```

<400> 141
agacagaggc agggcttgcg acggaagtgg cctctctgct tctgcagggc tggggaag      58
atg ctg cgt cca gcg tta ccg tgg ctg tac ctt ggc ctc tgc agc ctc      106
Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
-20 -15 -10
ctg gtg ggg gag gca gag gcc ccg agc ccc gtg gat ccg ctg gag cgg      154
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
-5 1 5
agc cgg ccg tac gcg gtg ctg cga ggg cag aac ctg gtg ttg atg gga      202
Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
10 15 20 25
acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt      250
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
30 35 40
gtc tac aag ccc att ccg cgt ccg tgacagccag acaagttctt caatgagtat      304
Val Tyr Lys Pro Ile Arg Arg Arg
45
ttgggaatag gataagttgt gttgcacaca ggccagtggg gaagttggaa ccaaaacttt      364
cctactttga aatgaccttt ggtctggaca gttggtaaata gctaaatgaa ttagaagaaa      424
acatgtacta gacattattt tttcctaaca ctgtagcgca aataattggc ccctgagtc      484
gcttctcagt gtttctgact gtacttggtta aaagtaagac ctgaaagctc caaagggtcag      544
tgtaaagatg gagtggtcat gagaaagaaa acatggtaac cttgtgagtg cctgtaagaa      604
ccacactgta aagaactcat cattaatgct tgaaaatggt attaagaagg agacttacca      664
tgcagacatt ccctatttta gaaccatttg gttacagtgg gttaagaatc acagattttt      724
ttttttaatc tcacctgagt tagcctagaa tgcgctgggt gcaaagtggg gtcagctgtg      784
gggatcttgg gccctcggtc ctcacctgca tcctgccttg cactcaggtg ctccccctga      844
agtcagggtc acatcaggta gacctgttac tatatgcacc tttggcctgg aatgctctga      904
agttggactg gaaatgttac taggttggcc tgttacaaaa aggaccccat cctgcttaaa      964
cacattgata tcaccttgccc tgcatttgag tctttctagc ccacgggtctg aaacttgagg      1024
cagctttcca gatttggaaat gtaaaaggct cagtgggcac tctgttcac cctgggtggg      1084
gagggccag ccaacagaag tgcattgtcca ctgtgcgggc cagtgtgtgt ttacacaaat      1144
ttcatctcag ctttgaaaat gctgctatta gtttccactg ttggtgaact ggattttttc      1204
ctcctattga aatgatactt tcatacttat aaagctgtcg tcaatattta tttcaagggtg      1264
ctagatttaa ttttggttatt aaattgaaat gcttatcttg tgttcaagca cagcactgat      1324
tttaacaacc tgcatttaat gtgaagtaac cgaagtagga tactgtaact gtgtaaggat      1384
tttgtttgta atcttgtaac attgaaccat tgaaatgttc agttctttgc ttttgagcaa      1444
aacgtcaatt aaaactaaag taaaatctta aaaaaaaaaa aaaaaa      1490

```

```

<210> 142
<211> 661
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 158..442

```

```

<220>
<221> sig_peptide
<222> 158..301
<223> Von Heijne matrix
score 7.53908709538105
seq FVILLLFIFTVVS/LV

```

```

<400> 142
aaaaacagac gataccatcg cttcagcagc atcctctcag acaagagcca ctatttctga      60
ttcagatcac ctgtcatcga agtttaaaga aggggaaaca ggagacagaa atacactgaa      120

```

```

ccaaaaagat tcaaaagagc aagtggaatc tctaaga atg gct tcc agc cac tgg      175
                                   Met Ala Ser Ser His Trp
                                   -45
aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa      223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln
-40 -35 -30
aaa att tac cct ttc cat gac aac tgg aac act gcc tgc ttt gtc atc      271
Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile
-25 -20 -15
ctg ctt tta ttt ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc      319
Leu Leu Leu Phe Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe
-10 -5 1 5
ctt tat gaa gtg ctt gac tgc tgc tgc tgt gta aaa aac aaa acc gtg      367
Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys Val Lys Asn Lys Thr Val
10 15 20
aaa gac ttg aaa agt gaa ccc aac cct ctt aga agt atg atg gac aac      415
Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu Arg Ser Met Met Asp Asn
25 30 35
atc aga aaa cgt gaa act gaa gtg gtc taacactcta tagaagatga      462
Ile Arg Lys Arg Glu Thr Glu Val Val
40 45
acaaaatctc tgaagcagc tcaacctctt ctgagaaaaa aaatatattc tgaggccaac      522
tggttgetaca aaacaaattc tgactgaatg tttaaaacat ttctagtaga aggggaaaaa      582
aaagttaaac atgcactgtt tgtgtgtata gccatttcat taaatataca gtaaaacttc      642
ataaaaaaaaa aaaaaaaaaa      661

<210> 143
<211> 1789
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..454

<220>
<221> sig_peptide
<222> 5..64
<223> Von Heijne matrix
score 6.64507667657896
seq LLPLLSLLVGAWL/KL

<400> 143
cctg atg gcc cgg cat ggg tta ccg ctg ctg ccc ctg ctg tcg ctc ctg      49
Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu
-20 -15 -10
gtc ggc gcg tgg ctc aag cta gga aat gga cag gct act agc atg gtc      97
Val Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val
-5 1 5 10
caa ctg cag ggt ggg aga ttc ctg atg gga aca aat tct cca gac agc      145
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
15 20 25
aga gat ggt gaa ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc      193
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
30 35 40
atc gac ata ttt cct gtc acc aac aaa gat ttc agg gat ttt gtc agg      241
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
45 50 55

```

| | |
|---|------|
| gag aaa aag tat cgg aca gaa gct gag atg ttt gga tgg agc ttt gtc | 289 |
| Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val | |
| 60 65 70 75 | |
| ttt gag gac ttt gtc tct gat gag ctg aga aac aaa gcc acc cag cca | 337 |
| Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro | |
| 80 85 90 | |
| atg aag gtc aag ttt acc cat ggg gga act ggt tcc agc caa acc gca | 385 |
| Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala | |
| 95 100 105 | |
| cca acc tgt ggc agg gaa agt tcc cca agg gag aca aag ctg agg atg | 433 |
| Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met | |
| 110 115 120 | |
| gct tcc atg gag tct ccc cag tgaatgcttt ccccgcccag aacaactacg | 484 |
| Ala Ser Met Glu Ser Pro Gln | |
| 125 130 | |
| ggctctatga cctcctgggg aacgtgtggg agtggacagc atcaccgtac caggctgctg | 544 |
| agcaggacat gcgcgtcctc cgggggggcat cctggatcga cacagctgat ggctctgcca | 604 |
| atcaccgggc ccgggtcacc accaggatgg gcaacactcc agattcagcc tcagacaacc | 664 |
| tgggtttccg ctgtgctgca gacgcaggcc ggccgcccagg ggagctgtaa gcagccgggt | 724 |
| ggtgacaagg agaaaagcct tctagggtca ctgtcattcc ctggccatgt tgcaaacagc | 784 |
| gcaattccaa gctcgagagc ttcagcctca ggaaagaact tccccttccc tgtctcccat | 844 |
| ccctctgtgg caggcgctc tcaccagggc aggagaggac tcagcctcct gtgttttgga | 904 |
| gaaggggccc aatgtgtgtt gacgatggct gggggccagg tgtttctgtt agaggccaag | 964 |
| tattattgac acaggattgc aaacacacaa acaattggaa cagagcactc tgaaaggcca | 1024 |
| ttttttaagc attttaaaat ctattctctc cccctttctc cctggatgat tcaggaagct | 1084 |
| gacattgttt cctcaaggca gaattttcct ggttctgttt tctcagccag ttgctgtgga | 1144 |
| aggagaatgc tttctttgtg gcctcatctg tggtttcgtg tccctctgaa ggaaactagt | 1204 |
| ttccactgtg taacaggcag acatgtaact atttaaagca cagttcagtc ctaaaagggt | 1264 |
| ctgggagaac cagatgatgt actaggtgaa gcattgcatt gtgggaatca caaagcaaat | 1324 |
| agtactccag aaagacaaat atcagaagct tcctattctt tttttttttt tttttttttt | 1384 |
| ttgagacagg gtctttctct gttgcccagg ctagagtgca ctggtgatca cggctcactc | 1444 |
| tagccttgaa ttcttgggcc caagcaattc tcccacctca gcctcctgag tagctgggac | 1504 |
| tacaagtgtg caccaccatg cctggctaatt tttttgaatt tttgtagtga tgggatctcg | 1564 |
| ctctgttgcc cagggtgggc tgcgaactcct ggccctcaagc gatectccca cctcgacctc | 1624 |
| ccaaagtgtg gggattacag gtgtgagcca cctgcgctgg gcccccttct ccatatgcct | 1684 |
| ccaaaaacat gtccctggag agtagcctgc tcccacactg tcactggatg tcatggggcc | 1744 |
| aataaaatct cctgcaattg tgtatctcaa aaaaaaaaaa aaaaa | 1789 |

<210> 144
 <211> 2006
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 241..1302

| | |
|--|-----|
| <400> 144 | |
| tagtgccgga gccccgccag agcccgactt cagccccagc cagatcccgc gtcaacggag | 60 |
| gcggaacggc ggaccccgta ccctggcagc atcggagcac cggcgggtga aggcaaggctc | 120 |
| cctggactgg tcatatacct cttgtggccc tggcagaatc aagatgaggc cctgtcatgc | 180 |
| ctccccagtg aggcctacag tctgagcaga cagcatggcc tgccactggc agtgaacacc | 240 |
| atg tct gca gga ggt ggc cgg gcc ttt gct tgg caa gtg ttc ccc ccc | 288 |
| Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro | |
| 1 5 10 15 | |
| atg ccc act tgc cgg gtc tat ggc aca gtg gca cac caa gat ggg cac | 336 |
| Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His | |
| 20 25 30 | |

| | |
|---|------|
| ctg ctg gtg ttg ggg ggt tgt ggc cgg gct gga ctg ccc ctg gac act | 384 |
| Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr | |
| 35 40 45 | |
| gct gag aca ctg gac atg gcc tcg cac aca tgg ctg gca ctg gca ccc | 432 |
| Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro | |
| 50 55 60 | |
| ctg ccc act gcc cgg gct ggt gca gct gcg gta gtt ctg ggc aag cag | 480 |
| Leu Pro Thr Ala Arg Ala Gly Ala Ala Ala Val Val Leu Gly Lys Gln | |
| 65 70 75 80 | |
| gtg cta gtg gtg tgt ggt gtg gat gag gtc cag agc ccg gta gct gct | 528 |
| Val Leu Val Val Cys Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala | |
| 85 90 95 | |
| gta gag gcc ttc ctg atg gat gag ggc cgc tgg gag cgt cgg gcc acc | 576 |
| Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr | |
| 100 105 110 | |
| ctc cct caa gca gcc atg ggg gtt gca act gtg gag aga gat ggt atg | 624 |
| Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met | |
| 115 120 125 | |
| gtg tat gct ctg ggg gga atg ggc cct gac acg gcc ccc cag gcc cag | 672 |
| Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln | |
| 130 135 140 | |
| gta cgt gtg tat gac ccc cgt cgg gac tgc tgg ctt tcg cta ccc tcc | 720 |
| Val Arg Val Tyr Asp Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser | |
| 145 150 155 160 | |
| atg ccc aca ccc tgc tat ggg gcc tcc acc ttc ctg cac ggg aac aag | 768 |
| Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys | |
| 165 170 175 | |
| atc tat gtc ctg ggg ggc cgc cag ggc aag ctc ccg gtg act gct ttt | 816 |
| Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe | |
| 180 185 190 | |
| gaa gcc ttt gat ctg gag gcc cgt aca tgg acc cgg cat cca agc cta | 864 |
| Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu | |
| 195 200 205 | |
| ccc agc cgt cgg gcc ttt gct ggc tgc gcc atg gct gaa ggc agc gtc | 912 |
| Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val | |
| 210 215 220 | |
| ttt agc ctg ggt ggc ctg cag cag cct ggg ccc cac aac ttc tac tct | 960 |
| Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser | |
| 225 230 235 240 | |
| cgc cca cac ttt gtc aac act gtg gag atg ttt gac ctg gag cat ggg | 1008 |
| Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly | |
| 245 250 255 | |
| tcc tgg acc aaa ttg ccc cgc agc ctg cgc atg agg gat aag agg gca | 1056 |
| Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala | |
| 260 265 270 | |
| gac ttt gtg gtt ggg tcc ctt ggg ggc cac att gtg gcc att ggg ggc | 1104 |
| Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly | |
| 275 280 285 | |
| ctt gga aac cag cca tgt cct ttg ggc tct gtg gag agc ttt agc ctt | 1152 |
| Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu | |
| 290 295 300 | |
| gca cgg cgg cgc tgg gag gca ttg cct gcc atg ccc act gcc cgc tgc | 1200 |
| Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys | |
| 305 310 315 320 | |
| tcc tgc tct agt ctg cag gct ggg ccc cgg ctg ttt gtt att ggg ggt | 1248 |
| Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly | |
| 325 330 335 | |
| gtg gcc cag ggc ccc agt caa gcc gtg gag gca ctg tgt ctg cgt gat | 1296 |

Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp
340 345 350

ggg gtc tgaaggcttg gtgggagctg tccactggag cagctcattg ccagaggcag 1352
Gly Val

ctattttctat ggctcctttt gctgctgagg acactcactg tggctctgtg ggatgagaga 1412
ggcatggggg tgagcacttg aaacactgcc ttggggcctt gggttagggg agcctttgtc 1472
tttagtgcag gacacacata tgcttacacc tacctttatc accatttcgtt catgaatcat 1532
gcctagctcc atccttgccc tgggacctac taggccttcc atccaactgg gaaatgggga 1592
gaagcaaagc tggcctcatg ctcttcaggg tcagttccta tctggagttg accaggccta 1652
ccccagttgc cattcctgaa aaatctcagc tgccaggctg ccttttagggt ccctgcagac 1712
ccaggagagt tgagaggggtg ggggacacac acagaataga gaggatgtgg gaactgccag 1772
agggccggag cgcaggagtt caagtggagg aatgctggct ttgagccctc tacactgctg 1832
gttgatgac cttggacaag tcacttcacc tctctgtgcc tcagcatcct catctataaa 1892
tggggatctc tgaaaccttc ctaccctacc tacctcacag ggctgttggtg aggaccagg 1952
gagtttggat gtggaagtaa aagtgtgtgct aaaaccgaaa aaaaaaaaaa aaaa 2006

<210> 145
<211> 1096
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..635

<400> 145

atccaaggcg caag atg gcg ctg ctt ttt gca cgt tct ttg cgc ttg tgc 50
Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys
1 5 10

cgc tgg gga gcc aaa cga ttg gga gtt gcc tcc aca gag gcc cag aga 98
Arg Trp Gly Ala Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg
15 20 25

ggc gtc agt ttc aaa ctg gaa gaa aaa acc gcc cac agc agc ctg gca 146
Gly Val Ser Phe Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala
30 35 40

ctc ttc aga gat gat acg ggt gtc aaa tat ggc ttg gtg gga ttg gag 194
Leu Phe Arg Asp Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu
45 50 55 60

ccc acc aag gtg gcc ttg aat gtg gag cgc ttc cgg gag tgg gca gtg 242
Pro Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val
65 70 75

gtg ctg gca gac aca gcg gtc acc agt ggc aga cac tac tgg gaa gtg 290
Val Leu Ala Asp Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val
80 85 90

aca gtg aag cgc tcc cag cag ttc cgg ata gga gtg gca gat gtg gac 338
Thr Val Lys Arg Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp
95 100 105

atg tcc cgg gat agc tgc att ggt gtt gat gat cgt tcc tgg gtg ttc 386
Met Ser Arg Asp Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe
110 115 120

acc tat gcc cag cgc aag tgg tac acc atg ttg gcc aac gag aaa gcc 434
Thr Tyr Ala Gln Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala
125 130 135 140

cca gtt gag ggt att ggg cag cca gag aag gtg ggg ctg ttg ctg gag 482
Pro Val Glu Gly Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu
145 150 155

tat gag gcc cag aag ctg agc ctg gtg gat gtg agc cag gtc tct gtg 530
Tyr Glu Ala Gln Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val

| | | | | |
|--|-----|-----|-------------|------|
| ggt cac acg cta cag aca gat ttc cgg ggt cca gtg gtg cct gcc ttt | 160 | 165 | 170 | 578 |
| Val His Thr Leu Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe | | | | |
| gct ctc tgg gat ggg gag ctg ctg acc cat tca ggg ctt gag gtg ccc | 175 | 180 | 185 | 626 |
| Ala Leu Trp Asp Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro | | | | |
| gag ggc ctc tagtatgtcc attactggag tccctaataca cgcttttggc | 190 | 195 | 200 | 675 |
| Glu Gly Leu | | | | |
| cagcctcctt ttgaaagtgt ccgaagcctt tttactttgc ctcaagcaac ctctagctcc | 205 | | | 735 |
| cacaattcag tggtgggtcc tctgtgcaat atcatgatca tcttcctcat cccctacctt | | | | 795 |
| gtgaaagcta ggcatacagc caaacctctc ttttccccac ccaccaacac tactgccaat | | | | 855 |
| ttcctaggct accatgggtg tatcttctct gacctgcttc cttcagtcctc tctgcctccc | | | | 915 |
| tttgcccagg cctttctcag actgtattcc atcctggggc cttatcattc agctttgttt | | | | 975 |
| gaattttatta atcaccatga tacctctccc tccctttgtc cacatgtaac ttgtttcttg | | | | 1035 |
| ggctctacca gatggctgaa gagtaaattcc tttctacctc tggcaaaaaa aaaaaaaaaa | | | | 1095 |
| a | | | | 1096 |
| | | | | |
| <210> 146 | | | | |
| <211> 1666 | | | | |
| <212> DNA | | | | |
| <213> Homo sapiens | | | | |
| | | | | |
| <220> | | | | |
| <221> CDS | | | | |
| <222> 109..738 | | | | |
| | | | | |
| <400> 146 | | | | |
| cccagcgttc ctctctcggc ccaggtcac cgccagcacg cgcttgcttc ccgtctgcgc | | | | 60 |
| gagtccacgc agctccccag gcccttcacc agcacagcag cagcaggc atg gca gca | | | | 117 |
| | | | Met Ala Ala | |
| | | | 1 | |
| agc gtg gag cag cgc gag ggc acc atc cag gtg cag ggc cag gcc ctc | | | | 165 |
| Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly Gln Ala Leu | | | | |
| 5 10 15 | | | | |
| ttc ttc cga gag gcc ctg ccc ggc agt ggg cag gct cgc ttc tct gta | | | | 213 |
| Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val | | | | |
| 20 25 30 35 | | | | |
| ctg ctg ctg cat ggt att cgc ttc tcc tcc gag acc tgg cag aac ctg | | | | 261 |
| Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp Gln Asn Leu | | | | |
| 40 45 50 | | | | |
| ggc aca ctg cac agg ctg gcc cag gct ggc tac cgg gct gtg gcc att | | | | 309 |
| Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile | | | | |
| 55 60 65 | | | | |
| gac ctg cca ggt ctg ggg cac tcc aag gaa gca gca gcc cct gcc cct | | | | 357 |
| Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Pro Ala Pro | | | | |
| 70 75 80 | | | | |
| att ggg gag ctg gcc cct ggc agc ttc ctg ggc gct gtg gtg gat gcc | | | | 405 |
| Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala | | | | |
| 85 90 95 | | | | |
| ttg gag ctg ggc ccc ccg gtt gtg atc agt cca tca ctg agt ggc atg | | | | 453 |
| Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met | | | | |
| 100 105 110 115 | | | | |
| tac tcc ctg ccc ttc ctc acg gcc cct ggc tcc cag ctc ccg ggc ttt | | | | 501 |
| Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu Pro Gly Phe | | | | |
| 120 125 130 | | | | |
| gtg cca gtg gcc ccc atc tgc act gac aaa atc aat gct gcc aac tat | | | | 549 |


```

aaagtccagt tgaactttct aagtctgtga tccccgtgct gactgtggaa gtgtatttat 1395
accaagatgg agatcttgac ttcttgaata tatctggact ggtaaaatct tgatgaggct 1455
cataaaatga gtttgggaat tgtgtatagc tgatttttttg tgggaaactg tttacttcat 1515
tcaaagggttc ttgagactct tgatatttct gtcttctcct tgtgctttcc tatggaaaaa 1575
atacatatat agtttagttt gttagacgtg agttatccaa gtattttattt tgtgtagtgt 1635
gtaagaatgc taaataaaat gttatacagg aaaaaaaaaa aaaaatgcga aa 1687

```

<210> 148
 <211> 1747
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..1596

```

<400> 148
gttgggcggc cggtagctgt tgctgttggg ggacccccctc attcctgccg ctgccgtccc 60
tgctgcccac atg gcg gcc atc gga gtt cac ctg ggc tgc acc tca gcc tgt 111
      Met Ala Ala Ile Gly Val His Leu Gly Cys Thr Ser Ala Cys
      1          5          10
gtg gcc gtc tat aag gat ggc cgg gct ggt gtg gtt gca aat gat gcc 159
Val Ala Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala
15          20          25          30
ggt gac cga gtt act cca gct gtt gtt gct tac tca gaa aat gaa gag 207
Gly Asp Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu
      35          40          45
att gtt gga ttg gca gca aaa caa agt aga ata aga aat att tca aat 255
Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn
      50          55          60
aca gta atg aaa gta aag cag atc ctg ggc aga agc tcc agt gat cca 303
Thr Val Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro
      65          70          75
caa gct cag aaa tac atc gcg gaa agt aaa tgt tta gtc att gaa aaa 351
Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys
      80          85          90
aat ggg aaa tta cga tat gaa ata gat act gga gaa gaa aca aaa ttt 399
Asn Gly Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe
      95          100          105          110
gtt aac cca gaa gat gtt gcc aga ctg ata ttt agt aaa atg aaa gaa 447
Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu
      115          120          125
acg gca cat tct gta ttg ggc tca gat gca aat gat gta gtt att act 495
Thr Ala His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr
      130          135          140
gtc ccg ttt gat ttt gga gaa aag caa aaa aat gct ctt gga gaa gca 543
Val Pro Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala
      145          150          155
gct aga gct gct gga ttt aat gtt ttg cga tta att cac gaa ccg tct 591
Ala Arg Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser
      160          165          170
gca gct ctt ctt gct tat gga att gga caa gac tcc cct act gga aaa 639
Ala Ala Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys
      175          180          185          190
agc aat att ttg gtg ttt aag ctt gga gga aca tcc tta tct ctc agc 687
Ser Asn Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser
      195          200          205
gtc atg gaa gtt aac agt gga ata tat cgg gtt ctt tca aca aac act 735

```

| | |
|--|------|
| Val Met Glu Val Asn Ser Gly Ile Tyr Arg Val Leu Ser Thr Asn Thr | |
| 210 215 220 | |
| gat gat aac atc ggt ggt gca cat ttc aca gaa acc tta gca cag tat | 783 |
| Asp Asp Asn Ile Gly Gly Ala His Phe Thr Glu Thr Leu Ala Gln Tyr | |
| 225 230 235 | |
| cta gct tct gag ttc caa aga tcc ttc aaa cat gat gtg aga gga aat | 831 |
| Leu Ala Ser Glu Phe Gln Arg Ser Phe Lys His Asp Val Arg Gly Asn | |
| 240 245 250 | |
| gcg cga gcc atg atg aaa tta acg aac agt gct gaa gta gcg aaa cat | 879 |
| Ala Arg Ala Met Met Lys Leu Thr Asn Ser Ala Glu Val Ala Lys His | |
| 255 260 265 270 | |
| tct ttg tca acc ttg gga agt gcc aac tgt ttt ctt gac tca tta tat | 927 |
| Ser Leu Ser Thr Leu Gly Ser Ala Asn Cys Phe Leu Asp Ser Leu Tyr | |
| 275 280 285 | |
| gaa ggt caa gat ttt gat tgc aat gtg tcc aga gca aga ttt gaa ctt | 975 |
| Glu Gly Gln Asp Phe Asp Cys Asn Val Ser Arg Ala Arg Phe Glu Leu | |
| 290 295 300 | |
| ctt tgt tct cca ctt ttt aat aag tgt ata gaa gca atc aga gga ctc | 1023 |
| Leu Cys Ser Pro Leu Phe Asn Lys Cys Ile Glu Ala Ile Arg Gly Leu | |
| 305 310 315 | |
| tta gat caa aat gga ttt aca aca gat gat atc aac aag gtt gtc ctt | 1071 |
| Leu Asp Gln Asn Gly Phe Thr Thr Asp Asp Ile Asn Lys Val Val Leu | |
| 320 325 330 | |
| tgt gga ggg tct tct cga atc cca aag cta cag caa ctg att aaa gat | 1119 |
| Cys Gly Gly Ser Ser Arg Ile Pro Lys Leu Gln Gln Leu Ile Lys Asp | |
| 335 340 345 350 | |
| ctt ttc cca gct gtt gag ctt ctc aat tct atc cct cct gat gaa gtg | 1167 |
| Leu Phe Pro Ala Val Glu Leu Leu Asn Ser Ile Pro Pro Asp Glu Val | |
| 355 360 365 | |
| atc cct att ggt gca gct ata gaa gca gga att ctt att ggg aaa gaa | 1215 |
| Ile Pro Ile Gly Ala Ala Ile Glu Ala Gly Ile Leu Ile Gly Lys Glu | |
| 370 375 380 | |
| aac ctg ttg gtg gaa gac tct ctt atg ata gag tgt tca gcc aga gat | 1263 |
| Asn Leu Leu Val Glu Asp Ser Leu Met Ile Glu Cys Ser Ala Arg Asp | |
| 385 390 395 | |
| att tta gtt aag ggt gtg gac gaa tca gga gcc agt aga ttc aca gtg | 1311 |
| Ile Leu Val Lys Gly Val Asp Glu Ser Gly Ala Ser Arg Phe Thr Val | |
| 400 405 410 | |
| ctg ttt cca tca ggg act cct ttg cca gct cga aga caa cac aca ttg | 1359 |
| Leu Phe Pro Ser Gly Thr Pro Leu Pro Ala Arg Arg Gln His Thr Leu | |
| 415 420 425 430 | |
| caa gcc cct gga agc ata tct tca gtg tgc ctt gaa ctc tat gag tct | 1407 |
| Gln Ala Pro Gly Ser Ile Ser Ser Val Cys Leu Glu Leu Tyr Glu Ser | |
| 435 440 445 | |
| gat ggg aag aac tct gcc aaa gag gaa acc aag ttt gca cag gtt gta | 1455 |
| Asp Gly Lys Asn Ser Ala Lys Glu Glu Thr Lys Phe Ala Gln Val Val | |
| 450 455 460 | |
| ctc cag gat tta gat aaa aaa gaa aat gga tta cgt gat ata tta gct | 1503 |
| Leu Gln Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala | |
| 465 470 475 | |
| gtt ctt act atg aaa agg gat gga tct tta cat gtg aca tgc aca gat | 1551 |
| Val Leu Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp | |
| 480 485 490 | |
| caa gaa act gga aaa tgt gaa gca atc tct att gag ata gca tct | 1596 |
| Gln Glu Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser | |
| 495 500 505 | |
| tagtggtttta gagaaatcaa gaattttttaa aaacaagaat atcaacattt gggttttgtgt | 1656 |
| ataagtgggtg tttgtatttaa aatacttttt caatgaactg tataaactat gttttattaa | 1716 |

actacaatat atcagtaaaaa aaaaaaaaaa a

1747

<210> 149
<211> 658
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 129..362

<400> 149
agtcaggaaa atgaagctga acatcaagtc ccagcaagaa aagaaggaaa aggaatgcca 60
agcagtcatg ttagcagttt gaaggggctg gagcaagatg gaatcaggaa taaggagtca 120
gtgggacc atg tac aac act gga aga cac gta tcc ctt cgc ctg gac aag 170
Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys
1 5 10
gag cac ttg gtc aac ata tct gga ggg ccc atg aca tac agc cac cgg 218
Glu His Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg
15 20 25 30
ctg gag gag atc cga cta cac ttt ggg agt gag gac agc caa ggg tcg 266
Leu Glu Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser
35 40 45
gag cac ctc ctc aat gga cag gcc ttc tct ggg gag ctt caa gag agg 314
Glu His Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg
50 55 60
gat ttg ttc atc ttg ttg act tct gta tca gga cat ctg ccc gat aca 362
Asp Leu Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
65 70 75
tagaaaaagt ctgctgaccc ctgaattaca gtatgagcca ttcggaatgc atttctcttt 422
aaaagtctc gcctcattca gtgtctggaa cacagtgggt gctccccaat aggtgacacc 482
ttcctcaagt ttccttggga gaacagactc aatgtcggat ccacaaagga gacctgcaca 542
tacctaaccc ctatttctgc agaagctgaa ggctgtatta tctattgctt gcataataaa 602
tattgcataa cgacaacaat agtaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaaa 658

<210> 150
<211> 2045
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 109..594

<400> 150
attattacta caggaaaaac tgttctcttc tgtggcacag agaaccctgc ttcaaagcag 60
aagtagcagt tccggagtcc agctggctaa aactcatccc agaggata atg gca acc 117
Met Ala Thr
1
cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg 165
His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val
5 10 15
ggc aca gtg gct gtc act gtc atg cct cag tgg ata gtg tcg gcc ttc 213
Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val Ser Ala Phe
20 25 30 35
att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg tgg 261
Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp
40 45 50

| | |
|---|------|
| atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc tat | 309 |
| Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr | |
| 55 60 65 | |
| gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg | 357 |
| Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu | |
| 70 75 80 | |
| atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc | 405 |
| Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile | |
| 85 90 95 | |
| ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag | 453 |
| Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys | |
| 100 105 110 115 | |
| gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg | 501 |
| Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met | |
| 120 125 130 | |
| gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat | 549 |
| Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp | |
| 135 140 145 | |
| ttc tat aac cca ata gtg aat gtt gcc caa aaa cgt gag ctt gga | 594 |
| Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly | |
| 150 155 160 | |
| taagctctct acttaggatg gaccacggca ctggtgctga ttgttggagg agctctgttc | 654 |
| tgctgcgttt tttgttgcaa cgaaaagagc agtagctaca gatactcgat accttcccat | 714 |
| cgcacaaccc aaaaaagtta tcacaccgga aagaagtcac cgagcgtcta ctccagaagt | 774 |
| cagtatgtgt agttgtgtat gtttttttaa ctttactata aagccatgca aatgacaaaa | 834 |
| atctatatta ctttctcaaa atggacccca aagaaaacttt gatttactgt tcttaactgc | 894 |
| ctaactttaa ttacaggaac tgtgcatcag ctatttatga ttctataagc tatttcagca | 954 |
| gaatgagata ttaaattcaa tgcttttgatt gttctagaaa gtatagtaat ttgttttcta | 1014 |
| aggtggttca agcatctact ctttttatca tttacttcaa aatgacattg ctaaaagactg | 1074 |
| cattatttta ctactgtaat ttctccacga catagcatta tgtacataga tgagtgtaac | 1134 |
| atttatatct cacatagaga catgcttata tggttttatt taaaatgaaa tgccagtcca | 1194 |
| ttacactgaa taaatagaac tcaactattg cttttcaggg aaatcatgga tagggttgaa | 1254 |
| gaaggttact attaattggt taaaaacagc ttagggatta atgtcctcca tttataatga | 1314 |
| agattaaaat gaaggcttta atcagcattg taaaggaaat tgaatggctt tctgatatgc | 1374 |
| tgttttttag cctaggaggt agaaatccta acttctttat cctcttctcc cagaggcttt | 1434 |
| ttttttcttg tgtattaaat taacattttt aaaaagcaga tattttgtca aggggctttg | 1494 |
| cattcaaaact gcttttccag ggctatactc agaagaaaga taaaagtgtg atctaagaaa | 1554 |
| aagtgatggt tttaggaaaag tgaaaatatt tttgtttttg tatttgaaga agaatgatgc | 1614 |
| attttgacaa gaaatcatat atgtatggat atattttaat aagtatttga gtacagactt | 1674 |
| tgaggtttca tcaatataaa taaaagagca gaaaaatatg tcttggtttt catttgctta | 1734 |
| ccaaaaaaac aacaacaaaa aaagttgttc tttgagaact tcacctgctc ctatgtgggt | 1794 |
| acctgagtca aaattgtcat ttttgttctg tgaaaaataa atttccttct tgtaccattt | 1854 |
| ctgttttagtt ttactaaaat ctgtaaaatac tgtatttttc tgtttattcc aaatttgatg | 1914 |
| aaactgacaa tccaatttga aagtttgtgt cgacgtctgt ctagcttaaa tgaatgtgtt | 1974 |
| ctatttgctt tatacatttta tattaataaa ttgtacattt ttctaattat ttggaaaaaa | 2034 |
| aaaaaaaaa a | 2045 |

<210> 151

<211> 788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 150..587

<400> 151

attttcaaat ttacctctct gtgacttgta agccatgcaa ttcgtagggc taaatatgca 60

<213> Homo sapiens

<220>

<221> CDS

<222> 100..441

<400> 153

```
ataccaggca ctttagaacc agagactctg ctgcttttcc tgggcagggc ctgcttgctc      60
cagctctcaa gtctgacttg catctacact gcgggcaag atg cgg ctg caa gac      114
                               Met Arg Leu Gln Asp
                               1           5
cgc atc gcc acg ttc ttc ttc cca aaa ggc atg atg ctc acc acg gct      162
Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met Met Leu Thr Thr Ala
                10           15           20
gcg ctg atg ctc ttc ttc tta cac ctg ggc atc ttc atc aga gac gtg      210
Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile Phe Ile Arg Asp Val
                25           30           35
cac aac ttc tgc atc acc tac cac tat gac cac atg agc ttt cac tac      258
His Asn Phe Cys Ile Thr Tyr His Tyr Asp His Met Ser Phe His Tyr
                40           45           50
acg gtc gtc ctg atg ttc tcc cag gtg atc agc atc tgc tgg gct gcc      306
Thr Val Val Leu Met Phe Ser Gln Val Ile Ser Ile Cys Trp Ala Ala
                55           60           65
atg ggg tca ctc tat gct gag atg aca gaa aac aat gct caa cgg agc      354
Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser
                70           75           80           85
cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg      402
His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro
                90           95           100
gga gga gca cca ctg agg cct ggg gag tcg gaa cag ggc taaggagggg      451
Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu Gln Gly
                105           110
gaagcaaaag gctgcctcgg gtgttttaat aaagttgttg tttattccaa aaaaaaaaaa      511
aaa                                                                514
```

<210> 154

<211> 1183

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 32..1132

<400> 154

```
acttctttcc tgcctctgat tccgggctgt c atg gcg acc ccc aac aat ctg      52
                               Met Ala Thr Pro Asn Asn Leu
                               1           5
acc ccc acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat      100
Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp
                10           15           20
gcg gcc aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc      148
Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro
                25           30           35
gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc      196
Ala His Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser
                40           45           50           55
ttc agc tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg      244
```


360
tgtcaaaaaa aaaaaaaaaa a

1183

<210> 155
<211> 1545
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..996

<400> 155
acacagcatg catttcttca acaagcgact cagaaggcac ttgcacatcg ttgctgttct 60
gcctctttgc ttcagcatga ttacccagag gcgcacccgt gccgtggcct gcccgtcgtc 120
tatgcacccg tgctgtggcg tgcccgtcgt ctgtgtggc atg cct gtc tgt gca 174
Met Pro Val Cys Ala
1 5
ccc gtg ctg tgg cgt gcc cgt cgt ctg tgt ggc atg cct gtc tgt gca 222
Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly Met Pro Val Cys Ala
10 15 20
ccc gtg ccg tgg cgt gcc cgt cgt ctg tgc acc cgt gct gtg gtg tgc 270
Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr Arg Ala Val Val Cys
25 30 35
cct tcg tct gtt cct ttt att gcc ggg cag ggt tgc acc cac atg tgc 318
Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly Cys Thr His Met Cys
40 45 50
aag cca gcg acg gac ccc agg ttc acc cgt tca ccg ctg gct gga ggc 366
Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser Pro Leu Ala Gly Gly
55 60 65
gtg atc ctg ggt gtg gcc ctg tgg ctc cgc cat gac ccg cag acc acc 414
Val Ile Leu Gly Val Ala Leu Trp Leu Arg His Asp Pro Gln Thr Thr
70 75 80 85
aac ctc ctg tat ctg gag ctg gga gac aag ccc gcg ccc aac acc ttc 462
Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe
90 95 100
tat gta ggc atc tac atc ctc atc gct gtg ggc gct gtc atg atg ttc 510
Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly Ala Val Met Met Phe
105 110 115
gtt ggc ttc ctg ggc tgc tac ggg gcc atc cag gaa tcc cag tgc ctg 558
Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu
120 125 130
ctg ggg acg ttc ttc act tgc ctg gtc atc ctg ttt gcc tgt gag gtg 606
Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu Phe Ala Cys Glu Val
135 140 145
gcc gcc ggc atc tgg ggc ttt gtc aac aag gac cag atc gcc aag gat 654
Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp Gln Ile Ala Lys Asp
150 155 160 165
gtg aag cag ttc tat gac cag gcc cta cag cag gcc gtg gtg gat gat 702
Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp
170 175 180
gac gcc aac aac gcc aag gct gtg gtg aag acc ttc cac gag acg ctt 750
Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr Phe His Glu Thr Leu
185 190 195
gac tgc tgt ggc tcc agc aca ctg act gct ttg acc acc tca gtg ctc 798
Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu Thr Thr Ser Val Leu
200 205 210
aag aac aat ttg tgt ccc tcg ggc agc aac atc atc agc aac ctc ttc 846

Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe
 215 220 225
 aag gag gac tgc cac cag aag atc gat gac ctc ttc tcc ggg aag ctg 894
 Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu
 230 235 240 245
 tac ctc atc ggc att gct gcc atc gtg gtc gct gtg atc atg atc ttc 942
 Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala Val Ile Met Ile Phe
 250 255 260
 gag atg atc ctg agc atg gtg ctg tgc tgt ggc atc cgg aac agc tcc 990
 Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly Ile Arg Asn Ser Ser
 265 270 275
 gtg tac tgaggccccg cagctctggc cacagggacc tctgcagtgc cccctaagtg 1046
 Val Tyr
 acccgagacac ttccgagggg gccatcacccg cctgtgtata taacgtttcc ggtattactc 1106
 tgetacacgt agccttttta cttttggggg tttgtttttg ttctgaactt tcctgttacc 1166
 ttttcagggc tgacgtcaca tgtaggtggc gtgtatgagt ggagacgggc ctgggtcttg 1226
 gggactggag ggcagggggtc cttctgccct ggggtcccag ggtgctctgc ctgctcagcc 1286
 aggcctctcc tgggagccac tcgcccagag actcagcttg gccaaacttg ggggctgtgt 1346
 ccaccacagcc cgcccgctcct gtgggctgca cagctcacct tgttccctcc tgccccggtt 1406
 cgagagccga gtctgtgggc actctctgcc ttcatgcacc tgccttttct aacacgtcgc 1466
 cttcaactgt aatcacaaca tctgactcc gtcatttaat aaagaaggaa catcaggcat 1526
 gcaaaaaaaaa aaaaaaaaa 1545

 <210> 156
 <211> 1068
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 11..529

 <400> 156
 gaagcacgga atg tgt ctc ctg ctg ggg gcc acg ggc gtc ggg aag acg 49
 Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr
 1 5 10
 ctg ctg gtg aaa cgg ctg cag gag gtg agc tcc cgg gat ggg aaa ggc 97
 Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly
 15 20 25
 gac ctg ggg gag ccg ccc ccg aca cgg ccc acg gtg ggc acc aat ctt 145
 Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu
 30 35 40 45
 act gac atc gtg gca cag aga aag atc acc atc cgg gag ctt ggg ggg 193
 Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly
 50 55 60
 tgc atg ggc ccc atc tgg tcc agt tac tat gga aac tgc cgt tct ctc 241
 Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu
 65 70 75
 ctg ttt gtg atg gac gcc tct gac ccc acc cag ctc tct gca tcc tgt 289
 Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys
 80 85 90
 gtg cag ctc tta ggt ctc ctt tct gca gaa caa ctt gca gaa gca tcg 337
 Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser
 95 100 105
 gtg ctg ata ctc ttc aat aaa atc gac cta ccc tgt tac atg tcc acg 385
 Val Leu Ile Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr
 110 115 120 125
 gag gag atg aag tca tta atc agg ctt cca gac atc att gct tgt gcc 433

| | | | | | | | | | | | | | | | | | |
|--------------------|------------|------------|------------|------------|------------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Glu | Met | Lys | Ser | Leu | Ile | Arg | Leu | Pro | Asp | Ile | Ile | Ala | Cys | Ala | | |
| | | | | 130 | | | | | 135 | | | | | 140 | | | |
| aag | cag | aac | atc | acc | acg | gca | gaa | atc | agc | gcc | cgt | gaa | ggc | act | ggc | 481 | |
| Lys | Gln | Asn | Ile | Thr | Thr | Ala | Glu | Ile | Ser | Ala | Arg | Glu | Gly | Thr | Gly | | |
| | | | 145 | | | | | 150 | | | | | 155 | | | | |
| tta | gca | ggg | gtg | ctg | gcc | tgg | ctc | cag | gcc | acc | cac | aga | gcc | aac | gat | 529 | |
| Leu | Ala | Gly | Val | Leu | Ala | Trp | Leu | Gln | Ala | Thr | His | Arg | Ala | Asn | Asp | | |
| | 160 | | | | | | 165 | | | | | 170 | | | | | |
| tgactgcacg | gcagaggcgc | agctggcctg | agctggggag | aggtggcaga | gggcagtatg | 589 | | | | | | | | | | | |
| gctttgctgc | caatagtttc | ttctcacagg | ggcagaataa | cccaaagtaa | ccctacatga | 649 | | | | | | | | | | | |
| tggggctctg | tgctgggatg | caatgatgtg | taaactgagg | catgtggaga | tggaagttga | 709 | | | | | | | | | | | |
| catctggcct | ctgaaaaaag | tgtccccagg | ggctaggcat | ggtggctcac | acctgtaac | 769 | | | | | | | | | | | |
| ccagcacttt | gagaggccga | ggcgggtgta | tcacctgagg | tcgggagttc | gagactagcc | 829 | | | | | | | | | | | |
| tgaccaacat | ggagaaaccc | tgtctctact | aaaaatacaa | aattagctgg | gtgtgctggg | 889 | | | | | | | | | | | |
| gcatgcctgt | aatctcagct | acttgggagg | ctgagacagg | agaatccctt | gaacctggga | 949 | | | | | | | | | | | |
| ggtggagggt | gcagtgagtc | gagatcatgc | cattgcactg | cacctgggca | acaagagtga | 1009 | | | | | | | | | | | |
| aactcgcgtc | taaaaaatat | aagaaataaa | aaaataaaaa | cctaaaaaaa | aaaaaaaaa | 1068 | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| <210> 157 | | | | | | | | | | | | | | | | | |
| <211> 1097 | | | | | | | | | | | | | | | | | |
| <212> DNA | | | | | | | | | | | | | | | | | |
| <213> Homo sapiens | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| <220> | | | | | | | | | | | | | | | | | |
| <221> CDS | | | | | | | | | | | | | | | | | |
| <222> 135..749 | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| <400> 157 | | | | | | | | | | | | | | | | | |
| aacgaaacgg | taaccagccc | tgggaagccc | gcaagaggcc | tcagcgggtg | ccgtccgagc | 60 | | | | | | | | | | | |
| gccgagagggt | gaggggtgcc | ccgcctcacc | tgcagagggg | ccgttccggg | ctcgaacccg | 120 | | | | | | | | | | | |
| gcaccttccg | gaaa | atg | gcg | gct | gcc | agg | ccc | agc | ctg | ggc | mga | gtc | ctc | | | | |
| | Met | Ala | Ala | Ala | Arg | Pro | Ser | Leu | Gly | Arg | Val | Leu | | | | | |
| | 1 | | | | 5 | | | | | 10 | | | | | | | |
| cca | gga | tcc | tct | gtc | ctg | ttc | ctg | tgt | gac | atg | cag | gag | aag | ttc | cgc | 218 | |
| Pro | Gly | Ser | Ser | Val | Leu | Phe | Leu | Cys | Asp | Met | Gln | Glu | Lys | Phe | Arg | | |
| | 15 | | | | 20 | | | | | 25 | | | | | | | |
| cac | aac | atc | gcc | tac | ttc | cca | cag | atc | gtc | tca | gtg | gct | gcc | cgc | atg | 266 | |
| His | Asn | Ile | Ala | Tyr | Phe | Pro | Gln | Ile | Val | Ser | Val | Ala | Ala | Arg | Met | | |
| | 30 | | | | 35 | | | | 40 | | | | | | | | |
| ctc | aag | gtg | gcc | cgg | ctg | ctt | gag | gtg | cca | gtc | atg | ctg | acg | gag | cag | 314 | |
| Leu | Lys | Val | Ala | Arg | Leu | Leu | Glu | Val | Pro | Val | Met | Leu | Thr | Glu | Gln | | |
| | 45 | | | 50 | | | | 55 | | | | | | 60 | | | |
| tac | cca | caa | ggc | ctg | ggc | ccc | acg | gtg | ccc | gag | ctg | ggg | act | gag | ggc | 362 | |
| Tyr | Pro | Gln | Gly | Leu | Gly | Pro | Thr | Val | Pro | Glu | Leu | Gly | Thr | Glu | Gly | | |
| | | | 65 | | | | 70 | | | | | | 75 | | | | |
| ctt | cgg | ccg | ctg | gcc | aag | acc | tgc | ttc | agc | atg | gtg | cct | gcc | ctg | cag | 410 | |
| Leu | Arg | Pro | Leu | Ala | Lys | Thr | Cys | Phe | Ser | Met | Val | Pro | Ala | Leu | Gln | | |
| | | 80 | | | | | 85 | | | | | 90 | | | | | |
| cag | gag | ctg | gac | agt | cgg | ccc | cag | ctg | cgc | tct | gtg | ctg | ctc | tgt | ggc | 458 | |
| Gln | Glu | Leu | Asp | Ser | Arg | Pro | Gln | Leu | Arg | Ser | Val | Leu | Leu | Cys | Gly | | |
| | 95 | | | | | 100 | | | | | 105 | | | | | | |
| att | gag | gca | cag | gcc | tgc | atc | ttg | aac | acg | acc | ctg | gac | ctc | cta | gac | 506 | |
| Ile | Glu | Ala | Gln | Ala | Cys | Ile | Leu | Asn | Thr | Thr | Leu | Asp | Leu | Leu | Asp | | |
| | 110 | | | | 115 | | | | | | 120 | | | | | | |
| cgg | ggg | ctg | cag | gtc | cat | gtg | gtg | gac | gcc | tgc | tcc | tca | cgc | agc | | 554 | |
| Arg | Gly | Leu | Gln | Val | His | Val | Val | Val | Asp | Ala | Cys | Ser | Ser | Arg | Ser | | |
| | 125 | | | 130 | | | | | 135 | | | | | 140 | | | |
| cag | gtg | gac | cgt | ctg | gtg | gct | ctg | gcc | cgc | atg | aga | cag | agt | ggt | gcc | 602 | |

Gln Val Asp Arg Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala
145 150 155
ttc ctc tcc acc agc gaa ggg ctc att ctg cag ctt gtg ggc gat gcc 650
Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala
160 165 170
gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc 698
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala
175 180 185
cca gac agc gga ctg ctg ggc ctc ttc caa ggc cag aac tcc ctc ctc 746
Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu
190 195 200
cac tgaactccaa ccctgccttg agggaagacc accctcctgt caccocggacc 799
His
205
tcagtggaag cccgttcccc ccattccctgg atcccaagag tgggtgcgac caccaggagt 859
gccgccccct tgtggggggg ggcaggggtgc tgccttccca ttggacagct gctcccggaa 919
atgcaaata gactcctgga aactgggtgg gaattggctg agccaagatg gagggcggggc 979
tcggccccgg gccacttcac ggggcgggaa ggggagggga agaagagtct cagactgtgg 1039
gacacggact cgcagaataa acatatatgt ggctgtggac caaaaaaaaa aaaaaaaaa 1097

<210> 158
<211> 894
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 98..637

<400> 158
ctttggggcc gaagtgggcg tgcggctcgc gctgttcgcg gccttcctgg tgacggagct 60
gctccccccg ttccagagac tcattccagcc ggaggag atg tgg ctc tac cgg aac 115
Met Trp Leu Tyr Arg Asn
1 5
ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att 163
Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile
10 15 20
gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag 211
Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys
25 30 35
aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt 259
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu
40 45 50
gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta 307
Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val
55 60 65 70
ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta 355
Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu
75 80 85
gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag 403
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu
90 95 100
ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt 451
Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly
105 110 115
ctg gcc ttt gcg tcc ttc tac ctg gca ggg aag tta cac tgc ttc aca 499
Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr
120 125 130

aaa taaacagctt gcacttgaaa aaaaaaaaaa aaa

703

Lys

150

<210> 160

<211> 849

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 165..674

<400> 160

aaaactgagg cctgggagca ggaacctgta ggcagcgctt gagggtagcg ggatagcagc 60
tgcaagcgcg cgtgggaggc gggggctctg ggcggaacaa aaatcacagg atgtcagagg 120
atgtttcccg ggaagaactg ggataaagga aggtcccag cacc atg gag gac ccg 176
Met Glu Asp Pro

1

aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224
Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
5 10 15 20

ccc cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc 272
Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys
25 30 35

acc cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac 320
Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His
40 45 50

atg aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg 368
Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly
55 60 65

gtc ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa 416
Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys
70 75 80

gcc cta atc acc cac cag cgc agc cac ggt cca gcc gcc aag ccc acc 464
Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala Ala Lys Pro Thr
85 90 95 100

ctg ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac 512
Leu Pro Val Ala Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp
105 110 115

tgt ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag 560
Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln
120 125 130

atg cat gag gtc cgt gcc cct cct gcc acc ttc gcc tgc aca gag tgc 608
Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys
135 140 145

ggc cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg 656
Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg
150 155 160

cat gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacgggtgac 704
His Ala Arg Gly Glu Leu
165 170

gggtggctct gtggctggta ggactcacc atgatatgg gtgcaggaac tctgggggcc 764
ctgaaggatt tgcttcctc ccttgggaag gcagagggct cttaataaag aggaccaga 824
agattctcaa aaaaaaaaaa aaaaa 849

<210> 161

<211> 846

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 165..671

<400> 161
 aaaactgagg cctgggagca ggaacctgta ggcagcgctt gagggtagcg ggatagcagc 60
 tgcaagcgcg cgtgggagggc gggggctctg ggcggaacaa aaatcacagg atgtcagagg 120
 atgtttcccg ggaagaactg ggataaagga aggggtcccag cacc atg gag gac ccg 176
 Met Glu Asp Pro
 1
 aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224
 Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
 5 10 15 20
 ccc cag ccc agg agg caa cat ctg cca cct ggg ggc ccc gaa gtg cac 272
 Pro Gln Pro Arg Arg Gln His Leu Pro Pro Gly Gly Pro Glu Val His
 25 30 35
 ccg ctg cct cat cac ctt cgc aga ttc caa gtt cca gga gcg tca cat 320
 Pro Leu Pro His His Leu Arg Arg Phe Gln Val Pro Gly Ala Ser His
 40 45 50
 gaa gcg gga gca ccc agc gga ctt cgt ggc cca gaa gct gca ggg ggt 368
 Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu Ala Ala Gly Gly
 55 60 65
 cct ctt cat ctg ctt cac ctg cgc ccg ctc ctt ccc ctc ctc caa agc 416
 Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro Leu Leu Gln Ser
 70 75 80
 cct aat cac cca cca gcg cag cac ggt cca gcc gcc aag ccc acc ctg 464
 Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala Lys Pro Thr Leu
 85 90 95 100
 ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac tgt 512
 Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys
 105 110 115
 ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag atg 560
 Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln Met
 120 125 130
 cat gag gtc cgt gcc cct cct ggc acc ttc gcc tgc aca gag tgc ggt 608
 His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys Gly
 135 140 145
 cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg cat 656
 Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg His
 150 155 160
 gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtgac gggtggctct 711
 Ala Arg Gly Glu Leu
 165
 gtggctggta ggactcacc atgatatggg gtgcaggaac tctgggggcc ctgaaggatt 771
 tgcttccctc ccctgggaag gcagagggct cttaataaag aggaccaga agattctcaa 831
 aaaaaaaaaa aaaaaa 846

<210> 162
 <211> 1176
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..1128

<400> 162

```

ctttcctgcc tctgattccg ggctgtc atg gcg acc ccc aac aat ctg acc ccc      54
               Met Ala Thr Pro Asn Asn Leu Thr Pro
               1               5
acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat gcg gcc      102
Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala Ala
10               15               20               25
aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc gcc cat      150
Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala His
               30               35               40
tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc agc      198
Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe Ser
               45               50               55
tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg tgc gag      246
Ser Gln Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val Cys Glu
               60               65               70
gag cgg gac gtg agc ctg cca cag agc gag cac aag gag ccc tgg ttc      294
Glu Arg Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro Trp Phe
               75               80               85
atg cgg ctc aac ctg ggc gag gag gtg ccc gtc atc atc cac cgc gac      342
Met Arg Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His Arg Asp
90               95               100               105
aac atc atc agt gac tat gac cag atc att gac tat gtg gag cgc acc      390
Asn Ile Ile Ser Asp Tyr Asp Gln Ile Ile Asp Tyr Val Glu Arg Thr
               110               115               120
ttc aca gga gag cac gtg gtg gcc ctg atg ccc gag gtg ggc agc ctg      438
Phe Thr Gly Glu His Val Val Ala Leu Met Pro Glu Val Gly Ser Leu
               125               130               135
cag cac gca cgg gtg ctg cag tac cgg gag ctg ctg gac gca ctg ccc      486
Gln His Ala Arg Val Leu Gln Tyr Arg Glu Leu Leu Asp Ala Leu Pro
               140               145               150
atg gat gcc tac acg cat ggc tgc atc ctg cat ctc gag ctc acc acc      534
Met Asp Ala Tyr Thr His Gly Cys Ile Leu His Leu Glu Leu Thr Thr
155               160               165
gac tcc atg atc ccc aag tac gcc acg gcc gag atc cgc aga cat tta      582
Asp Ser Met Ile Pro Lys Tyr Ala Thr Ala Glu Ile Arg Arg His Leu
170               175               180               185
gcc aat gcc acc acg gac ctc atg aaa ctg gac cat gaa gag gag ccc      630
Ala Asn Ala Thr Thr Asp Leu Met Lys Leu Asp His Glu Glu Glu Pro
               190               195               200
cag ctc tcc gag ccc tac ctt tct aaa caa aag aag ctc atg gcc aag      678
Gln Leu Ser Glu Pro Tyr Leu Ser Lys Gln Lys Lys Leu Met Ala Lys
               205               210               215
atc ttg gag cat gat gat gtg agc tac ctg aag aag atc ctc ggg gaa      726
Ile Leu Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu
               220               225               230
ctg gcc atg gtg ctg gac cag att gag gcg gag ctg gag aag agg aag      774
Leu Ala Met Val Leu Asp Gln Ile Glu Ala Glu Leu Glu Lys Arg Lys
235               240               245
ctg gag aac gag ggg cag aaa tgc gag ctg tgg ctc tgt ggc tgt gcc      822
Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Ala
250               255               260               265
ttc acc ctc gct gat gtc ctc ctg gga gcc acc ctg cac cgc ctc aag      870
Phe Thr Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg Leu Lys
               270               275               280
ttc ctg gga ctg tcc aag aaa tac tgg gaa gat ggc agc cgg ccc aac      918
Phe Leu Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg Pro Asn

```

| | | | |
|---|-----|-----|------|
| 285 | 290 | 295 | |
| ctg cag tcc ttc ttt gag agg gtc cag aga cgc ttt gcc ttc cgg aaa | | | 966 |
| Leu Gln Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys | | | |
| 300 | 305 | 310 | |
| gtc ctg ggt gac atc cac acc acc ctg ctg tcg gcc gtc atc ccc aat | | | 1014 |
| Val Leu Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn | | | |
| 315 | 320 | 325 | |
| gct ttc cgg ctg gtc aag agg aaa ccc cca tcc ttc ttc ggg gcg tcc | | | 1062 |
| Ala Phe Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser | | | |
| 330 | 335 | 340 | 345 |
| ttc ctc atg ggc tcc ctg ggt ggg atg ggc tac ttt gcc tac tgg tac | | | 1110 |
| Phe Leu Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr | | | |
| 350 | 355 | 360 | |
| ctc aag aaa aaa tac atc tagggccagg cctggggcctt ggtgtctgac | | | 1158 |
| Leu Lys Lys Lys Tyr Ile | | | |
| 365 | | | |
| aaaaaamaaa aaaaaaaa | | | 1176 |

<210> 163
 <211> 1084
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 135..194

| | |
|--|------|
| <400> 163 | |
| aacgaaacgg taaccagccc tgggaagccc gcaagaggcc tcagcgggtgg ccgtccgagc | 60 |
| gccgagaggt gaggtgccc cgcctcacc tgcagagggg ccgttccggg ctggaacccg | 120 |
| gcaccttccg gaaa atg gcg gct gcc agg ccc agc ctg ggc cga gtc ctc | 170 |
| Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu | |
| 1 5 10 | |
| cca gga tcc tct cct gtt cct gtg tgacatgcag gagaagtcc gccacaacat | 224 |
| Pro Gly Ser Ser Pro Val Pro Val | |
| 15 20 | |
| cgctacttcc ccacagatcg tctcagtggc tgcccgcgat ctcaaggtgg cccggtgct | 284 |
| tgaggtgcca gtcagtctga cggagcagta cccacaaggc ctgggccccg cgtgcccga | 344 |
| gctgggggact gagggccttc ggccgctggc caagacctgc ttcagcatgg tgcttgcct | 404 |
| gcagcaggag ctggacagtc ggccccagct gcgctctgtg ctgctctgtg gcattgaggc | 464 |
| acaggcctgc atcttgaaca cgacctgga cctcctagac cgggggctgc aggtccatgt | 524 |
| ggtggtggac gcctgtcct caccagcca ggtggaccgg ctggtggctc tggcccgcat | 584 |
| gagacagagt ggtgccttcc tctccaccag cgaagggtc attctgcagc ttgtgggcga | 644 |
| tgccgtccac cccagttca aggagatcca gaaactcatc aaggagcccg cccagacag | 704 |
| cggactgctg ggctcttcc aaggccagaa ctccctctc cactgaactc caaccctgcc | 764 |
| ttgagggaag accaccctcc tgtcaccgg acctcagtgg aagcccgttc ccccatccc | 824 |
| tgatcccaa gagtgggtgc atccaccagg agtgccggcc ccttgggggg ggcagggtgc | 884 |
| tgcttccca ttggacagct gctccggaa atgcaaatga gactcctgga aactgggtgg | 944 |
| gaattggctg agccaagatg gagggggggc tcggccccgg gccacttcac ggggcgggaa | 1004 |
| ggggagggga agaagagtct cagactgtgg gacacggact cgcagaataa acatatatgt | 1064 |
| ggcaaaaaaa aaaaaaaaaa | 1084 |

<210> 164
 <211> 1793
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 173..847

<400> 164

```
gsmggrggcc attacctaga acatcstaac cgaarratta tttgaaaaac cactggggttc      60
cgagttcatt actacaggaa aaactgttct cttctgtggc acagagaacc ctgcttcaaa      120
gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca      178
                                         Met Ala
                                         1
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg      226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
      5      10      15
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc      274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
      20      25      30
ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg      322
Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu
      35      40      45      50
tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc      370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile
      55      60      65
tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga      418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly
      70      75      80
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc      466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala
      85      90      95
atc ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg      514
Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val
      100      105      110
aag gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc      562
Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly
      115      120      125      130
atg gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga      610
Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg
      135      140      145
gat ttc tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga      658
Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly
      150      155      160
gaa gct ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga      706
Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly
      165      170      175
gga gct ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc      754
Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser
      180      185      190
tac aga tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac      802
Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
      195      200      205      210
acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg      847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
      215      220      225
tagttgtgta tgttttttta actttactat aaagccatgc aaatgacaaa aatctatatatt      907
acttttctcaa aatggacccc aaagaaaactt tgatttactg ttcttaactg cctaattctta      967
attacaggaa ctgtgcatca gctattttatg atttctataag ctatttcagc agaatgagat      1027
attaaaccca atgcttttgat tgttctagaa agtattgttaa tttgttttct aaggtgggttc      1087
aagcatctac tcttttttata atttacttca aaatgacatt gctaaagact gcattattct      1147
actactgtaa tttctccacg acatagcatt atgtacatag atgagtgtaa catttatatc      1207
tcacatagag acatgcttat atgggttttat ttaaaatgaa atgccagtcc attacactga      1267
```

```

ataaatagaa ctcaactatt gcttttcagg gaaatcatgg ataggggttga agaagggttac 1327
tattaattgt ttaaaaacag cttatggatt aatgtcctcc atttataatg aagattaaaa 1387
tgaaggcttt aatcagcatt gtaaaggaaa ttgaatggct ttctgatatg ctgtttttta 1447
gcctaggagt tagaaatcct aacttcttta tcctcttctc ccagaggctt tttttttctt 1507
gtgtattaaa ttaacatttt taaaaagcag atattttgtc aaggggcttt gcattcaaac 1567
tgcttttcca gggctatact cagaagaaag ataaaaagtgt gatctaagaa aaagtgatgg 1627
tttttaggaaa gtgaaaatat ttttgttttt gtatttgaag aagaatgatg cattttgaca 1687
agaaatcata tatgtatgta tatattttta taagtatttg agtacagact ttgagggttc 1747
atcaatataa ataaaagagc agaaaagtaa aaaaaaaaaa aaaaaa 1793

```

```

<210> 165
<211> 1849
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 8..1141

```

```

<220>
<221> misc_feature
<222> 1707
<223> n=a, g, c or t

```

```

<400> 165
cgttgcc atg gat cct ggg gac gac tgg ctg gtg gaa tcc ttg cgc ttg 49
      Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu
      1          5          10
tac cag gat ttc tat gca ttc gac ctg tca gga gcc act cga gtc ctt 97
Tyr Gln Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu
15          20          25          30
gaa tgg att gat gac aaa gga gtc ttt gtt gct ggc tat gaa agc ctg 145
Glu Trp Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu
      35          40          45
aaa aag aat gaa att ctt cat ctg aaa tta cct ctc aga ctt tct gta 193
Lys Lys Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val
      50          55          60
aag gaa aac aag ggc tta ttc cca gaa aga gat ttc aaa gtg cgc cat 241
Lys Glu Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His
      65          70          75
gga gga ttt tca gac agg tct atc ttt gat cta aag cat gtg cca cat 289
Gly Gly Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His
      80          85          90
acc aga ttg ctg gtt acc agt ggc ctt cca ggt tgt tat ctg cag gtg 337
Thr Arg Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val
95          100          105          110
tgg cag gtt gca gag gac agt gat gtc att aaa gct gtc agc acc att 385
Trp Gln Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile
      115          120          125
gct gtg cat gag aaa gag gag agt ctc tgg cct agg gtg gcc gtc ttc 433
Ala Val His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe
      130          135          140
tcc aca ttg gca ccc gga gtc ctc cat ggg gcg agg ctc cga agt ctg 481
Ser Thr Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu
      145          150          155
cag gtc gtt gat ctg gag tcc cgg aag acc acg tac acc tca gat gtc 529
Gln Val Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val
      160          165          170

```


| | |
|--|------|
| agt gac agt gag gag ctg agt agc ctg cag gtc cta gat gcg gac acc | 577 |
| Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr | |
| 175 180 185 190 | |
| ttt gcc ttc tgc tgt gct tgc ggc cgg ctg ggg ctt gtt gac acc cgg | 625 |
| Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg | |
| 195 200 205 | |
| cag aag tgg gca ccg ttg gag aat cgc agc cct ggc cct ggg tct ggt | 673 |
| Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly | |
| 210 215 220 | |
| gga gag aga tgg tgt gct gaa gtt ggg agc tgg ggc cag ggc cct ggg | 721 |
| Gly Glu Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly | |
| 225 230 235 | |
| ccc agc att gcc agc ctt agc tca gat ggg cgt ctt tgt ctt ctt gac | 769 |
| Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp | |
| 240 245 250 | |
| ccc cgg gat ctc tgc cat cct gtg agc tca gtc cag tgc cca gta tcc | 817 |
| Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser | |
| 255 260 265 270 | |
| gta cct agc cct gac cca gag ctg ctg cga gtg act tgg gcc cca ggc | 865 |
| Val Pro Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly | |
| 275 280 285 | |
| ctg aag aat tgc ttg gcc atc tca ggt ttt gat ggt aca gtc cag gtc | 913 |
| Leu Lys Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val | |
| 290 295 300 | |
| tat gat gcc aca tct tgg gat gga aca cgg agc caa gat gga aca cgg | 961 |
| Tyr Asp Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg | |
| 305 310 315 | |
| agc caa gta gaa cct ctc ttc act cac aga ggt cac atc ttc cta gat | 1009 |
| Ser Gln Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp | |
| 320 325 330 | |
| gga aat ggg atg gac cct gct cct ttg gtc acc acc cac acc tgg cat | 1057 |
| Gly Asn Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His | |
| 335 340 345 350 | |
| ccc tgc aga cca agg act ttg tta tca gca aca aat gat gcc tct ctg | 1105 |
| Pro Cys Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu | |
| 355 360 365 | |
| cat gtg tgg gac tgg gtg gac ctt tgt gcc ccc cgc tgacaccagc | 1151 |
| His Val Trp Asp Trp Val Asp Leu Cys Ala Pro Arg | |
| 370 375 | |
| atctttccat ctaggcctct agaaagggga ggagctgctg tagtagcaag ggtgctgatg | 1211 |
| taggactcaa gtgactacca gtccctgtta ccagctgtgt ggccttgggc aagtctgcc | 1271 |
| gcgtcactta gcctcagttt ccttatctgt aaaatgagga tagtaagaac tacctcgtag | 1331 |
| tgatattgcg aagggttagaa gaaacgcatg gcataattac ttggtagcta ttgttagatc | 1391 |
| tgggagtgtg aaatggtagc gttttgtccc tgtcttcaca ctatcatagg gagaatcaaa | 1451 |
| agagctaaca aatataaaca tgctttgtga atttttttaa agaaaaaaat gtaggggggc | 1511 |
| caataaacat gaaaaaatcc cagccctagt agcaattaag gaaatagcaa aacaggattt | 1571 |
| ctgctcctct tgaggggggtc tcatgggaac acaggtgcac tttcccacac ttgtccccc | 1631 |
| aggtgactag gttcaagaga catttgcttt tggtggcccc acaaacattt ccttttgagg | 1691 |
| gcccatagtg aatatntaaa gtgtgtctgga catggtggct catgcctgta atcccagcac | 1751 |
| tttcagaggc tgaggtgggc agattgcttg agctgaggag tttgagacca gcctgggcaa | 1811 |
| catagcaaga tcccttcccc aaaaaaaaaa aaaaaaaaaa | 1849 |

<210> 166

<211> 1748

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> 136..264

```

<400> 166
attattttgaa aaaccactgg gttccgagtt cattactaca ggaaaaactt tctcttctgt      60
ggcacagaga accctgcttc aaagcagaag tagcagttcc ggagtccagc tggctaaaac      120
tcattcccaga ggata atg gca acc cat gcc tta gaa atc gct ggg ctg ttt      171
          Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe
                1                5                10
ctt ggt ggt gtt gga atg gtg ggc aca gtg gct gtc act gtc atg cct      219
Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro
          15                20                25
cag tgg aga gtg tgc gcc ttc att gaa aac aac atc gtg gtt ttt      264
Gln Trp Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe
          30                35                40
taaaacttct gggaaggact gtggatgaat tgcgtgaggc aggctaacat caggatgcag      324
tgcaaaatct atgattccct gctggctcct tctccggacc tacaggcagc cagaggactg      384
atgtgtgctg cttccgtgat gtccttcttg gctttcatga tggccatcct tggcatgaaa      444
tgcaccaggt gcacggggga caatgagaag gtgaaggctc acattctgct gacggctgga      504
atcatcttca tcatcacggg catggtgggt ctcatccctg tgagctgggt tgccaatgcc      564
atcatcagag atttctataa ctcaatagtg aatgttggcc aaaaacgtga gcttggagaa      624
gctctctact taggatggac cacggcactg gtgctgattg ttggaggagc tctgttctgc      684
tgcgtttttt gttgcaacga aaagagcagt agctacagat actcgatacc ttcccatcgc      744
acaacccaaa aaagttatca caccggaaag aagtcaccga gcgtctactc cagaagtcag      804
tatgtgtagt tgtgtatggt tttttaactt tactataaag ccatgcaaat gacaaaaatc      864
tatattactt tctcaaaatg gaccccaaag aaactttgat ttactgttct taactgccta      924
atcttaatta caggaactgt gcatcagcta tttatgattc tataagctat ttcagcagaa      984
tgagatatta aaccgaatgc tttgattggt ctagaaagta tagtaatttg ttttctaagg     1044
tggktaagc atctactcct tttatcattt acttcaaaat gacattgcta aagactgcat     1104
tatttttacta ctgtaatttc tccacgacat agcattatct acatagatga gtgtaacatt     1164
tatatctcac atagagacat gcttatatgg ttkcatttaa aatgaaatgc cagtccatta     1224
cactgaataa atagaactca actattgctt ttcagggaaa tcatggatag ggttgaagaa     1284
ggttactatt aattgtttta aaacagctta gggattaatg tcctccattt ataatgaaga     1344
ttaaagttaa ggctttaatc agcattgtaa aggaaattga atggctttct gatatgctgt     1404
tttttagcct aggagttaga aatcctaact tctttatcct cttctcccag aggccttttt     1464
tttcttgtgt attaaattaa cttttttaaa aagcagatat tttgtcaagg ggctttgcat     1524
tcaaactgct tttccagggc tatactcaga agaaagataa aagtgtgatc taagaaaaag     1584
tgatggtttt aggaagtga aaatatTTTT gtttttgtat ttgaagaaga atgatgcatt     1644
ttgacaagaa atcatatatg tatggatata ttttaataag tatttgagta cagactttga     1704
ggtttcatca atataataaa aagagcaaaa aaaaaaaaaa aaaa                        1748

```

<210> 167
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..1048

```

<400> 167
agaggttggg aag atg gcg tgg cga ggc tgg gcg cag aga ggc tgg ggc      49
          Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
                1                5                10
tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag      97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
          15                20                25
ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac      145

```

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|--------|-----|------|--|
| Leu | Thr | Ala | Val | Leu | Thr | Pro | Pro | Gln | Leu | Leu | Gly | Arg | Arg | Phe | Asn | | |
| 30 | | | | | | 35 | | | | | 40 | | | | | | |
| ttc | ttt | att | caa | caa | aaa | tgc | gga | ttc | aga | aaa | gca | ccc | agg | aag | gtt | 193 | |
| Phe | Phe | Ile | Gln | Gln | Lys | Cys | Gly | Phe | Arg | Lys | Ala | Pro | Arg | Lys | Val | | |
| 45 | | | | | 50 | | | | | 55 | | | | | 60 | | |
| gaa | cct | cga | aga | tca | gac | cca | ggg | aca | agt | ggg | gaa | gca | tac | aag | aga | 241 | |
| Glu | Pro | Arg | Arg | Ser | Asp | Pro | Gly | Thr | Ser | Gly | Glu | Ala | Tyr | Lys | Arg | | |
| | | | | 65 | | | | | 70 | | | | | 75 | | | |
| agt | gct | ttg | att | cct | cct | gtg | gaa | gaa | aca | gtc | ttt | tat | cct | tct | ccc | 289 | |
| Ser | Ala | Leu | Ile | Pro | Pro | Val | Glu | Glu | Thr | Val | Phe | Tyr | Pro | Ser | Pro | | |
| | | | 80 | | | | | 85 | | | | | 90 | | | | |
| tat | cct | ata | agg | agt | ctc | ata | aaa | cct | tta | ttt | ttt | act | gtt | ggg | ttt | 337 | |
| Tyr | Pro | Ile | Arg | Ser | Leu | Ile | Lys | Pro | Leu | Phe | Phe | Thr | Val | Gly | Phe | | |
| | | 95 | | | | | 100 | | | | | 105 | | | | | |
| aca | ggc | tgt | gca | ttt | gga | tca | gct | gct | att | tgg | caa | tat | gaa | tca | ctg | 385 | |
| Thr | Gly | Cys | Ala | Phe | Gly | Ser | Ala | Ala | Ile | Trp | Gln | Tyr | Glu | Ser | Leu | | |
| | 110 | | | | | 115 | | | | | 120 | | | | | | |
| aaa | tcc | agg | gtc | cag | agt | tat | ttt | gat | ggg | ata | aaa | gct | gat | tgg | ttg | 433 | |
| Lys | Ser | Arg | Val | Gln | Ser | Tyr | Phe | Asp | Gly | Ile | Lys | Ala | Asp | Trp | Leu | | |
| | 125 | | | | 130 | | | | | | 135 | | | | 140 | | |
| gat | agc | ata | aga | cca | caa | aaa | gaa | gga | gac | ttc | aga | aag | gag | att | aac | 481 | |
| Asp | Ser | Ile | Arg | Pro | Gln | Lys | Glu | Gly | Asp | Phe | Arg | Lys | Glu | Ile | Asn | | |
| | | | | 145 | | | | | 150 | | | | | 155 | | | |
| aag | tgg | tgg | aat | aac | cta | agt | gat | ggc | cag | cgg | act | gtg | aca | ggg | att | 529 | |
| Lys | Trp | Trp | Asn | Asn | Leu | Ser | Asp | Gly | Gln | Arg | Thr | Val | Thr | Gly | Ile | | |
| | | | 160 | | | | | 165 | | | | | 170 | | | | |
| ata | gct | gca | aat | gtc | ctt | gta | ttc | tgt | tta | tgg | aga | gta | cct | tct | ctg | 577 | |
| Ile | Ala | Ala | Asn | Val | Leu | Val | Phe | Cys | Leu | Trp | Arg | Val | Pro | Ser | Leu | | |
| | | 175 | | | | | 180 | | | | | 185 | | | | | |
| cag | cgg | aca | atg | atc | aga | tat | ttc | aca | tcg | aat | cca | gcc | tca | aag | gtc | 625 | |
| Gln | Arg | Thr | Met | Ile | Arg | Tyr | Phe | Thr | Ser | Asn | Pro | Ala | Ser | Lys | Val | | |
| | | 190 | | | | 195 | | | | | 200 | | | | | | |
| ctt | tgt | tct | cca | atg | ttg | ctg | tca | aca | ttc | agt | cat | ttc | tcc | tta | ttt | 673 | |
| Leu | Cys | Ser | Pro | Met | Leu | Leu | Ser | Thr | Phe | Ser | His | Phe | Ser | Leu | Phe | | |
| | 205 | | | | 210 | | | | | 215 | | | | | 220 | | |
| cac | atg | gca | gca | aat | atg | tat | gtt | ttg | tgg | agc | ttc | tct | tcc | agc | ata | 721 | |
| His | Met | Ala | Ala | Asn | Met | Tyr | Val | Leu | Trp | Ser | Phe | Ser | Ser | Ser | Ile | | |
| | | | | 225 | | | | | 230 | | | | | 235 | | | |
| gtg | aac | att | ctg | ggg | caa | gag | cag | ttc | atg | gca | gtg | tac | cta | tct | gca | 769 | |
| Val | Asn | Ile | Leu | Gly | Gln | Glu | Gln | Phe | Met | Ala | Val | Tyr | Leu | Ser | Ala | | |
| | | | 240 | | | | 245 | | | | | | 250 | | | | |
| ggg | gtt | att | tcc | aat | ttt | gtc | agt | tac | gtg | ggg | aaa | gtt | gcc | aca | gga | 817 | |
| Gly | Val | Ile | Ser | Asn | Phe | Val | Ser | Tyr | Val | Gly | Lys | Val | Ala | Thr | Gly | | |
| | | 255 | | | | 260 | | | | | | 265 | | | | | |
| aga | tat | gga | cca | tca | ctt | ggg | gca | gcc | ctg | aaa | gcc | att | atc | gcc | atg | 865 | |
| Arg | Tyr | Gly | Pro | Ser | Leu | Gly | Ala | Ala | Leu | Lys | Ala | Ile | Ile | Ala | Met | | |
| | | 270 | | | | 275 | | | | | 280 | | | | | | |
| gat | aca | gca | gga | atg | atc | ctg | gga | tgg | aaa | ttt | ttt | gat | cat | gcg | gca | 913 | |
| Asp | Thr | Ala | Gly | Met | Ile | Leu | Gly | Trp | Lys | Phe | Phe | Asp | His | Ala | Ala | | |
| | | 285 | | | | 290 | | | | 295 | | | | | 300 | | |
| cat | ctt | ggg | gga | gct | ctt | ttt | gga | ata | tgg | tat | gtt | act | tac | ggg | cat | 961 | |
| His | Leu | Gly | Gly | Ala | Leu | Phe | Gly | Ile | Trp | Tyr | Val | Thr | Tyr | Gly | His | | |
| | | | | 305 | | | | 310 | | | | | | 315 | | | |
| gaa | ctg | att | tgg | aag | aac | agg | gag | ccg | cta | gtg | aaa | atc | tgg | cat | gaa | 1009 | |
| Glu | Leu | Ile | Trp | Lys | Asn | Arg | Glu | Pro | Leu | Val | Lys | Ile | Trp | His | Glu | | |
| | | | 320 | | | | | 325 | | | | | 330 | | | | |
| ata | agg | act | aat | ggc | ccc | aaa | aaa | gga | ggg | ggc | tct | aag | taaaa | actggg | | 1058 | |
| Ile | Arg | Thr | Asn | Gly | Pro | Lys | Lys | Gly | Gly | Gly | Ser | Lys | | | | | |

| | | | |
|------------|------------|-------------|------------|
| 335 | 340 | 345 | |
| attggacagt | agtggtgcat | ctggctccttg | ccgcctgaga |
| gagtgacat | ggctatgctc | ccgtctggaa | gatgccagca |
| agctgtgtcc | cccagtcctg | gtcttttttag | aatgtgaatg |
| aggtttctat | ctagtttgca | aaaaaaaaaa | aaaaaaa |

1118
1178
1238
1275

<210> 168
<211> 1023
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..777

| | |
|---|-----|
| <400> 168 | |
| aataggtccg gttccggggg cgcgtggctg cagcggggcc cgcgtggtgc ctccctgagggc | 60 |
| ggcccccg atg aag aga tct ggg aac ccg gga gcc gag gta acg aac agc | 111 |
| Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser | |
| 1 5 10 | |
| tcg gtg gca ggg cct gac tgc tgc gga ggc ctc ggc aat att gat ttt | 159 |
| Ser Val Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe | |
| 15 20 25 30 | |
| aga cag gca gac ttc tgc gtt atg acc cgg ctg ctg ggc tac gtg gac | 207 |
| Arg Gln Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp | |
| 35 40 45 | |
| ccc ctg gat ccc agc ttt gtg gct gcc gtc atc acc atc acc ttc aat | 255 |
| Pro Leu Asp Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn | |
| 50 55 60 | |
| ccg ctc tac tgg aat gtg gtt gca cga tgg gaa cac aag acc cgc aag | 303 |
| Pro Leu Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys | |
| 65 70 75 | |
| ctg agc agg gcc ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc | 351 |
| Leu Ser Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser | |
| 80 85 90 | |
| atc acc atc ctg ctc ctg aac ttc ctg cgc tgc cac tgc ttc acg cag | 399 |
| Ile Thr Ile Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln | |
| 95 100 105 110 | |
| gcc atg ctg agc cag ccc agg atg gag agc ctg gac acc ccc gcg gcc | 447 |
| Ala Met Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala | |
| 115 120 125 | |
| tac agc ctg gtc ctc gca ctc ctg gga ctg ggc gtc gtg ctc gtg ctc | 495 |
| Tyr Ser Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu | |
| 130 135 140 | |
| tcc agc ttc ttt gca ctg ggg ttc gct gga act ttc cta ggt gat tac | 543 |
| Ser Ser Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr | |
| 145 150 155 | |
| ttc ggg atc ctc aag gag gcg aga gtg acc gtg ttc ccc ttc aac atc | 591 |
| Phe Gly Ile Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile | |
| 160 165 170 | |
| ctg gac aac ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg | 639 |
| Leu Asp Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp | |
| 175 180 185 190 | |
| gcc atc atg cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg | 687 |
| Ala Ile Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val | |
| 195 200 205 | |
| gcc ctc acc tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct | 735 |
| Ala Leu Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala | |

| | | | |
|--|-------------------------|-----|------|
| 210 | 215 | 220 | |
| gag atc tac cgg cag aaa gcc tcc ggg tcc cac aag agg agc | | | 777 |
| Glu Ile Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser | | | |
| 225 | 230 | 235 | |
| tgattgagct gcaacagctt tgctgaaggc ctggccagcc tcttggcctg ccccaagtgg | | | 837 |
| caggccctgc gcagggcgag aatggtgcct gctgctcagg gctcgccccc ggcgtgggct | | | 897 |
| gccccagtgc cttggaacct gctgccttgg ggaccctgga cgtgccgaca tatggccatt | | | 957 |
| gagctccaac ccacacattc ccattcacca ataaaggcac cctgacctca aaaaaaaaaa | | | 1017 |
| aaaaaa | | | 1023 |
| | | | |
| <210> 169 | | | |
| <211> 1085 | | | |
| <212> DNA | | | |
| <213> Homo sapiens | | | |
| | | | |
| <220> | | | |
| <221> CDS | | | |
| <222> 38..400 | | | |
| | | | |
| <400> 169 | | | |
| aacaattcat gaagttgaag aaaagacact gtcagaa atg aac aca gaa gcg gag | | | 55 |
| | Met Asn Thr Glu Ala Glu | | |
| | 1 5 | | |
| caa cag ctt ctc cat cac gcc aga aat ggc aat gct gaa gaa gta aga | | | 103 |
| Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg | | | |
| | 10 15 20 | | |
| caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat | | | 151 |
| Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn | | | |
| | 25 30 35 | | |
| tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg | | | 199 |
| Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu | | | |
| | 40 45 50 | | |
| gca tgc tat ttt gga cac aga caa gtg gtc cag gat ctg ttg aag gct | | | 247 |
| Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala | | | |
| | 55 60 65 70 | | |
| ggg gca gaa gtg aat gtg ttg aat gac atg gga gac acg ccg ctt cat | | | 295 |
| Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His | | | |
| | 75 80 85 | | |
| cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg | | | 343 |
| Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met | | | |
| | 90 95 100 | | |
| ttt gta agt gag gta ttt gga gga gta gtt acc att gtt ttc tct gtt | | | 391 |
| Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val | | | |
| | 105 110 115 | | |
| ata acc atc tgaccagcaa ccgaagaaag ccacacaaaa aaatgtatac | | | 440 |
| Ile Thr Ile | | | |
| | 120 | | |
| accagcactt tgggtcaaaa ggccacagga tcttttgagt ctgacagtga ggtccagtac | | | 500 |
| taagggtcatg gagaccccc ctctgtagca tccctgtgag gagatcattc cgtttctgct | | | 560 |
| tgtgtactcc agcaatgggg aactcctgat tattcttttt ttttaaaaaa aaatagcttc | | | 620 |
| attgaggtat aacttacatt gcataaactt cacctgtgat attgtgaaat atataatttgg | | | 680 |
| tctttgacct tgtacactaa agatgtacaa aaagatgact ggcaaccctt ggcttcagga | | | 740 |
| tgggggctgg tcaccagaaa gaccaaggca ggactagggg gttgggactt tcagccgaac | | | 800 |
| tttgcaacct ccaggggagg tagaggggct gaaggggaaa tggctcgcta atggccagtg | | | 860 |
| gtttcatcaa tcatgcctat ttaatggaac ctccataaaa acctgaaagg acagggttct | | | 920 |
| aggagctcct gggtagctga acacgtggag gttcttgaat gatcacacc agggagggca | | | 980 |
| tgggtgctct gtgcccttcc tccatgcctt gctttatgta tctcttcac tgtatccttt | | | 1040 |
| gtaataaagc agtaaacatg ttttcttgaa aaaaaaaaaa aaaaa | | | 1085 |

<210> 170
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..572

<400> 170
 atatgtcatc aggcccccgc cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggaggac gcccagggtg gggaggaaga gtctgcaagc agggctgttg agttagggtt 652
 caccccaatg ggaccaccct cctgggtccc ctgggtgccg ttttccttag aaatcagaga 712
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagcaaaaaa 772
 aaaa 776

<210> 171
 <211> 1219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..867

<400> 171

```
gtagtttagga gtctggagtc gtgagccgga gtcagaactg cgtctcgcga cccaggcgcg      60
ggtttccgga ggacagccaa caagcgatgc tgccgccgcc gtttctgat tggttgtggg      120
tggctacctc ttcgttctga ttggccgcta gtgagcaag atg ctg agc aag ggt      174
                               Met Leu Ser Lys Gly
                               1           5

ctg aag cgg aaa cgg gag gag gag gag gag aag gaa cct ctg gca gtc      222
Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val
                               10           20

gac tcc tgg tgg cta gat cct ggc cac aca gcg gtg gca cag gca ccc      270
Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro
                               25           30           35

ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc      318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu
                               40           45           50

cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg      366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu
                               55           60           65

gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct      414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala
70           75           80           85

gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac      462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp
                               90           95           100

aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc      510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser
                               105           110           115

ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa      558
Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln
120           125           130

ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg      606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala
135           140           145

ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta      654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu
150           155           160           165

ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg      702
Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met
170           175           180

tat gac aat gaa ctt tgg gca cca gcc tct gag ggc ctc aaa cca ggc      750
Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly
185           190           195

cct gag gat ggg ccg ggc aag gag gaa gct ccg gag ctg gac gag gcc      798
Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala
200           205           210

gaa ttg gac tac ctc atg gat gtg ctg gtg ggc aca cag gca ctg gag      846
Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu
215           220           225

cga ccg ccg ggg cca ggg cgc tgagccctcg tgctggaatg gttgtctggt      897
Arg Pro Pro Gly Pro Gly Arg
230           235

atctgaactg agcctgctgg ctggaccaac tgtcctcgaa aagacacagc tggcttcct      957
agtacagaga acagggcttg ggccactttg gagagacaga atctagtcct gggcaacttc      1017
acatccgtcc tctgtctca gggctggcag ggggagcctg gaattacccc ctagtgatgg      1077
aatgacaggg tctgggtggg acttaattcc ctggccctgg ggtcatagct tgggctgttc      1137
cttctctgat acgggaagag accccaatca gatttttcaa attaaagcca gtcctgggaa      1197
atctcaaaaa aaaaaaaaaa aa      1219
```

<210> 172
 <211> 1487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..640

```

<400> 172
gacgaaggac tggaaggtgg cgggtggtgaa ggtgcaggcc gttggggcgg ctcagaggca      60
ggtgact atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa      109
      Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
      1          5          10
ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat      157
Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp
15          20          25          30
aac ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat      205
Asn Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn
      35          40          45
aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt      253
Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val
      50          55          60
ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca      301
Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser
      65          70          75
ttc ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct      349
Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser
      80          85          90
gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg      397
Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu
      95          100          105          110
gtt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att      445
Val His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile
      115          120          125
cgg gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc      493
Arg Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu
      130          135          140
tct cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt      541
Ser Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly
      145          150          155
aca ata gct att cag tta gca cat cat aga gga gcc aaa gta ttt caa      589
Thr Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln
      160          165          170
cag cat gca gcc ttg aag ata agc agt gcc ttg aaa gat tca gac ctc      637
Gln His Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu
      175          180          185          190
cca tagccccgagt gattgatgta tctaattggga aagttcatgt tgctgaaagc      690
Pro
tgtttgaag aaacaggtgg cctgggagta gatattgtcc tagatgctgg agtgagatta      750
tatagtaaag atgatgaacc agctgtaaaa ctacaactac taccacataa acatgatatc      810
atcacacttc ttggtgttgg aggccactgg gtaacaacag aagaaaacct tcagttggat      870
cctccagata gccactgcct tttcctcaag ggagcaacgt tagctttcct gaatgatgaa      930
gtttggaatt tgtcaaattgt acaacaggga aaatatcttt gtatcttaaa ggaatgtgatg      990
gagaagttat caactggtgt tttcagacct cagttggatg aaccatttcc actgtatgag      1050
gcaaaagtgt ccatggaagc tggttcagaaa aatcaaggaa gaaaaaagca agttgttcaa      1110
ttttaatttt cttctttctc agacctcagt cggatgaaca tattccagta tttgaagcca      1170

```


| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| gaattttctt | tggaattgt | tgagaaaaac | caaggaagat | aaaacaagtt | gcatttttaa | 1230 |
| gcacgtttct | ctgctaagac | aagatgctca | gttgacacat | ttgaaaagtg | tttgaaaaat | 1290 |
| tcttggtcaa | atgatcaaga | taattctata | attaacatct | taagggaatt | tttctaaaaa | 1350 |
| ccttttcatt | gtttctatat | attttgcccc | tgctataaaa | ttccttccat | gaagaaaact | 1410 |
| gctgctttca | gcaaaagtca | cactactctt | gataaaagct | gttgcaggcc | tttgctaagc | 1470 |
| aaaaaaaaaa | aaaaaaa | | | | | 1487 |

<210> 173
 <211> 1915
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 132..1298

| | | | | | | | | | | | | | | | |
|---|---|-------------|---------------------|------------|------------|-----|--|--|--|--|--|--|--|--|--|
| <400> 173 | | | | | | | | | | | | | | | |
| aactccatt | tctggtgccg | tcacgggaca | gagcagtcgg | tgacaggaca | gagcagtcgg | 60 | | | | | | | | | |
| tgacgggaca | cagtggttgg | tgacgggaca | gagcggtcgg | tgacagcctc | aagggcttca | 120 | | | | | | | | | |
| gcaccgcgcc | c atg gca gag cca gac ccc tct cac cct ctg gag acc cag | 170 | | | | | | | | | | | | | |
| | Met Ala Glu Pro Asp | Pro Ser His | Pro Leu Glu Thr Gln | | | | | | | | | | | | |
| | 1 | 5 | 10 | | | | | | | | | | | | |
| gca ggg aag gtg cag gag gct cag gac tca gat tca gac tct gag gga | 218 | | | | | | | | | | | | | | |
| Ala Gly Lys Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly | | | | | | | | | | | | | | | |
| 15 | 20 | 25 | | | | | | | | | | | | | |
| gga gcc gct ggt gga gaa gca gac atg gac ttc ctg cgg aac tta ttc | 266 | | | | | | | | | | | | | | |
| Gly Ala Ala Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe | | | | | | | | | | | | | | | |
| 30 | 35 | 40 | 45 | | | | | | | | | | | | |
| tcc cag acg ctc agc ctg ggc agc cag aag gag cgt ctg ctg gag gag | 314 | | | | | | | | | | | | | | |
| Ser Gln Thr Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu | | | | | | | | | | | | | | | |
| | 50 | 55 | 60 | | | | | | | | | | | | |
| ctg acc ttg gaa ggg gtg gcc cgg tac atg cag agc gaa cgc tgt cgc | 362 | | | | | | | | | | | | | | |
| Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg | | | | | | | | | | | | | | | |
| | 65 | 70 | 75 | | | | | | | | | | | | |
| aga gtc atc tgt ttg gtg gga gct gga atc tcc aca tcc gca ggc atc | 410 | | | | | | | | | | | | | | |
| Arg Val Ile Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile | | | | | | | | | | | | | | | |
| | 80 | 85 | 90 | | | | | | | | | | | | |
| ccc gac ttt cgc tct cca tcc acc ggc ctc tat gac aac cta gag aag | 458 | | | | | | | | | | | | | | |
| Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys | | | | | | | | | | | | | | | |
| | 95 | 100 | 105 | | | | | | | | | | | | |
| tac cat ctt ccc tac cca gag gcc atc ttt gag atc agc tat ttc aag | 506 | | | | | | | | | | | | | | |
| Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys | | | | | | | | | | | | | | | |
| | 110 | 115 | 120 | 125 | | | | | | | | | | | |
| aaa cat ccg gaa ccc ttc ttc gcc ctc gcc aag gaa ctc tat cct ggg | 554 | | | | | | | | | | | | | | |
| Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly | | | | | | | | | | | | | | | |
| | 130 | 135 | 140 | | | | | | | | | | | | |
| cag ttc aag cca acc atc tgt cac tac ttc atg cgc ctg ctg aag gac | 602 | | | | | | | | | | | | | | |
| Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp | | | | | | | | | | | | | | | |
| | 145 | 150 | 155 | | | | | | | | | | | | |
| aag ggg cta ctc ctg cgc tgc tac acg cag aac ata gat acc ctg gag | 650 | | | | | | | | | | | | | | |
| Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu | | | | | | | | | | | | | | | |
| | 160 | 165 | 170 | | | | | | | | | | | | |
| cga ata gcc ggg ctg gaa cag gag gac ttg gtg gag gcg cac ggc acc | 698 | | | | | | | | | | | | | | |
| Arg Ile Ala Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr | | | | | | | | | | | | | | | |
| | 175 | 180 | 185 | | | | | | | | | | | | |
| ttc tac aca tca cac tgc gtc agc gcc agc tgc cgc cac gaa tac ccg | 746 | | | | | | | | | | | | | | |
| Phe Tyr Thr Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro | | | | | | | | | | | | | | | |
| | 190 | 195 | 200 | 205 | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|--------------------|------------|------------|-------------|-------------|-------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|------|
| Gly | Asp | Asp | Ala | Ser | Glu | Glu | Lys | Ala | Ala | Asn | Gln | Ile | Arg | Lys | Cys | |
| 285 | | | | | 290 | | | | | 295 | | | | | | |
| cag | cag | agc | aca | tct | gca | gtc | att | ggc | gtg | cgt | gtg | tgt | ggc | atg | cag | 1203 |
| Gln | Gln | Ser | Thr | Ser | Ala | Val | Ile | Gly | Val | Arg | Val | Cys | Gly | Met | Gln | |
| 300 | | | | | 305 | | | | | 310 | | | | | 315 | |
| gtg | tac | caa | gca | ggc | agt | ggg | cag | ctc | atg | ttc | atg | aac | aag | tac | cat | 1251 |
| Val | Tyr | Gln | Ala | Gly | Ser | Gly | Gln | Leu | Met | Phe | Met | Asn | Lys | Tyr | His | |
| | | | | 320 | | | | | | 325 | | | | | 330 | |
| gga | cgg | aag | cta | tcg | gtg | cag | ggc | ttc | aag | gag | gca | ctt | ttc | cag | ttc | 1299 |
| Gly | Arg | Lys | Leu | Ser | Val | Gln | Gly | Phe | Lys | Glu | Ala | Leu | Phe | Gln | Phe | |
| | | | 335 | | | | | 340 | | | | | 345 | | | |
| ttc | cac | aat | ggg | cgg | tac | ctg | cgc | cgt | gaa | ctc | ctg | ggc | cct | gtg | ctc | 1347 |
| Phe | His | Asn | Gly | Arg | Tyr | Leu | Arg | Arg | Glu | Leu | Leu | Gly | Pro | Val | Leu | |
| | | 350 | | | | | 355 | | | | | 360 | | | | |
| aag | aag | ctg | act | gag | ctc | aag | gca | gtg | ttg | gag | cga | cag | gag | tcc | tac | 1395 |
| Lys | Lys | Leu | Thr | Glu | Leu | Lys | Ala | Val | Leu | Glu | Arg | Gln | Glu | Ser | Tyr | |
| | | 365 | | | | 370 | | | | | 375 | | | | | |
| cgc | ttc | tac | tca | agc | tcc | ctg | ctg | gtc | att | tat | gat | ggc | aag | gag | cgg | 1443 |
| Arg | Phe | Tyr | Ser | Ser | Ser | Leu | Leu | Val | Ile | Tyr | Asp | Gly | Lys | Glu | Arg | |
| | | | | 385 | | | | | | 390 | | | | | 395 | |
| ccc | gaa | gtg | gtc | ctg | gac | tca | gat | gct | gag | gat | ttg | gag | gac | ctg | tca | 1491 |
| Pro | Glu | Val | Val | Leu | Asp | Ser | Asp | Ala | Glu | Asp | Leu | Glu | Asp | Leu | Ser | |
| | | | | 400 | | | | | 405 | | | | | 410 | | |
| gag | gaa | tca | gct | gat | gag | tct | gct | ggc | gcc | tat | gcc | tac | aaa | ccc | atc | 1539 |
| Glu | Glu | Ser | Ala | Asp | Glu | Ser | Ala | Gly | Ala | Tyr | Ala | Tyr | Lys | Pro | Ile | |
| | | | 415 | | | | | 420 | | | | | 425 | | | |
| ggc | gcc | agc | tct | gta | gat | gtg | cgc | atg | atc | gac | ttt | gca | cac | acc | acc | 1587 |
| Gly | Ala | Ser | Ser | Val | Asp | Val | Arg | Met | Ile | Asp | Phe | Ala | His | Thr | Thr | |
| | | 430 | | | | | 435 | | | | | 440 | | | | |
| tgc | agg | ctg | tat | ggc | gag | gac | acc | gtg | gtg | cat | gag | ggc | cag | gat | gct | 1635 |
| Cys | Arg | Leu | Tyr | Gly | Glu | Asp | Thr | Val | Val | His | Glu | Gly | Gln | Asp | Ala | |
| | | 445 | | | | 450 | | | | | 455 | | | | | |
| ggc | tat | atc | ttc | ggg | ctc | cag | agc | ctg | ata | gac | att | gtc | aca | gag | ata | 1683 |
| Gly | Tyr | Ile | Phe | Gly | Leu | Gln | Ser | Leu | Ile | Asp | Ile | Val | Thr | Glu | Ile | |
| | | 460 | | | 465 | | | | 470 | | | | | | 475 | |
| agt | gag | gag | agt | ggg | gag | tgagcttgct | agctgctcca | gtacttgaga | | | | | | | | 1731 |
| Ser | Glu | Glu | Ser | Gly | Glu | | | | | | | | | | | |
| | | | | 480 | | | | | | | | | | | | |
| gcgactctgt | gtcccaggma | cagctgtgct | gcgtcagggg | ggaagccagt | atggccaggt | | | | | | | | | | | 1791 |
| gggtggctcct | gcagcctgga | gctgatgtgc | agtggcctct | gtgagcccca | gcctgagcca | | | | | | | | | | | 1851 |
| gtcccagctg | tgcttgaggt | ctttatttat | tttaactatt | tcttcaacat | tccacatttg | | | | | | | | | | | 1911 |
| atgatgatac | ctctttcttc | cctgagtgtg | tatgtttctaa | tacaaatctt | tttgtttatt | | | | | | | | | | | 1971 |
| ataaaaaaaaa | aaaaaaaaa | | | | | | | | | | | | | | | 1990 |
| <210> 175 | | | | | | | | | | | | | | | | |
| <211> 1971 | | | | | | | | | | | | | | | | |
| <212> DNA | | | | | | | | | | | | | | | | |
| <213> Homo sapiens | | | | | | | | | | | | | | | | |
| <220> | | | | | | | | | | | | | | | | |
| <221> CDS | | | | | | | | | | | | | | | | |
| <222> 213..1274 | | | | | | | | | | | | | | | | |
| <400> 175 | | | | | | | | | | | | | | | | |
| ttcagcccc | gccagatccc | gcgtcaacgg | acgcggaacg | gcggaccccc | taccctggca | | | | | | | | | | | 60 |
| gcatcggagc | accggcgggg | gaaggcaagg | tccctggact | ggcatatac | ctcttggtggc | | | | | | | | | | | 120 |
| cctggcagaa | tcaagatgag | gccctgtcat | gcctccccag | tgaggcctac | agtcctgagca | | | | | | | | | | | 180 |
| gacagcatgg | cctgccactg | gcagtgaaca | cc atg tct | gca gga ggt | ggc cgg | | | | | | | | | | | 233 |

| | Met | Ser | Ala | Gly | Gly | Gly | Arg | |
|---|-----|-----|-----|-----|-----|-----|-----|------|
| | 1 | | | 5 | | | | |
| gcc ttt gct tgg caa gtg ttc ccc ccc atg ccc act tgc cgg gtc tat | | | | | | | | 281 |
| Ala Phe Ala Trp Gln Val Phe Pro Pro Met Pro Thr Cys Arg Val Tyr | | | | | | | | |
| 10 15 20 | | | | | | | | |
| ggc aca gtg gca cac caa gat ggg cac ctg ctg gtg ttg ggg ggt tgt | | | | | | | | 329 |
| Gly Thr Val Ala His Gln Asp Gly His Leu Leu Val Leu Gly Gly Cys | | | | | | | | |
| 25 30 35 | | | | | | | | |
| ggc cgg gct gga ctg ccc ctg gac act gct gag aca ctg gac atg gcc | | | | | | | | 377 |
| Gly Arg Ala Gly Leu Pro Leu Asp Thr Ala Glu Thr Leu Asp Met Ala | | | | | | | | |
| 40 45 50 55 | | | | | | | | |
| tgc cac aca tgg ctg gca ctg gca ccc ctg ccc act gcc cgg gct ggt | | | | | | | | 425 |
| Ser His Thr Trp Leu Ala Leu Ala Pro Leu Pro Thr Ala Arg Ala Gly | | | | | | | | |
| 60 65 70 | | | | | | | | |
| gca gct gcg gta gtt ctg ggc aag cag gtg cta gtg gtg ggt ggt gtg | | | | | | | | 473 |
| Ala Ala Ala Val Val Leu Gly Lys Gln Val Leu Val Val Gly Gly Val | | | | | | | | |
| 75 80 85 | | | | | | | | |
| gat gag gtc cag agc ccg gta gct gct gta gag gcc ttc ctg atg gat | | | | | | | | 521 |
| Asp Glu Val Gln Ser Pro Val Ala Ala Val Glu Ala Phe Leu Met Asp | | | | | | | | |
| 90 95 100 | | | | | | | | |
| gag ggc cgc tgg gag cgt cgg gcc acc ctc cct caa gca gcc atg ggg | | | | | | | | 569 |
| Glu Gly Arg Trp Glu Arg Arg Ala Thr Leu Pro Gln Ala Ala Met Gly | | | | | | | | |
| 105 110 115 | | | | | | | | |
| gtt gca act gtg gag aga gat ggt atg gtg tat gct ctg ggg gga atg | | | | | | | | 617 |
| Val Ala Thr Val Glu Arg Asp Gly Met Val Tyr Ala Leu Gly Gly Met | | | | | | | | |
| 120 125 130 135 | | | | | | | | |
| ggc cct gac acg gcc ccc cag gcc cag gta cgt gtg tat gag ccc cgt | | | | | | | | 665 |
| Gly Pro Asp Thr Ala Pro Gln Ala Gln Val Arg Val Tyr Glu Pro Arg | | | | | | | | |
| 140 145 150 | | | | | | | | |
| cgg gac tgc tgg ctt tgc cta ccc tcc atg ccc aca ccc tgc tat ggg | | | | | | | | 713 |
| Arg Asp Cys Trp Leu Ser Leu Pro Ser Met Pro Thr Pro Cys Tyr Gly | | | | | | | | |
| 155 160 165 | | | | | | | | |
| gcc tcc acc ttc ctg cac ggg aac aag atc tat gtc ctg ggg ggc cgc | | | | | | | | 761 |
| Ala Ser Thr Phe Leu His Gly Asn Lys Ile Tyr Val Leu Gly Gly Arg | | | | | | | | |
| 170 175 180 | | | | | | | | |
| cag ggc aag ctc ccg gtg act gct ttt gaa gcc ttt gat ctg gag gcc | | | | | | | | 809 |
| Gln Gly Lys Leu Pro Val Thr Ala Phe Glu Ala Phe Asp Leu Glu Ala | | | | | | | | |
| 185 190 195 | | | | | | | | |
| cgt aca tgg acc cgg cat cca agc cta ccc agc cgt cgg gcc ttt gct | | | | | | | | 857 |
| Arg Thr Trp Thr Arg His Pro Ser Leu Pro Ser Arg Arg Ala Phe Ala | | | | | | | | |
| 200 205 210 215 | | | | | | | | |
| ggc tgc gcc atg gct gaa ggc agc gtc ttt agc ctg ggt ggc ctg cag | | | | | | | | 905 |
| Gly Cys Ala Met Ala Glu Gly Ser Val Phe Ser Leu Gly Gly Leu Gln | | | | | | | | |
| 220 225 230 | | | | | | | | |
| cag cct ggg ccc cac aac ttc tac tct cgc cca cac ttt gtc aac act | | | | | | | | 953 |
| Gln Pro Gly Pro His Asn Phe Tyr Ser Arg Pro His Val Asn Thr | | | | | | | | |
| 235 240 245 | | | | | | | | |
| gtg gag atg ttt gac ctg gag cat ggg tcc tgg acc aaa ttg ccc cgc | | | | | | | | 1001 |
| Val Glu Met Phe Asp Leu Glu His Gly Ser Trp Thr Lys Leu Pro Arg | | | | | | | | |
| 250 255 260 | | | | | | | | |
| agc ctg cgc atg agg gat aag agg gca gac ttt gtg gtt ggg tcc ctt | | | | | | | | 1049 |
| Ser Leu Arg Met Arg Asp Lys Arg Ala Asp Phe Val Val Gly Ser Leu | | | | | | | | |
| 265 270 275 | | | | | | | | |
| ggg ggc cac att gtg gcc att ggg ggc ctt gga aac cag cca tgt cct | | | | | | | | 1097 |
| Gly Gly His Ile Val Ala Ile Gly Gly Leu Gly Asn Gln Pro Cys Pro | | | | | | | | |
| 280 285 290 295 | | | | | | | | |
| ttg ggc tct gtg gag agc ttt agc ctt gca cgg cgg cgc tgg gag gca | | | | | | | | 1145 |
| Leu Gly Ser Val Glu Ser Phe Ser Leu Ala Arg Arg Arg Trp Glu Ala | | | | | | | | |

| | | | | | | |
|--|-----|--|-----|--|-----|------|
| | 300 | | 305 | | 310 | |
| ttg cct gcc atg ccc act gcc cgc tgc tcc tgc tct agt ctg cag gct | | | | | | 1193 |
| Leu Pro Ala Met Pro Thr Ala Arg Cys Ser Cys Ser Ser Leu Gln Ala | | | | | | |
| | 315 | | 320 | | 325 | |
| ggg ccc cgg ctg ttt gtt att ggg ggt gtg gcc cag ggc ccc agt caa | | | | | | 1241 |
| Gly Pro Arg Leu Phe Val Ile Gly Gly Val Ala Gln Gly Pro Ser Gln | | | | | | |
| | 330 | | 335 | | 340 | |
| gcc gtg gag gca ctg tgt ctg cgt gat ggg gtc tgaaggcttg gtgggagctg | | | | | | 1294 |
| Ala Val Glu Ala Leu Cys Leu Arg Asp Gly Val | | | | | | |
| | 345 | | 350 | | | |
| tccactggag cagctcattg ccagaggcag ctattttctat ggctcctttt gctgctgagg | | | | | | 1354 |
| acactcactg tggctctgtg ggatgagaga ggcattgggg tgagcacttg aaacactgcc | | | | | | 1414 |
| ttggggcctt gggttagggg agcctttgtc tttagtgcag gacacacata tgcttacacc | | | | | | 1474 |
| tacctttatc accattcgtt catgaatcat gcctagctcc atccttgccc tgggacctac | | | | | | 1534 |
| taggccttcc atccaactgg gaaatgggga gaagcaaagc tggcctcatg ctcttcaggg | | | | | | 1594 |
| tcagttccta tctggagttg accaggccta cccaggttgc cattcctgaa aaatctcagc | | | | | | 1654 |
| tgccaggctg cctttagggg ccctgtagac ccaggagagt tgagaggggtg ggggacacag | | | | | | 1714 |
| agagaataga gaggatgtgg gaactgccag agggccggag cgcaggaggt caagtggagg | | | | | | 1774 |
| aatgctggct ttgagccctc tacactgctg gttgtatgac cttggacaag tcacttcacc | | | | | | 1834 |
| tctctgtgcc tcagcatcct catctataaa tggggtatctc tgaaaccttc ctaccctacc | | | | | | 1894 |
| tacctcacag ggctgttgtg aggaccagg gagtttgat gtggaagtaa aagtgtgcc | | | | | | 1954 |
| aaaaaaaaa aaaaaaa | | | | | | 1971 |
| <210> 176 | | | | | | |
| <211> 1613 | | | | | | |
| <212> DNA | | | | | | |
| <213> Homo sapiens | | | | | | |
| <220> | | | | | | |
| <221> CDS | | | | | | |
| <222> 68..127 | | | | | | |
| <400> 176 | | | | | | |
| gacgaaggac tggaaaggtgg cgggtggtgaa ggtgcaggcc gttggggcgg ctcagaggca | | | | | | 60 |
| ggtgact atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa | | | | | | 109 |
| Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu | | | | | | |
| 1 5 10 | | | | | | |
| ata aca ttt gta ttt caa taaaaggaag atcttcctgt tacagaggat | | | | | | 157 |
| Ile Thr Phe Val Phe Gln | | | | | | |
| 15 20 | | | | | | |
| aactttgtga aacttcaagt taaagcttgt gctctgagcc agataaatac aaagcttctg | | | | | | 217 |
| gcagaaatga agatgaaaaa ggattttattt cctgtttggga gagaaattgc tggaaattgta | | | | | | 277 |
| ttagatgttg gaagcaagggt atcattcttt caaccagatg atgaagtagt tggaaattttg | | | | | | 337 |
| ccctggact ctgaagaccc tggactttgt gaagttgtta gagtacatga gcattacttg | | | | | | 397 |
| gttcataaac cagaaaagggt cacatggacg gaagcagcag gaagcattcg ggatggagtg | | | | | | 457 |
| cgtgcctata cagctctgca ttatctttct catctctctc ctggaaaatc agtgctgata | | | | | | 517 |
| atggatggag caagtgcatt tgggtacaata gctattcagt tagcacatca tagaggagcc | | | | | | 577 |
| aaagtgtattt caacagcatg cagccttgaa gataagcagt gccttgaaag attcagacct | | | | | | 637 |
| cccatagccc gagtgattga tgtatctaata gggaaagtgc atgttgctga aagctgtttg | | | | | | 697 |
| gaagaaacag gtggcctggg agtagatatt gtcctagatg ctggagttag attatatagt | | | | | | 757 |
| aaagatgatg aaccagctgt aaaactacaa ctactaccac ataaacatga tatcatcaca | | | | | | 817 |
| cttcttggtg ttggaggcca ctgggtaaca acagaagaaa accttcagtt ggatcctcca | | | | | | 877 |
| gatagccact gccttttctt caagggagca acgttagctt tcctgaatga tgaagtttgg | | | | | | 937 |
| aatttgtcaa atgtacaaca gggamaata tctttgtatc ttaaaggatg tgatggagaa | | | | | | 997 |
| gttatcaact ggtgttttca gacctcagt ggatgaaccc attccactgt atgaggcaaa | | | | | | 1057 |
| agtttccatg gaagctgttc agaaaaatca aggaagaaaa aagcaagttg ttcaatttta | | | | | | 1117 |
| attttcttct ttctcagacc tcagtcggat gaacatatcc cagtatttga agccagaatt | | | | | | 1177 |
| ttcttttgaa attgttgaga aaaaccaagg aagataaaac aagttgcatt tttaagcacg | | | | | | 1237 |

```

tttctctgct aagacaagat gctcagttga cacatttgaa aagtgtttga aaaattcttg 1297
tgcaaatgat caagataatt ctataattaa catcttaagg gaatttttct aaaaaccttt 1357
tcattgtttc tatatatattt gccctgcta taaaattcct tccatgaaga aaactgctgc 1417
tttcagcaaa agtcacacta ctcttgataa aagctgttgc aggcctttgc taagctatca 1477
aagtaacgta ttaattttgt atcaactccg ttctcaacac cttccttaag tctttgctgt 1537
cataatttaa gcatttgagt atattttgaa gtcttaaaag acttagccca taggcactca 1597
aaaaaaaaa aaaaaa 1613

```

<210> 177
 <211> 1361
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..1024

```

<400> 177
gaaggactgg aaggtggcgg tggatgaagg gcaggccggt ggggcggctc agaggcaggt 60
gact atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa ata 109
      Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile
      1          5          10          15
aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat aac 157
Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn
      20          25          30
ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat aca 205
Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr
      35          40          45
aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt ggg 253
Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly
      50          55          60
aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca ttc 301
Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe
      65          70          75
ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct gaa 349
Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu
      80          85          90
gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg gtt 397
Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val
      100          105          110
cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att cgg 445
His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg
      115          120          125
gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc tct 493
Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser
      130          135          140
cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt aca 541
Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr
      145          150          155
ata gct att cag tta gca cat cat aga gga gcc aaa gtg att tca aca 589
Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Ile Ser Thr
      160          165          170          175
gca tgc agc ctt gaa gat aag cag tgc ctt gaa aga ttc aga cct ccc 637
Ala Cys Ser Leu Glu Asp Lys Gln Cys Leu Glu Arg Phe Arg Pro Pro
      180          185          190
ata gcc cga gtg att gat gta tct aat ggg aaa gtt cat gtt gct gaa 685
Ile Ala Arg Val Ile Asp Val Ser Asn Gly Lys Val His Val Ala Glu
      195          200          205

```

```

agc tgt ttg gaa gaa aca ggt ggc ctg gga gta gat att gtc cta gat      733
Ser Cys Leu Glu Glu Thr Gly Gly Leu Gly Val Asp Ile Val Leu Asp
      210      215      220
gct gga gtg aga tta tat agt aaa gat gat gaa cca gct gta aaa cta      781
Ala Gly Val Arg Leu Tyr Ser Lys Asp Asp Glu Pro Ala Val Lys Leu
      225      230      235
caa cta cta cca cat aaa cat gat atc atc aca ctt ctt ggt gtt gga      829
Gln Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly
      240      245      250      255
ggc cac tgg gta aca aca gaa gaa aac ctt cag ttg gat cct cca gat      877
Gly His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp
      260      265      270
agc cac tgc ctt ttc ctc aag gga gca acg tta gct ttc ctg aat gat      925
Ser His Cys Leu Phe Leu Lys Gly Ala Thr Leu Ala Phe Leu Asn Asp
      275      280      285
gaa gtt tgg aat ttg tca aat gta caa cag gga aaa tat ctt tat ctt      973
Glu Val Trp Asn Leu Ser Asn Val Gln Gln Gly Lys Tyr Leu Tyr Leu
      290      295      300
aaa gga tgt gat gga gaa gtt atc aac tgg tgt ttt cag acc tca gtc      1021
Lys Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val
      305      310      315
gga tgaacatatatt ccagtatttg aagccagaat tttctttgga aattggttag      1074
Gly
320
aaaaaccaag gaagataaaa caagttgcat ttttaagcac gtttctctgc taagacaaga      1134
tgctcagttg acacatttga aaagtgtttg aaaaattctg gcttctaata ctgcctctgt      1194
tcccttttct ctccttgaaa gtccagcaca ccattcttgt ccttccccag tttcctcgcc      1254
ctccaccctt ccagcttcat gctcagtgtt gtgcttaata aaatggacat atttttctct      1314
aaaaaaaaaa aaaaaakaaa aaaaaaaaaat aaaaaaaaaa aaaaaaaa      1361

<210> 178
<211> 1113
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 109..585

<400> 178
gcgggaccgg acttccggct ggtctgtggg gtttcggggt cgggggtttcc tgggtgggcgt      60
caggggcagg caacagagtg gcggccgcta cggccctgga acggggcc atg gag aag      117
                                   Met Glu Lys
                                   1
ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag ggc ctg act      165
Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln Gly Leu Thr
      5      10      15
gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc aga ttg aaa      213
Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr Arg Leu Lys
      20      25      30      35
tgg ttt gcc atc tgc ttc gta tgt ggc gtt ttc ttt tct att ctt gga      261
Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser Ile Leu Gly
      40      45      50
act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt gca gtg ttt      309
Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe Ala Val Phe
      55      60      65
tat acc ctc ggc aat ctt gct gcg tta gcc agt aca tgc ttt tta atg      357
Tyr Thr Leu Gly Asn Leu Ala Ala Leu Ala Ser Thr Cys Phe Leu Met

```


| | | | |
|--|---------------------------------|-----|------|
| 70 | 75 | 80 | |
| gga cct gtg aag caa ctg aag aaa atg ttt gaa gca aca aga ttg ctt | | | 405 |
| Gly Pro Val Lys Gln Leu Lys Lys Met Phe Glu Ala Thr Arg Leu Leu | | | |
| 85 | 90 | 95 | |
| gca aca att gtt atg ctt ttg tgt ttc ata ttt acc ctg tgt gct gct | | | 453 |
| Ala Thr Ile Val Met Leu Leu Cys Phe Ile Phe Thr Leu Cys Ala Ala | | | |
| 100 | 105 | 110 | 115 |
| ctt tgg tgg cat aag aag gga ctg gct gtg tta ttc tgc ata ttg cag | | | 501 |
| Leu Trp Trp His Lys Lys Gly Leu Ala Val Leu Phe Cys Ile Leu Gln | | | |
| 120 | 125 | 130 | |
| ttc ttg tca atg acc tgg tat agc ctg tcg tac atc cca tat gca agg | | | 549 |
| Phe Leu Ser Met Thr Trp Tyr Ser Leu Ser Tyr Ile Pro Tyr Ala Arg | | | |
| 135 | 140 | 145 | |
| gat gca gtt att aaa tgc tgt tct tct ctc cta agt tgaaaatcag | | | 595 |
| Asp Ala Val Ile Lys Cys Cys Ser Ser Leu Leu Ser | | | |
| 150 | 155 | | |
| aaacattgtg gaaaagagca cttgaatgta tggactacta tgtttggtga agtttgcttt | | | 655 |
| tccccataaa acactccagg aacaactgac gtgacagttg aagaccgttt tgtactaagt | | | 715 |
| ctcattttgt atactggtaa aaactacatg cttgattaaa ccattaaatg cttgtaactt | | | 775 |
| taaattcatt atgtgtcatt aatatacttt tccaaagata agatttttaa tcaactgccag | | | 835 |
| ttgtaaatta ttttttagcca attttttaaatt cttttcaaag cagctttgaa atgtgaatat | | | 895 |
| ttaaaggtag acctcgtgct gcaagataat taaacttttt tgctttttaa aaatgtctgc | | | 955 |
| atttttaaga ttttttttac tttaaatgtg aaacttattt taagctagaa amattgctta | | | 1015 |
| ttatatgtaa taaaaataat atataaatct ttacaatktt tgaaataaac ccatccttg | | | 1075 |
| aaaaataaaa aaaaaaaaaa agaaaaaaaa aaaaaaaaa | | | 1113 |
| | | | |
| <210> 179 | | | |
| <211> 1960 | | | |
| <212> DNA | | | |
| <213> Homo sapiens | | | |
| | | | |
| <220> | | | |
| <221> CDS | | | |
| <222> 29..577 | | | |
| | | | |
| <400> 179 | | | |
| atcggccaac ggacgcgagg cgcgcgcc atg gaa cag cgg tta gct gag ttt | | | 52 |
| | Met Glu Gln Arg Leu Ala Glu Phe | | |
| | 1 5 | | |
| cgg gcg gcg cgg aaa cgg gcg ggt ctg gcg gcc caa ccc cct gct gcc | | | 100 |
| Arg Ala Ala Arg Lys Arg Ala Gly Leu Ala Ala Gln Pro Pro Ala Ala | | | |
| 10 15 20 | | | |
| agt cag ggc gca caa acc cca gga gag aag gcg gaa gca gca gcg act | | | 148 |
| Ser Gln Gly Ala Gln Thr Pro Gly Glu Lys Ala Glu Ala Ala Ala Thr | | | |
| 25 30 35 40 | | | |
| cta aag gca gcc cca ggc tgg cta aag cgg ttc ctg gta tgg aaa cct | | | 196 |
| Leu Lys Ala Ala Pro Gly Trp Leu Lys Arg Phe Leu Val Trp Lys Pro | | | |
| 45 50 55 | | | |
| agg ccc gcg agt gcc cgg gcc cag ccc ggc cta gtt cag gaa gcg gct | | | 244 |
| Arg Pro Ala Ser Ala Arg Ala Gln Pro Gly Leu Val Gln Glu Ala Ala | | | |
| 60 65 70 | | | |
| cag ccc cag ggc agc aca tca gag aca cca tgg aac aca gcc att cct | | | 292 |
| Gln Pro Gln Gly Ser Thr Ser Glu Thr Pro Trp Asn Thr Ala Ile Pro | | | |
| 75 80 85 | | | |
| ctg ccg tcg tgc tgg gac cag tct ttc ctg acc aat atc acc ttc ttg | | | 340 |
| Leu Pro Ser Cys Trp Asp Gln Ser Phe Leu Thr Asn Ile Thr Phe Leu | | | |
| 90 95 100 | | | |
| aag gtt ctt ctc tgg ttg gtc ctg ctg gga ctg ttt gtg gaa ctg gaa | | | 388 |

| | |
|--|------|
| tat aaa agt cag gtg ttc agc tat cct cac cgc tac ctg gtc ctc gat | 196 |
| Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp | |
| 45 50 55 | |
| ctt gct ctg ctg ttt ctg atg ggg att cta gaa gca gtt cgg tta tac | 244 |
| Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr | |
| 60 65 70 | |
| ctg ggc acc agg ggc aac ctg aca gag gct gag agg ccg ctg gcc gcc | 292 |
| Leu Gly Thr Arg Gly Asn Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala | |
| 75 80 85 90 | |
| agc ctg gcc ctc acg gct ggc acc gcc ctc ctc tct gcc cac ttc ctg | 340 |
| Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Ser Ala His Phe Leu | |
| 95 100 105 | |
| ctt tgg cag gcc cta gtg ttg tgg gcg gac tgg gcc ctc agc gcc acg | 388 |
| Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr | |
| 110 115 120 | |
| ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc | 436 |
| Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile | |
| 125 130 135 | |
| gcg gcc ttc acc agg tagctacgga caccgggat accccacact gggggccctcc | 491 |
| Ala Ala Phe Thr Arg | |
| 140 | |
| tcctgggcct gaccagtccc ccagctgtca cctccccatt cctggacagg aagggcactt | 551 |
| ttcctagtga ctggccatag atgggttttg atggttccat ctgttctggc aggagtggga | 611 |
| gcaggagcca gggcagaaca aactgctgga ggccctgggtg ttgggaacag ctgcggggag | 671 |
| ggtagggacc agacagaact gccttcaaga tgagtcccag gagcgcacac tcagccctgt | 731 |
| cagtggggtc tggcttttagc agccaggcct ccacagaccc ccatgggccc ccagggccga | 791 |
| gagggaggac agagcccttc agaacagagg cctcatctca ctgcatcccc catcaccccc | 851 |
| tagttcccca atggtcctaa tttgtgttct gagatcccag tttactctgt ggccaggccc | 911 |
| cacctgtgtt tccaagtccg gctggagacg caggatgggg taggccttgt gctctgagca | 971 |
| accccagctc tgccctcacag gcaggcaggc ccggtgcaag agtggactct gggttcctaa | 1031 |
| agcaataaat gcaaacaaagc caacagctct gctgcctagc aatttccatc ttagccacac | 1091 |
| ttctcccttc aggggcttcg gaggagaggt cagggtctaa gccggggatg atactgcagg | 1151 |
| agagagagca gcggagggcc acattcggag cctccgtcca ctccagtttt atcagctttt | 1211 |
| gcttttgcac ggagtgttaa acaaattcta gctctgtgtt tttttcccat tcccagattt | 1271 |
| actatcagtt ctccttaaaa agtatctaag ctgttacagt agctttccct tcaacttgatt | 1331 |
| ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc | 1391 |
| accgcatttt gtaataaaag agatgtgtat gcctcaaaaa aaaaaaaaaa aa | 1443 |
| <210> 181 | |
| <211> 605 | |
| <212> DNA | |
| <213> Homo sapiens | |
| <220> | |
| <221> CDS | |
| <222> 232..450 | |
| <400> 181 | |
| caaatacaaa tgccccaaga agactgagga taggagaaaag aatatctcta cctgtgaaac | 60 |
| attgttagac tgccctggcta ggagttcatt gttgttttct gaaggacgta accaaccact | 120 |
| ccaaaactta caggcttaaa acaacaaaca tgtatcattt cttatgattc tgtgggttgg | 180 |
| ctgggtggtt cttctagctg aggcaggatg gtctaggata gctacatcca c atg tct | 237 |
| Met Ser | |
| 1 | |
| ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtg | 285 |
| Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu Pro Val | |
| 5 10 15 | |
| gtg tca tcc tcc aga agg ctg ccc aga ttt gtc cat atg gta gca gga | 333 |

| | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|
| Val | Ser | Ser | Ser | Arg | Arg | Leu | Pro | Arg | Phe | Val | His | Met | Val | Ala | Gly | |
| 20 | | | | | | 25 | | | | 30 | | | | | | |
| g | t | t | c | c | a | a | a | a | a | a | a | a | a | a | a | a |
| g | t | t | c | c | a | a | a | a | a | a | a | a | a | a | a | a |
| Val | Ser | Ser | Lys | Gln | Glu | Arg | Ala | Arg | Ser | Asn | Thr | Glu | Ala | Leu | Phe | |
| 35 | | | | 40 | | | | | 45 | | | | | 50 | | |
| a | a | a | a | a | a | a | a | a | a | a | a | a | a | a | a | a |
| Lys | Leu | Cys | Phe | His | His | Ile | Cys | Gln | Cys | Leu | Thr | Asp | Glu | His | Lys | |
| | | | | 55 | | | | 60 | | | | | 65 | | | |
| t | t | c | a | a | a | a | a | a | a | a | a | a | a | a | a | a |
| Phe | His | Gly | Gln | Val | Gln | Phe | | | | | | | | | | |
| 70 | | | | | | | | | | | | | | | | |
| t | g | g | c | t | a | a | a | a | a | a | a | a | a | a | a | a |
| agg | a | g | a | t | t | c | c | a | a | a | a | a | a | a | a | a |
| aaaaa | | | | | | | | | | | | | | | | |

<210> 182
 <211> 1724
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 758..1183

| | | | | | | | | | | | | | | | | | |
|-----------|--------|-------|--------|------|---------|------|-------|-------|------|------|-------|------|-------|-------|------|--------|-----------|
| <400> 182 | | | | | | | | | | | | | | | | | |
| a | a | a | a | a | a | a | a | a | a | a | a | a | a | a | a | a | a |
| g | a | t | c | c | c | c | c | c | c | c | c | c | c | c | c | c | c |
| gat | cccc | ctg | aac | ctg | cacc | tcc | atc | cag | a | ccc | att | cagg | agc | ctc | cagg | agc | ccagagaca |
| ccag | cccc | ccc | acc | atg | gtaa | gtc | ctt | caag | gg | tggg | gat | ct | gga | agag | gaa | agagg | agggga |
| cacc | agcc | cag | gt | ggag | gtg | cct | aaaa | aatg | acc | atc | cagaa | att | ggg | gtg | a | gggg | aggggc |
| at | ggt | ggact | tct | gt | ggggg | tgg | gggt | gtct | ctc | agt | gcag | ctc | agg | tgcc | tcc | agc | atcc |
| ctt | acc | aggg | ag | caag | ctcc | cat | ct | gtagg | tgg | tggg | gat | gcc | agg | gggtg | tat | ccct | tgga |
| tcca | aggata | gggc | aggacc | tgg | aagacag | aag | gt | ggccc | agg | gaga | atc | ac | agag | tctg | | | |
| cagg | gaca | aag | gac | atag | cct | cctt | tgctt | g | caa | atta | aagg | gag | ccctt | tc | ccag | tccagc | |
| ccag | tctctc | gtct | ccct | gt | tagc | ctt | gg | gctag | tca | ct | agc | tccc | ctct | t | tg | cccc | cggt |
| tccc | acagat | gtc | atatt | tg | gaa | atcc | g | tc | atg | cgga | agt | tgt | ctt | cag | gggt | ctt | |
| tcag | ttgcaa | catt | tctca | aag | gtct | gt | gggt | tct | gcc | acag | agt | ctc | cg | gc | tg | agat | ggga |
| agct | atgtct | aaca | agcgat | ggg | gtgg | att | gac | gc | ctcc | ct | gtg | cc | gg | g | gac | ggg | cggt |
| at | ggct | gcag | cag | agg | gcag | ag | agg | ctgaa | tac | gtcc | atg | cca | ccc | ttt | ggt | ggg | |
| | | | | | | | | | | | | Met | Pro | Pro | Phe | Gly | Gly |
| | | | | | | | | | | | | 1 | | | | 5 | |
| cat | ccc | tta | tcc | caa | gag | gag | gat | ggc | agc | cag | agg | tgt | tgc | tgc | ctg | | |
| His | Pro | Leu | Ser | Gln | Glu | Glu | Asp | Gly | Ser | Gln | Arg | Cys | Cys | Cys | Leu | | |
| | | | | 10 | | | | 15 | | | | | 20 | | | | |
| tca | agt | ctg | agg | tct | gtc | gat | gat | agc | aac | ggg | gag | act | gtc | gtg | atc | | |
| Ser | Ser | Leu | Arg | Ser | Val | Asp | Asp | Ser | Asn | Gly | Glu | Thr | Val | Val | Ile | | |
| | | | | 25 | | | | 30 | | | | 35 | | | | | |
| atg | gcg | cta | ttc | cta | gca | gta | tcg | tac | cac | cat | aag | acg | caa | agt | aag | | |
| Met | Ala | Leu | Phe | Leu | Ala | Val | Ser | Tyr | His | His | Lys | Thr | Gln | Ser | Lys | | |
| | | | | 40 | | | | 45 | | | | 50 | | | | | |
| agg | tgg | cca | ggg | ctg | acc | cca | ccc | cac | agc | tct | ctg | ctg | tgt | aga | cca | | |
| Arg | Trp | Pro | Gly | Leu | Thr | Pro | Pro | His | Ser | Ser | Leu | Leu | Cys | Arg | Pro | | |
| | | | | 55 | | | | 60 | | | 65 | | | 70 | | | |
| ctt | cag | ctt | tca | ttt | ctc | gtc | att | cag | tca | gtg | agg | atg | aga | gca | tgt | | |
| Leu | Gln | Leu | Ser | Phe | Leu | Val | Ile | Gln | Ser | Val | Arg | Met | Arg | Ala | Cys | | |
| | | | | 75 | | | | 80 | | | | | | 85 | | | |
| ggc | tgt | gac | agc | ggc | cac | tgc | agg | att | ctt | ggc | agg | tac | agc | tta | cta | | |
| Gly | Cys | Asp | Ser | Gly | His | Cys | Arg | Ile | Leu | Gly | Arg | Tyr | Ser | Leu | Leu | | |
| | | | | 90 | | | | 95 | | | | | | 100 | | | |

```

ggg tgg agt cag gga cat agg gca aga ggc aga ggt ggt gtt agt ctg      1111
Gly Trp Ser Gln Gly His Arg Ala Arg Gly Arg Gly Gly Val Ser Leu
      105              110              115
aga gac aac acc ttc ttt cag gaa gcc agt gag ggc cag gga cag tgg      1159
Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp
      120              125              130
ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag      1213
Leu Met Pro Val Ile Pro Ala Phe
135              140
gtcagggtgtt cgagaccagc ctggccaacg tggtgaaacc tcgtctctac taaaaaatac      1273
aaaaaattaa ctgggcgtgg tggcacacgc ctgtaatccc agctacatat gaggctgagg      1333
caagagaata acttgaaccc aggaggcgga ggggtgcagtg agctgagatc ctgccgctgc      1393
actccagcct ggggtgacaga gcacactccg tctcaaaaaa ggaaagctga tgagaaattg      1453
ggcatcccg aattcacacc caaacatca gctggagctc tgagactgtt ggggtgggaa      1513
ttcttccaag atgagaagca agccagggag gctcaggtcc tgggatgggc agggctttga      1573
tcaaaagaac acaggaagtg atttgctact tgaaagaaag gcaaccctc cccaaggaag      1633
ccctctgaaa atgcttagtc aacagtcggc ttggcagaca aggtctggga ggggccaccc      1693
gtatcgcaga ggacaaaaaa aaaaaaaaaa a      1724

<210> 183
<211> 1686
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 486..932

<400> 183
cggctcactg cagcctcttc ctcccagtct caagtgatcc tcctgtctca gcctcctgag      60
tggctgggat tacagggtgtg caccactacc acttggttaa tttttatact ttagtagag      120
atgggggttt accatgttgg ccaggctggc cttgaactcc tgacctcagg tgatccgccc      180
gcctcggcct cccaaagtgc tgggggttaca ggcattagacc accgcacccg gcccccttcc      240
ttcgtcttag tcaatcctat cccacctctt cttccaccag tcccctcacc tgatggtccc      300
aacacttcat catccaccac ctctctggagg gggtagcccg aggtgctccg ctggggactc      360
tgctcattct ggggggtgcag ttgacggctg gtcgtgatct ttcccgtaat ctgtcccctc      420
ttacggaacc tagtctccgt tctgtccatg gccttcttct ggacactgct aggatccaga      480
agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca      530
      Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
      1              5              10              15
gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt      578
Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
      20              25              30
ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat      626
Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
      35              40              45
gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct      674
Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
      50              55              60
gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt      722
Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
      65              70              75
ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc      770
Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
      80              85              90              95
ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct      818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
      100              105              110

```

gaa gca tgt tgg ggt ctc ttt gtc tct gta cat gcc cat ttc aga gtc 866
Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val
115 120 125
cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc 914
Gln Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser
130 135 140
aga aac gat gaa acc tta taagagtga attatcatgt gcaagagtga 962
Arg Asn Asp Glu Thr Leu
145
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag 1022
cactcagttt tggcagagct ttttctgccg aatgtttact cacattcact gtccgagatt 1082
ctatactggg ggtacacacg tcctctgccc taaggcaatt ttgagtccaa gagacatttt 1142
gaggcctaaa aatcatagga aactgcccct gagctcacac atatttccaa tgggtgtcccc 1202
aatctcaggg aatccatgga ttacctaagc cagcccctcc agttcggcta agaaactcta 1262
gtctatatgt caagttttgt atcatatgta ttgctctgaa ctcagaaatt tcccttccat 1322
ttatggattc tatgaataaa atatcacatg tacaaaaaga ctaagtcaaa aaatttcagc 1382
tgtgcacagt ggctcatgct tgtaatccca gcactttggg tggccgaggg gggaggattg 1442
cctgaggcca gcagttcaag accagtatgg gcaacatggc aagagcccat ctctaaaaaa 1502
acaaaaccaa accaaattgg ccaggtgtgg tggctggcac ctgtgttcca actacttggg 1562
agactcatgt gacaggaaga tcacttgagc ccgggggtta gaggctgcag tgagctatga 1622
tcttgccact gcactccagc ctgggtgaca gagcgagaca ccgtcgcaaa aaaaaaaaaa 1682
aaaa 1686

<210> 184
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..304

<400> 184
cttttaacag ctgaggtctc tctttaattc tcttaaatac catttctccc tcaaaaaaga 60
ccattagatc atttcacaa atg tat ctg cca cca aac agg tca gag ctt tgc 112
Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys
1 5 10
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg 160
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu
15 20 25
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc 208
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly
30 35 40
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg 256
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu
45 50 55
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac 304
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
60 65 70 75
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt 364
gtcctgtttc ccccttttta attttatccc ttgctagaat taagatacta tatgcctcac 424
ttatcaatta cagtctaaat ccaaaagaaa aaaaaaaaaa 463

<210> 185
<211> 773
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 188..691

<400> 185
 agttgctgggt tgcaggagtt caggaaagga ggtgggacta gagtcaacct ggaatagctc 60
 tacagtaaca atggcagcct ttttgctgct gggacatcca tacaggcaac ttagctgggtg 120
 aaaggactct ggattgggtg gcagctctgct ttttttttc caaggatgatc actttactgt 180
 agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys
 1 5 10
 ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277
 Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln
 15 20 25 30
 cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325
 Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp
 35 40 45
 aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373
 Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr
 50 55 60
 tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421
 Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr
 65 70 75
 gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469
 Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr
 80 85 90
 cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517
 Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His
 95 100 105 110
 tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac 565
 Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His
 115 120 125
 ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca 613
 Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr
 130 135 140
 att ctt tcc ctt tct ttc ttt att ctt ctt gta ctt ctg ctt ctg ctt 661
 Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu
 145 150 155
 ttt att att gtc ttc att ctg atc ttc ttc tgattctttt gtttcaataa 711
 Phe Ile Ile Val Phe Ile Leu Ile Phe Phe
 160 165
 acagcaatga gcatgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 771
 aa 773

<210> 186
 <211> 753
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..573

<400> 186
 acttttcagg ggacattcag aggcattcag cccttcctcc tcaccagctc ccagagttcc 60
 catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
 Met Pro Arg Ser Ser Arg Ser
 1 5

| | |
|---|-----|
| cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga | 162 |
| Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg | |
| 10 15 20 | |
| ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag | 210 |
| Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu | |
| 25 30 35 | |
| gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac | 258 |
| Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn | |
| 40 45 50 55 | |
| aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc | 306 |
| Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser | |
| 60 65 70 | |
| tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt | 354 |
| Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val | |
| 75 80 85 | |
| ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg | 402 |
| Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp | |
| 90 95 100 | |
| tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga | 450 |
| Ser Gln Thr Pro Val Ile Leu Pro Pro Gln Pro Ser Glu Val Leu Gly | |
| 105 110 115 | |
| tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat | 498 |
| Leu Gln Met Gln Ala Ala Val Pro Glu Ala His Gly Glu Asp Arg His | |
| 120 125 130 135 | |
| tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca | 546 |
| Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro | |
| 140 145 150 | |
| ggg gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca | 593 |
| Gly Gly Gly Ile Pro Gly Pro Trp His | |
| 155 160 | |
| agacactgca ctgccacgtg actcagtttc cccatctgcc tgatgggtgt tgctgtgaga | 653 |
| attatgaaat gaaatgatga ccatgaaaat attgtagaag ccaagaaatg cttcagaagt | 713 |
| tataaagctc tccccaaacc gtgttaaaaa aaaaaaaaaa | 753 |

<210> 187
 <211> 754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 181..462

| | |
|---|-----|
| <400> 187 | |
| atcctatcaa aagttacggt gaagtcaggg tgggtggcga gtccctgcaa ggtcgccct | 60 |
| ctgtgccaac acagcctgat ggcttcttgt ttcaggaaac atccagaatt acaactggcc | 120 |
| attgagttat tacatatcaa ttgaacaagg tagttttaaa atgaaagaaa atcttgcaac | 180 |
| atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc | 228 |
| Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe | |
| 1 5 10 15 | |
| ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct | 276 |
| Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser | |
| 20 25 30 | |
| gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga | 324 |
| Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg | |
| 35 40 45 | |
| ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg | 372 |
| Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro | |

| | | | |
|---|----|----|-----|
| 50 | 55 | 60 | |
| tcc gcc ctc cat aag cct ggg ggc atc tgc cct gca gca ctg ggg agg | | | 420 |
| Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg | | | |
| 65 | 70 | 75 | 80 |
| agc cac ctc ctt gtc tgg gaa cag cca agc ctc cgt gac agc | | | 462 |
| Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser | | | |
| 85 | 90 | | |
| tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca | | | 522 |
| tagctctgtg ccttgctggg gtctgaggtt cacaggtcag atgctgctgt ctggtccttc | | | 582 |
| ccaattgchg cgtgaattcc ttcacctca ccagtagctt cttgctctcc ccaaggagg | | | 642 |
| cacgtgctta gtagggagag aggcctacca aggttgccat ctgccatggg ctcaattgtg | | | 702 |
| tccccaaccc ccctgcaaat tatatatattga agtccccaaa aaaaaaaaaa aa | | | 754 |

<210> 188
 <211> 998
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..290

<220>
 <221> misc_feature
 <222> 871
 <223> n=a, g, c or t

| | |
|--|-----|
| <400> 188 | |
| gattc atg aag gcc tcg ggt cct gac ctc tct gat gga ctc cac tgc ccc | 50 |
| Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro | |
| 1 5 10 15 | |
| agt cta att aga cat tta aga acc ttc tct gca gct gct gcc tta gcc | 98 |
| Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala | |
| 20 25 30 | |
| cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc | 146 |
| Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu | |
| 35 40 45 | |
| tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc | 194 |
| Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser | |
| 50 55 60 | |
| cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca | 242 |
| His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr | |
| 65 70 75 | |
| gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat | 290 |
| Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp | |
| 80 85 90 95 | |
| taaagacttt caccagaaaa aaaaattacc tgattttgcc ctgaggcagc cagggagggc | 350 |
| tttgtccttg acaatcccac tgacttattt aacaggtagc tcaaaaccca acaaaaactg | 410 |
| gaggaggctg ctccactgca gggatggttt caattcggtta actggagtat tgtactctcc | 470 |
| ttgcaccctg gctcatcccc acaaaagacc tttcaaagaa aacacttaat tacctccttg | 530 |
| cacaagccct gtaagcccta aggtgaaaag aaactcagca gacaaggtcc acagagaagg | 590 |
| agaaggcaca attcagtagg gacctacgct cagcaccagg ataaagaaac tgtccattcc | 650 |
| tgccacctcc taggaagcta aaagaattaa ggggaggccg ggcacggtgg ctcacgctg | 710 |
| taatcccagc acttttgggag gccgaggcgg gtggatcatg aggtcaggag atcgagacca | 770 |
| tcctggctaa catggtgaaa ccccatctct actaaaaata caaaaaatta gccgggcgtg | 830 |
| gtggcgggcg ccctgtagtc ccagctactc gggaggctga nggcaggaga atggtgtgaa | 890 |
| ctggggaggg ggagcttgca gtgagccgag attgcgccct gctccactcc agcctgagcg | 950 |
| acagagcgag actccgtctc aaaaaaaaaa argaaaaaaaa aaaaaaaaaa | 998 |

<210> 189
 <211> 605
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 115..411

<400> 189
 aagaaagggg tgaggcctaa gggacaatca ggatgttttt cagagagaag tgtggatgct 60
 ggacaggaag aaccacagat accagatacg ggtactgttg taactctgtt ctcc atg 117
 Met
 1
 aaa aaa aag gaa gaa aca aca ctt tca gag atg gag cct gtt gag cca 165
 Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu Pro
 5 10 15
 cag tac caa cta gtc aat gct gaa tcg act tct ccc ttt cta cat tgc 213
 Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His Cys
 20 25 30
 ctg aga gaa gtc att ggg gaa tac tct gta cac gaa ttt tca ctg ttg 261
 Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu Leu
 35 40 45
 ggg aaa aca gag agt caa ggg att gga ttg tgg att gca ttg gtg gtt 309
 Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val Val
 50 55 60 65
 ttc ctc agt ttc ctc atc ttc tcc aca agt ttc tac ata tcg aat gca 357
 Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn Ala
 70 75 80
 gag cag ccc ttc ttc aaa gaa cct cct acg gaa gct gct aag gaa ctc 405
 Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu Leu
 85 90 95
 agt ctg tagctctgcg tggagccatg tgtaaact gaactgagac ctgccacctc 461
 Ser Leu
 ctactaccta agggcccatt ttcattctgat atcatccccc agaaacaaac tcatgatgac 521
 ttccatgttt ttttttagatt agatacatgg agaattttcc tttcccttag aattaaaatc 581
 ctgcattcta aaaaaaaaaa aaaa 605

<210> 190
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..368

<400> 190
 ag atc cga gcg acc atg gtg gcc cgg gtg tgg tcg ctg atg agg ttc 47
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe
 1 5 10 15
 ctc atc aag gga agt gtg gct ggg ggc gcc gtc tac ctg gtg tac gac 95
 Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp
 20 25 30
 cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag 143
 Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys
 35 40 45

| | |
|---|-----|
| gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg | 191 |
| Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val | |
| 50 55 60 | |
| tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag | 239 |
| Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys | |
| 65 70 75 | |
| att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg | 287 |
| Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val | |
| 80 85 90 95 | |
| atg tca gct ctg tcg gtg gcc ccc tcc aag gcc cgc gag tac tcc aag | 335 |
| Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys | |
| 100 105 110 | |
| gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcagagtca gcagggggccg | 388 |
| Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys | |
| 115 120 | |
| cctgccccgg ccagaacggg cagggctgcc actgacctga agactccgga ctgggacccc | 448 |
| actccgaggg cagctcccg ccttgccggc ccaataaagg acttcagaag tgaaaaaaaa | 508 |
| ataaaaaaaaa aaaaaaaaa | 526 |

<210> 191
 <211> 910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 174..527

| | |
|--|-----|
| <400> 191 | |
| attttcctgt taggccaaga gagaagagga tccttctctca gagcctccag cctcccttga | 60 |
| tcccttgctt gtgggcatat gtgggtcata tttccctccc atcaccctct gcacgccacc | 120 |
| cccatcaccg ccacagaccc ccagcccttc agttgccttg cacctccttg gtg atg | 176 |
| Met | |
| 1 | |
| cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg | 224 |
| Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu | |
| 5 10 15 | |
| tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc | 272 |
| Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser | |
| 20 25 30 | |
| tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa | 320 |
| Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln | |
| 35 40 45 | |
| ctc ctt ctc tgg gtt tgg cct gga gat cct ggc cct gaa ctc cag gaa | 368 |
| Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu | |
| 50 55 60 65 | |
| aca ggc ttc cct ggc cca cct cgc cca gct cac ctc aaa act gac cga | 416 |
| Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg | |
| 70 75 80 | |
| gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt ggc ata ggt | 464 |
| Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly | |
| 85 90 95 | |
| gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag | 512 |
| Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu | |
| 100 105 110 | |
| agg act tcc tcc ctc taaggagctc cccatacccc ccatcacctt ggcattccca | 567 |
| Arg Thr Ser Ser Leu | |
| 115 | |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| gctcctccag | aatccctccc | tccctcagcc | tagagaagga | caactgcttc | cccttggggc | 627 |
| ttgtcccctc | acctccttga | ggaaagaact | gggagtaa | ctgcttgaag | ttctcctcat | 687 |
| tgacaattcc | gctgggacat | tcctggaagg | agagggcacc | aggctgaggg | cagagacaaa | 747 |
| atcccccttc | gttcaccgcc | cccaccctcc | atggcccaag | actcccaggg | agggggataa | 807 |
| tcttcaagcc | tccagaggac | tcaccacgtg | gctcatgtga | tgggagggaa | gacttctttc | 867 |
| ccagtgcaca | aataaaaaac | atggaacgaa | aaaaaaaaaa | aaa | | 910 |

<210> 192
 <211> 668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..203

| | | | | | | | | | | | | | | | | |
|------------|------------|--------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 192 | | | | | | | | | | | | | | | | |
| tcctgtcgac | gtgttcttcc | ggtagggcggag | cggcggatta | gccttcgcgg | ggcaaa | atg | | | | | | | | | 59 | |
| | | | | | | Met | | | | | | | | | | |
| | | | | | | 1 | | | | | | | | | | |
| gag | ctc | gag | gcc | atg | agc | aga | tat | acc | agc | cca | gtg | aac | cca | cct | gtc | 107 |
| Glu | Leu | Glu | Ala | Met | Ser | Arg | Tyr | Thr | Ser | Pro | Val | Asn | Pro | Pro | Val | |
| | | | 5 | | | | | | 10 | | | | 15 | | | |
| ttc | ccc | cat | ctg | acc | gtg | gtg | ctt | ttg | gcc | att | ggc | atg | ttc | ttc | acc | 155 |
| Phe | Pro | His | Leu | Thr | Val | Val | Leu | Leu | Ala | Ile | Gly | Met | Phe | Phe | Thr | |
| | | 20 | | | | 25 | | | | | 30 | | | | | |
| gcc | tgg | ttc | ttc | gtg | tat | cct | ttc | act | gag | cag | cca | gag | gac | cag | cat | 203 |
| Ala | Trp | Phe | Phe | Val | Tyr | Pro | Phe | Thr | Glu | Gln | Pro | Glu | Asp | Gln | His | |
| | 35 | | | | | 40 | | | | | 45 | | | | | |
| tagtgatgtg | ggaagctcag | ggagaaacca | cgctaggtac | atggaccccg | ccggttttgt | | | | | | | | | | | 263 |
| acattggatt | ggggctgaga | gaagattgcc | gtgggctggg | ctctctgcac | tccacagtcc | | | | | | | | | | | 323 |
| acccttctgc | tttgcttaaa | ctgctgtgcc | cagttacgag | gtcacctcta | ccaagtacac | | | | | | | | | | | 383 |
| tcgtgatatc | tataaagagc | tcctcatctc | attagtggcc | tcactcttca | tgggcttttg | | | | | | | | | | | 443 |
| agtcctcttc | ctgctgtctc | gggttggcat | ctacgtgtga | gcacccaagg | gtaacaacca | | | | | | | | | | | 503 |
| gatggcttca | ctgaaacctg | ctttttgtaa | ttactttttt | ttactgttgc | tgggaagtgc | | | | | | | | | | | 563 |
| ccacctgctg | ctcataataa | atgcagatgt | atagcaaaaa | aaaaaaaaaa | aaaaaaaaaa | | | | | | | | | | | 623 |
| aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | aaaaaa | | | | | | | | | | | | 668 |

<210> 193
 <211> 637
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..334

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 193 | | | | | | | | | | | | | | | | |
| agttatgaag | ttctaaaagc | aagtcttaat | caggaagtgt | ccttgatcac | caacggctcg | | | | | | | | | | | 60 |
| cccaggc | atg | ctg | gct | ctc | ttc | cac | ttc | cac | ctt | cca | cca | tgg | gat | gac | | 109 |
| | Met | Leu | Ala | Leu | Phe | His | Phe | His | Leu | Pro | Pro | Trp | Asp | Asp | | |
| | 1 | | | | 5 | | | | | 10 | | | | | | |
| gca | gta | aga | agg | cca | tca | gta | gat | gcc | agt | ccc | tca | acc | ttg | aac | ttt | 157 |
| Ala | Val | Arg | Arg | Pro | Ser | Val | Asp | Ala | Ser | Pro | Ser | Thr | Leu | Asn | Phe | |
| | 15 | | | | 20 | | | | 25 | | | | 30 | | | |
| cca | gac | gca | gaa | ctt | tat | gcc | tcc | att | ttc | ctc | tgc | tgc | atg | gcc | cca | 205 |
| Pro | Asp | Ala | Glu | Leu | Tyr | Ala | Ser | Ile | Phe | Leu | Cys | Cys | Met | Ala | Pro | |
| | | 35 | | | | | | 40 | | | | | 45 | | | |

| | |
|--|-----|
| gga gag att tta att agc ttt cta acc ttg gtc cag att gca cat gca | 253 |
| Gly Glu Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala | |
| 50 55 60 | |
| aat ggt aga gga tgc aac acc ccc gct tgt gga gct gcc gct tgt gtc | 301 |
| Asn Gly Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val | |
| 65 70 75 | |
| tgg cat gaa aat tca caa gaa gag agg aaa tac tgaggagaaa atggcagatt | 354 |
| Trp His Glu Asn Ser Gln Glu Glu Arg Lys Tyr | |
| 80 85 | |
| gtgtttgctg aatttgattg acgaagaagt caccatgaaa atcacagtga accatttgga | 414 |
| aagcaaactg ccaaaaaaat aatagttagt catgctctca ggctggttgt tttggctggt | 474 |
| gtgggtttct tgcattttcca gatgattgca aagagctggt tctcaatttc tgcaacaagt | 534 |
| gccagctgaa attttggtac cagtttcatt aaatatgtat aacaaaaakaa aaaaaaaaaa | 594 |
| aaaaaaaaaa aaaaaaaaaa aaaaaaagaa aaaaaaaaaa aaa | 637 |

<210> 194
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 183..443

| | |
|--|-----|
| <400> 194 | |
| agaagttctc agaggggtgag ggtcccacat ctctgcagg acaggcccta gctaccgagt | 60 |
| cacagaaacc cagggccgaa gcaaagtccc aatcccagag aggctggggc acacctacaa | 120 |
| ctgaaaggag gcttagaaat ctttcagaga ccaccctatc ggttctcctc cacctggaca | 180 |
| gg atg agc cag caa cac aga agg aag agg cct tcc tcc gaa aga aaa | 227 |
| Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys | |
| 1 5 10 15 | |
| agc aca aga aag atg gac aca tgg cag agt ctt aaa gtc aaa gaa gta | 275 |
| Ser Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val | |
| 20 25 30 | |
| ttc tgt aag cat aat tct tcc tat gaa tgc ctt ctc tat aaa gag gtt | 323 |
| Phe Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val | |
| 35 40 45 | |
| gaa gca aga cag gtt tct aag aca gcc acc gat ggg tcc tac ctc ctc | 371 |
| Glu Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu | |
| 50 55 60 | |
| gta ttc aca tcc tat gta atc tcc tcc cca gtg tgg act gga cct ggt | 419 |
| Val Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly | |
| 65 70 75 | |
| gac ttg ctt cca gtg aat aga ata tagcaaaagt gattgatgtc acctccaaga | 473 |
| Asp Leu Leu Pro Val Asn Arg Ile | |
| 80 85 | |
| ttcagctata gaagactatg actatgactt tcctcttggt tagcattctc gctaaccctt | 533 |
| cctgcttgct tgtactgagc tgccctatga agaggcccat gtaggggtggc ctgggtgggg | 593 |
| gtgatctgtg gccaacagcc agcaaggaac taaatcctgt ttacaaccac atgagcttgg | 653 |
| aaggagatcc ttccccagta aagccaggag atgaatacaa aaaaaaaaaa aaa | 706 |

<210> 195
 <211> 670
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 94..228

<400> 195

```
acttttcagg ggacattcag aggcattcag cccttcctcc tcaccagctc ccagagttcc      60
catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc      114
                               Met Pro Arg Ser Ser Arg Ser
                               1           5
cct ggg gac cca ggc gcc cta ctc gaa gat ggc cca caa tcc cag acc      162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Gly Pro Gln Ser Gln Thr
      10           15           20
ccg gag gat tgc cca gcg agg ccg gaa cac cag cag gat ggc aga gga      210
Pro Glu Asp Cys Pro Ala Arg Pro Glu His Gln Gln Asp Gly Arg Gly
      25           30           35
cac ctc ccc aaa cat gaa tgacaacatc ctgttgccctg tccgcaacaa      258
His Leu Pro Lys His Glu
      40           45
tgaccaagcc ctaggcctga ctcagtgcac gctgggatgt gtgtcctggt tcacctgttt      318
tgctgtctcc ctgagaactc aggccagca gggtctgttt aacacgtgca gatgcaagct      378
gctgtgccag aagctcatgg agaagacagg cattctgctc ctctgtgctt tcggtgtgtc      438
ccagggccct gccagtcctc aggtggaagg tatccctggg ccctggcact gattatagga      498
cactgggcaa gacactgcac cgccacgtga ctcagtttcc ccatctgcct gatgggtgtt      558
gctgtgagaa ttatgaaatg aaatgatgac catgaaaata ttgtagaagc caagaaatgc      618
ttcagaagtt ataaagctct ccccaaaccg tgttatgaaa aaaaaaaaaa aa      670
```

<210> 196

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..327

<400> 196

```
aacctcaagg agccctgttg tgctaccgac tgcagagctc atggacatcc atcaggaagc      60
ctccaatacc caaaccaggg gtagttgcct aatccatcct catgtggata gctctttact      120
taggaaacct tg atg gct tat ttg gat gac aaa ggt tcc ctt ttg gcg ata      171
                               Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile
                               1           5           10
cat agc cat gcg aga caa cat agc cat gaa aca aac caa gtc cac cag      219
His Ser His Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln
      15           20           25
tgg ctt cct agg aac aca ttt gct ttc ctg ata aaa gag gac aga tgc      267
Trp Leu Pro Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys
      30           35           40           45
agt tgc aga agt acc tgt gcc tct ttt tct tct tct tct ttt tct      315
Ser Cys Arg Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser
      50           55           60
ttt tta atc tct taaatgcaga tataagaact ggtactgaag cagccatctt      367
Phe Leu Ile Ser
      65
gtgaccataa ggaagaagcc aagaacatca gaaccagtgg cctagccatt gcacagtcac      427
ctaaacacac ctctggactt gttattatgt aaaaaaaaaa aaacacctgc tcttgttatt      487
tgcaatccaa aaaaaaaaaa aaa      510
```

<210> 197

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..357

<400> 197

```
atagaatata cacaaaagga a atg aga aag aaa tgt aaa tgc ttc act ata      51
                        Met Arg Lys Lys Cys Lys Cys Phe Thr Ile
                        1          5          10
aaa aaa aca aat aca tac gaa gaa agt aat gca gga aat gaa gga caa      99
Lys Lys Thr Asn Thr Tyr Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln
                        15          20          25
aaa gaa gct ata agc att tgt att tgc aga aga gat ggt tta ctt cct      147
Lys Glu Ala Ile Ser Ile Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro
                        30          35          40
ctg tgg gta acc agg tta tca gat ttg gtg ttt tcc aaa gaa aag gca      195
Leu Trp Val Thr Arg Leu Ser Asp Leu Val Phe Ser Lys Glu Lys Ala
                        45          50          55
cat ggc atg att cca ctt ctt ggc tcc cat agg gaa aag aag aca agt      243
His Gly Met Ile Pro Leu Leu Gly Ser His Arg Glu Lys Lys Thr Ser
                        60          65          70
aaa gag atg aag act tct tcc agg aac ctg agg tac ttc att gtc tgc      291
Lys Glu Met Lys Thr Ser Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys
                        75          80          85          90
aga gat gcc tca tcc tac acc cct cag tca ctc ata tct gga tac att      339
Arg Asp Ala Ser Ser Tyr Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile
                        95          100          105
gga cct tgt caa cat caa taatggacat acctctgata tttgaactct      387
Gly Pro Cys Gln His Gln
                        110
gaatctcact ctgtgaccac aactttgtat ctttctaagt ctttaatctt caacctcaca      447
gaactcttca taccctaaaa tatagtattt tcacctggaa aaaaaaaaaa aaa      500
```

<210> 198

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..333

<400> 198

```
aaa atg gtg ttt gga gcc atg gtc ctt ctt gtg gga ctt gaa gaa ctg      48
      Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu
      1          5          10          15
acc aat atc cgc aac gtg gag aga ctg aag aag gac ttg agg gcc agt      96
Thr Asn Ile Arg Asn Val Glu Arg Leu Lys Lys Asp Leu Arg Ala Ser
      20          25          30
tat tgc ctc atc gac agc ttc ctg ggg gac tgc gag ctc atc ggg gac      144
Tyr Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp
      35          40          45
ctg acc cag tgt gtg gac tgc gtg att cct cca gag ggg tcc ctc ttg      192
Leu Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu
      50          55          60
cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct      240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro
```

| | | | |
|--|-----|-----|-----|
| 65 | 70 | 75 | |
| ggg gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt | | | 288 |
| Gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu | | | |
| 80 | 85 | 90 | 95 |
| ctc tac gtt gct aat ggt gcc tac tgc gca tgt aac agg cct gga | | | 333 |
| Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly | | | |
| 100 | 105 | 110 | |
| tgaacggtag ctgctgcggt tacattatta gcttcagttt gcccgcgccag gctagatggt | | | 393 |
| taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaaagtgaa | | | 453 |
| ggaactcagg ctccagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct | | | 513 |
| ggctgtgggt ttctcccat tccctgccc tctgggaagt cgctgccacc ccctacgctt | | | 573 |
| gtctgctgac tcccagttcc cctaaccctc cagaatgtaa acagcagcag atgaacaaaa | | | 633 |
| ataaaaaatc aaaaggccga aaaaaaaaaa aaaa | | | 667 |

<210> 199
 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..363

| | |
|---|-----|
| <400> 199 | |
| acg agt tct tcc ggg gcg gag gtc acc atg gca gct gcc ttg gct cgg | 48 |
| Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg | |
| 1 | 5 |
| ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc | 96 |
| Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe | |
| 20 | 25 |
| gag aaa aac gtg gaa tgc acg agg acc ttc ctg cag acg gtg agc agt | 144 |
| Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser | |
| 35 | 40 |
| gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg | 192 |
| Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val | |
| 50 | 55 |
| agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg | 240 |
| Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly | |
| 65 | 70 |
| cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc | 288 |
| His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu | |
| 85 | 90 |
| acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg | 336 |
| Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly | |
| 100 | 105 |
| gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca | 383 |
| Asp Lys Pro Gly Ala Asp Thr Gly Arg | |
| 115 | 120 |
| acaagatgat ttgcgtggac taggacactt aacctaagaa gagtttcact taatcattca | 443 |
| aatcactatc tgaagggtca cggagcgcaa aataaagttt aaaaccctgc taccaaaaaa | 503 |
| aaaaaaaaa a | 514 |

<210> 200
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 41..337

```

<400> 200
cttcaccacc aaaactctcc actccaccag cacagccaaa atg ctc gca cgt gct      55
                                         Met Leu Ala Arg Ala
                                         1      5
act ttc cgc gcc gcc tcg gcc cca act ctc gtc gcc cgc cgc ggc ttc      103
Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val Ala Arg Arg Gly Phe
              10              15              20
cag tcg acc cgc gcg caa atg gcc agc cca tac cac tac ccc gag ggt      151
Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr His Tyr Pro Glu Gly
              25              30              35
cct cgc agc aac ttg cca ttc gac ccg ctg aag aag ggc ttt gct ttc      199
Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys Lys Gly Phe Ala Phe
              40              45              50
aag tac tgg ggc ttt atg ggc acc gga ttc gcc ctt ccc ttc ctc ctt      247
Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala Leu Pro Phe Leu Leu
              55              60              65
gct gtc tgg caa aca gaa caa gcc gta aat gcg ctg aga cac ggc gtg      295
Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala Leu Arg His Gly Val
              70              75              80              85
gac atg cgt atc ggg atc ccg ggg aac acg gca ttt gta gat      337
Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala Phe Val Asp
              90              95
taggtggagg gcccgcatac ggctatacta gacatcacag catcaatttc attgtctgtc      397
ccccaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      457
aaaaa                                              462

```

<210> 201
<211> 551
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..549

```

<400> 201
aga gag gga gcc cga gcc agg cca tct cca acc atg tcc gac gag gcc      48
Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1      5      10      15
tcg gcc atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc      96
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
              20              25              30
cca ctc ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag      144
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
              35              40              45
ccg ggc tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc      192
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
              50              55              60
cat cgc acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta      240
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
              65              70              75              80
act tct tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg      288
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
              85              90              95
ttt tca tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta      336

```

| | |
|---|-----|
| Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu | |
| gat gat cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc | 384 |
| Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val | |
| tgc agt gat gtc tct tct tct att agc act tac tgg gat tgg tca gat | 432 |
| Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp | |
| agc gag ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt | 480 |
| Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser | |
| gat gta ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg | 528 |
| Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu | |
| ctt cct aaa aaa aaa aaa aa | 551 |
| Leu Pro Lys Lys Lys Lys | |

<210> 202
 <211> 550
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..315

<220>
 <221> misc_feature
 <222> 483
 <223> n=a, g, c or t

| | |
|--|-----|
| agagagggag cccgagccag gccatctcca acc atg tcc gac gag gcc tcg gcc | 54 |
| Met Ser Asp Glu Ala Ser Ala | |
| atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc cca ctc | 102 |
| Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu | |
| ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc | 150 |
| Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly | |
| tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc | 198 |
| Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg | |
| acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct | 246 |
| Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser | |
| tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca | 294 |
| Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser | |
| tct gtc tgt tgg aga tca aga tgattgctat tccctgtag atgatcagga | 345 |
| Ser Val Cys Trp Arg Ser Arg | |
| cttcacttct ttgattttat ttcctgaggg gagtgtctgc agtgatgtct cttcttctat | 405 |
| tagcacttac tgggattggt cagatagcga gtttgaatgg cagttaccag gcagtgcacat | 465 |
| tgccagtggg agtgatgnta ctttctgatg tcataccag tattccaagt tcaccttgcc | 525 |
| tgcttcctaa aaaaaaaaaa aaaaa | 550 |

<210> 203
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..315

<400> 203
 atc ggg ccg cga gcg ccc tcc ccg tcg ttt tcc gtg aga gac gta gag 48
 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 ctg agc gac cca gcc cgc gag cga ggt gag atg ccg gtg gcc gtg ggt 96
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc 144
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc 192
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc 240
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 288
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac 335
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105
 atctgtccct tcccatcaat cccagcccat gtactaataa aagaaagtct ttgagcaaaa 395
 aaaaaaaaaa aaa 408

<210> 204
 <211> 665
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..582

<400> 204
 acttttcagg ggacattcag aggcattcagc cccttctctc tcaccagctc ccagagttcc 60
 catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
 Met Pro Arg Ser Ser Arg Ser
 1 5
 cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga 162
 Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
 10 15 20
 ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag 210
 Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
 25 30 35
 gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac 258
 Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
 40 45 50 55

| | |
|--|-----|
| aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc | 306 |
| Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser | |
| 60 65 70 | |
| tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt | 354 |
| Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val | |
| 75 80 85 | |
| ctg ttt aac acg tgc aga tgc aag ctg ctg tgc cag aag ctc atg gag | 402 |
| Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu | |
| 90 95 100 | |
| aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct | 450 |
| Lys Thr Gly Ile Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro | |
| 105 110 115 | |
| gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg | 498 |
| Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg | |
| 120 125 130 135 | |
| aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg | 546 |
| Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu | |
| 140 145 150 | |
| cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgacccat | 592 |
| Pro Asp Gly Cys Cys Cys Glu Asn Tyr Glu Met Lys | |
| 155 160 | |
| gaaaatattg tagaagccaa gaaatgcttc agaagttata aagctctccc caaacccgcaa | 652 |
| aaaaaaaaaaa aaa | 665 |
| <210> 205 | |
| <211> 1008 | |
| <212> DNA | |
| <213> Homo sapiens | |
| <220> | |
| <221> CDS | |
| <222> 540..923 | |
| <400> 205 | |
| atttaggtga gctgccacgt ccggaggagg gcagcaagaa tgaaagacct ctagtgttcc | 60 |
| agactcccgg agccctgggtc tctacaccac atggacgtta tccacctcct ctgtgtcctc | 120 |
| ccaaggcagc atttcagaag gtgatccacg gcaaagccgt cccctcaaat ccgtctttgt | 180 |
| gcccactgcc atagtcaacc ccgtgagaag cacagccggc cctgggactt taggacaagg | 240 |
| gtctcttcgg aaagggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc | 300 |
| cctgcagaga cccctccagt ccgggatccc cactctcgtg gtaggctccc tcagacgcag | 360 |
| ccccaccatg gtccttcggc ctcagcagtt ccaattctac cagccacagg ggatcacctc | 420 |
| ctccccctca gccgtgggtg tggagatggg gtccaagcct gccctcacgg gggagcccgc | 480 |
| cctcacgtgc atcagcaggg gcagtgaggg ggatccactc cgcggccagc tccctcatt | 539 |
| atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg | 587 |
| Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro | |
| 1 5 10 15 | |
| ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga | 635 |
| Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg | |
| 20 25 30 | |
| aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc | 683 |
| Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser | |
| 35 40 45 | |
| cct cct ccc acc aaa cat tac acc tcc cat ccc acc tcc gga aag cct | 731 |
| Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro | |
| 50 55 60 | |
| gaa cag cca gcc acc ctc aag gcg tcc cag cct gaa gca gcg tcc ttg | 779 |
| Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu | |
| 65 70 75 80 | |

```

ggc cca gag atg acc gtc cta ttt gcc cac cga agt ggc tgc cac tcc      827
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
      85                      90                      95
gga cag cag aca gac ctc cgg aga aag tca gct ctt gcc aag gcc aca      875
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
      100                    105                    110
acc ctg gtg tcc act gcc tca ggc acg cag acc gtg ttt ccc agc aaa      923
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
      115                    120                    125
tgaacctacg ggtggctttt cctagacccc aaagaggtga attgcattta aatacagtct      983
gcctycactg aaaaaaaaaa aaaaaa
                                         1008

```

<210> 206
 <211> 455
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..364

```

<400> 206
tggacaaatg gacctgCGGT aggagagagg gacaacagta ggagcaggca gatcttgctg      60
tttcaaccaa aacctc atg ctg acc aga gtt gag gaa cag aag aag atg gtg      112
      Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val
      1                      5                      10
aag gcc tgc agg tat agg tgt tca gca tgt cat ctg aaa tat tcc cca      160
Lys Ala Cys Arg Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro
      15                    20                    25
cag agg caa aaa gaa agg aaa tta tct ctg aaa agg ggg agg aca agt      208
Gln Arg Gln Lys Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser
      30                    35                    40
cag cag aat atg tca atg ttt tgg ttg aag aag ctg ctt gaa tct ggg      256
Gln Gln Asn Met Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly
      45                    50                    55                    60
ctt ttc tgt gcc atg tgt tct ccc agg gcc agc aca aag aag ggc ttt      304
Leu Phe Cys Ala Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe
      65                    70                    75
tgg tgc agg ccc aag acc acc ata atc atc att gat tat tcc tct cca      352
Trp Cys Arg Pro Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro
      80                    85                    90
cgc cag tgt ctc taaataaact ttctcttctt tctctgaaaa aaaaaaaaaa      404
Arg Gln Cys Leu
      95
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa a      455

```

<210> 207
 <211> 749
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..544

```

<400> 207
cttttacgac gcgccggaaa gcaacggcaa gggccgcagc cagcaccggg cggagagggc      60
tacc atg ggg aaa atc gcg ctg caa ctc aaa gcc acg ctg gag aac atc      109

```


| | | | |
|---|-----|-----|-----|
| 35 | 40 | 45 | |
| gcg ctg agg agg gcc ccc gag cca gta cca gga aag gat aga ctc ctg | | | 311 |
| Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu Leu | | | |
| 50 | 55 | 60 | 65 |
| ctt gca gca ttc cca gca gag gca tcg cct gtg gac acc gcg tct gtg | | | 359 |
| Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser Val | | | |
| 70 | 75 | 80 | |
| tct gta tat ggc aga gct ccc aga tat atg cac aag gga gtg aaa aaa | | | 407 |
| Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys Lys | | | |
| 85 | 90 | 95 | |
| tgt gtt tgc acc cca gtc tct aaa aat tca aca gcc tgg tta ctt ctg | | | 455 |
| Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu Leu | | | |
| 100 | 105 | 110 | |
| ggg ggt ata tcg taggtggcct taatacgtgt tatttgcctca tctgtatttc | | | 507 |
| Gly Gly Ile Ser | | | |
| 115 | | | |
| ttactctttg cacaattaaa ccatgttcct tttacttatg tacattttta ataaaagaaa | | | 567 |
| gttggttaacg aaaaaaaaaa aaaaaaaa | | | 594 |

<210> 209
 <211> 2098
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 893..1897

| | | | |
|---|---------|----|----|
| <400> 209 | | | |
| accaggtcct cctgggtgca cctgaaatgg tcaacagaag tcttgtgaca cgtggaatca | 60 | | |
| tttcagagtc accccttctg cctcctgctc aagcaacaga cctgccgatc acccccgtcg | 120 | | |
| ggcccgcggt tctcagggtc ttccataatcc cctgggcttt cgggcttgct gtgtgcctgg | 180 | | |
| agtcaggccg ccgtgcggca ggctgttaac cttagcctcg ggagagtggg atggagccac | 240 | | |
| cttctcatgg aacgatcctc gccttccctc atctccattg ttttatggct tcacacggac | 300 | | |
| cgtggctttc tgcattggaag cttgggtggc aggggtgctgt cactttggga agcagccaga | 360 | | |
| gaaccacagg atgcgtgaat cggctctcct gtcttcatgg gcattctccg ccagggtggt | 420 | | |
| gtcttgtgct gtgattagtg ggtcactggc aagtgtctga atgaagtgga gggtccgggtg | 480 | | |
| gcaacagtga cggggaaggg ctatgggtcc gcctcaatgt catctgcccc atccctgggc | 540 | | |
| ctccaggaat ccagggtctc agcccctgct ttagaaggaa gtcctgacgg ccacgctgga | 600 | | |
| tctggaggac gtccggagct acagggcgga gatttcatct cgaaacctgg cggccagcag | 660 | | |
| ggcagagccc taccacagag tgaagggtgga ctttgccctc tcgtgccacg aggacttgc | 720 | | |
| ggcaccatc tctgagccca tcgagtggaa ataccacagc cctgaggagg agataagcct | 780 | | |
| tggacctgcc tgctggctct gggatttttt aagacgaagt caacaggcag ggtttttgc | 840 | | |
| gcccttgagt ggcgggggtgg acagcgcagc caccgcctgc ctcactact cc atg tgc | 898 | | |
| | Met Cys | | |
| | 1 | | |
| tgc cag gtc tgc gag gcc gtg agg agt gga aat gag gaa gtg ctg gct | 946 | | |
| Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val Leu Ala | | | |
| 5 | 10 | 15 | |
| gat gtc cgc acc atc gtg aac cag atc agc tac acc ccc cag gat ccc | 994 | | |
| Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln Asp Pro | | | |
| 20 | 25 | 30 | |
| cga gac ctc tgt gga cgc ata ctg acc acc tgc tac atg gcc agc aag | 1042 | | |
| Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala Ser Lys | | | |
| 35 | 40 | 45 | 50 |
| aac tcc tcc cag gag acg tgc acc cgg gcc aga gag ttg gcc cag cag | 1090 | | |
| Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala Gln Gln | | | |
| 55 | 60 | 65 | |

| | |
|---|------|
| att gga agc cac cac atc agt ctc aac atc gat cca gcc gtg aag gcc | 1138 |
| Ile Gly Ser His His Ile Ser Leu Asn Ile Asp Pro Ala Val Lys Ala | |
| 70 75 80 | |
| gtc atg ggc atc ttc agc ctg gtg acg ggg aag agc cct ctg ttt gca | 1186 |
| Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu Phe Ala | |
| 85 90 95 | |
| gct cat gga gga agc agc agg gaa aac ctg gcg ctg caa aat gtg cag | 1234 |
| Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn Val Gln | |
| 100 105 110 | |
| gct cga ata cgg atg gtc ctc gcc tat ctg ttt gct cag ttg agc ctc | 1282 |
| Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu Ser Leu | |
| 115 120 125 130 | |
| tgg tct cgg ggt gtc cac ggt ggg ctc ctc gtg ctg gga tcc gcc aac | 1330 |
| Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser Ala Asn | |
| 135 140 145 | |
| gtg gat gag agt ctc ctg ggc tac ctg acc aag tac gac tgc tcc agt | 1378 |
| Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys Ser Ser | |
| 150 155 160 | |
| gcg gac atc aac ccc ata ggc ggg atc agc aag acg gac ctc agg gcc | 1426 |
| Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu Arg Ala | |
| 165 170 175 | |
| ttc gtc cag ttc tgc atc cag cgc ttc cag ctt cct gcc ctg cag agc | 1474 |
| Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu Gln Ser | |
| 180 185 190 | |
| atc ctg ttg gcg ccg gcc acc gca gag ctg gag ccc ttg gct gat gga | 1522 |
| Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala Asp Gly | |
| 195 200 205 210 | |
| cag gtg tcc cag acc gac gag gaa gat atg ggg atg aca tat gcg gag | 1570 |
| Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr Ala Glu | |
| 215 220 225 | |
| ctc tcg gtc tat ggg aaa ctc agg aag gtg gcc aag atg ggg ccc tac | 1618 |
| Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly Pro Tyr | |
| 230 235 240 | |
| agc atg ttc tgc aaa ctc ctc ggc atg tgg aga cac atc tgc acc ccg | 1666 |
| Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys Thr Pro | |
| 245 250 255 | |
| aga cag gtc gct gac aaa gtg aag cgg ttt ttc tcc aag tac tcc atg | 1714 |
| Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr Ser Met | |
| 260 265 270 | |
| aac aga cac aag atg acc acg ctc aca ccc gcg tac cac gcc gag aac | 1762 |
| Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala Glu Asn | |
| 275 280 285 290 | |
| tac agc cct gag gac aac agg ttt gat ctg cga cca ttt ctg tac aac | 1810 |
| Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu Tyr Asn | |
| 295 300 305 | |
| aca agc tgg cct tgg cag ttt cgg tgc ata gaa aat cag gtg cta cag | 1858 |
| Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val Leu Gln | |
| 310 315 320 | |
| ctc gag agg gca gag cca cag tcc ctg gac ggc gtg gac tgaggccggt | 1907 |
| Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp | |
| 325 330 335 | |
| tccttcctgg aggcctcctg tcctcgggga cccagcacc tcctcctcag cattgctgga | 1967 |
| gccaagggtgta ggagccctac actaggagcc caggatggga cggcgcatca gccgagaggg | 2027 |
| agggaacttt tcagtcaaat tcctcaaaaa gaggctggaa taaagcctgg gctcaaaaaa | 2087 |
| aaaaaaaaa a | 2098 |

<210> 210

<211> 428

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 85..342

<400> 210
acactggtac agtcacctag cccatcagtt ccttcgtcga cagcgccggg gacatccaga 60
ctacaattta cagttcctct atcc atg tgc tgg gtt ata aat cat gcc atc 111
Met Cys Trp Val Ile Asn His Ala Ile
1 5
ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat 159
Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His
10 15 20 25
tcg gca tct ctt tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag 207
Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln
30 35 40
ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc 255
Leu Cys Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe
45 50 55
agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc 303
Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr
60 65 70
acg gcg aas cca ggc ggg aga cgg cag gag cag ctc agg taaccagggg 352
Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg
75 80 85
aagcttgctg gcccacggag atgcagccgt ggagctgtga ggaaagacgg tctggcttca 412
aaaaaaaaa aaaaaa 428

<210> 211
<211> 769
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 155..433

<400> 211
atatttcccc ccttgctcgg gatggtgcc aaggaggctg tgcgggcccc gctccgcttc 60
gaatggtgga tgctgtgggg caccacctcc ttgaggacca aggcactcca gctgccagga 120
atattggtgc taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa 175
Met Lys Ile Ala Leu Cys Gln
1 5
aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act 223
Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr
10 15 20
gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act 271
Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr
25 30 35
gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc 319
Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu
40 45 50 55
tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt 367
Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys
60 65 70
aaa agc tgt gct tca aga aat cac aaa aac att ttc ctg cac cta cta 415

Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu
 75 80 85
 cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg 463
 His Ser Leu Ser Ala Ala
 90
 caagaaatgc ttttttgtat gtgtcatgtc tgtttgtttt tcaattaaga gaggaaagca 523
 ttaggcagat ggaatgtaca tgtgaggatg aggagacaga aaacaagtag ccctttccat 583
 caagatagag ggttttctgg ggttgctggc tattgaatgt cactcctgat ttctctttcc 643
 aaggcactgt accaccagcc tactgagatt gtgtgggagc tttcatgggg gttgtatttc 703
 actgatgaaa ataaattttt tgcataatgt gaaaaaaaaa aaaaaaaaga aaaaaaaaaa 763
 aaaaaa 769

 <210> 212
 <211> 914
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 63..386

 <400> 212
 ctttttaggg agtccaaggt acagtgcgcg cgtgcggagc ttgttactgg ttacttgccc 60
 tc atg gcg gtc cga gct tcg ttc gag aac aac tgt gag atc ggc tgc 107
 Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys
 1 5 10 15
 ttt gcc aag ctc acc aac acc tac tgt ctg gta gcg atc gga ggc tca 155
 Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser
 20 25 30
 gag aac ttc tac agt gtg ttc gag ggc gag ctc tcc gat acc atc ccc 203
 Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro
 35 40 45
 gtg gtg cac gcg tct atc gcc ggc tgc cgc atc atc ggg cgc atg tgt 251
 Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys
 50 55 60
 gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt 299
 Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu
 65 70 75
 cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt 347
 Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu
 80 85 90 95
 cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag 396
 Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
 100 105
 gatgagctgt cctctcttct tcaagtcccc cttgtggcgg ggactgtgaa ccgaggcagt 456
 gaggtgattg ctgctgggat ggtggtgaat gactggtgtg ctttctgtgg cctggacaca 516
 accagcacag agctgtcagt ggtggagagt gtcttcaagc tgaatgaagc ccagcctagc 576
 accattgccca ccagcatgcg ggattccctc attgacagcc tcacctgagt caccttccaa 636
 gttgttccat gggctcctgg ctctggaactg tggccaacct tctccacatt ccgcccaatc 696
 tgtacctgat gctggcaggg aggtggcaga gagctcactg ggactgaggg gctgggcacc 756
 caaccctttt ccacctgtgc ttatgccttg gatctatcat tactgcaaaa acctgctctg 816
 ttgtgctggc tggcaggccc tgtggctgct ggctgagggg tctgctgtcc tgtgccaccc 876
 cattaagtgt cagttccctc caaaaaaaaaa aaaaaaaa 914

 <210> 213
 <211> 1489
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 460..1290

<400> 213

```

cttctttccc tctccgtttt ggtgggctgg ttgaagatga aatccactga ggaggggaagt    60
ccagcaccct gtgtgccagt ccagaactgg cccatctgta gacccccctga aaatcatatg    120
ggcttggaatt tggatattct caacagaaaag gggttaaaggc tgatgggtacc taaagcctgg    180
tacttgaatt ttgatcaaga taagctgcct taagttctct tcattacaca aatgatccta    240
gataattgat agatcctgtg gttcaactgg atttctagat agaagctgga ttcagtgtgat    300
gccagaggag taaaatttca agagactgaa accagatctg agtttcgctg ttccagtctg    360
gacctctttg gtgctgtaaa tcctggatat actgtagatg agtactgcgt ttttctttta    420
tggaactctct tcagcttctg gagacctcac tatectatt atg tct ttg tgt gaa    474
                                     Met Ser Leu Cys Glu
                                     1      5

gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctc tct ggc    522
Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly
                                     10      15      20

tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc    570
Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly
                                     25      30      35

agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt    618
Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser
                                     40      45      50

acc ctt tct gga aag cta gat att gtc cgc aca gaa ctc agt cca tca    666
Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser
                                     55      60      65

gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg    714
Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val
                                     70      75      80      85

ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat    762
Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His
                                     90      95      100

cag gaa cgt ctc tat caa gaa tac aat ttc agc aag gct gag ggc cat    810
Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His
                                     105      110      115

ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat    858
Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp
                                     120      125      130

gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta    906
Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val
                                     135      140      145

cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg    954
Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met
                                     150      155      160      165

gag cgc aat cgt cag tat caa aag ctc caa ggc ctc tat gat agc ctt    1002
Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu
                                     170      175      180

agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca    1050
Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro
                                     185      190      195

tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac    1098
Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn
                                     200      205      210

tcc aag ttt cct ttg gat aat aca cct gtt cga aat cgg ggc gat gga    1146
Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg Asn Arg Gly Asp Gly
                                     215      220      225

```

| | |
|---|------|
| gat gga gat ttt cag ttc aga cca ttt ttt gcg ggt tct ccc aca gca | 1194 |
| Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala Gly Ser Pro Thr Ala | |
| 230 235 240 245 | |
| cct gaa ccc agc aac agc ttt ttt agt ttt gtc tct cca agt cgt gaa | 1242 |
| Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val Ser Pro Ser Arg Glu | |
| 250 255 260 | |
| tta gag cag cag caa gtt tct agc agg gcc ttc aaa gta aaa aga att | 1290 |
| Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe Lys Val Lys Arg Ile | |
| 265 270 275 | |
| tgagccacgc atagtgtcac gcacctgtga tcccagctac ttaggaggtt gaggctggga | 1350 |
| ggatcacttg agcccaggag tctgaggctt tagtgatcta agatcatgcc actgcactcc | 1410 |
| agcctgggca acagagtgg acacctgtttc taaaaaaaaa taaagataat ttagctaact | 1470 |
| tcaaaaaaaaaa aaaaaaaaaa | 1489 |

<210> 214
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..539

| | |
|---|-----|
| <400> 214 | |
| caaatattttc catcacggggg atg ctt gtc atg tac ctg ctt gcc gcc ctc ttt | 53 |
| Met Leu Val Met Tyr Leu Leu Ala Ala Leu Phe | |
| 1 5 10 | |
| ggt tac cta acc ttc tat gga gaa gtt gaa gat gaa tta ctt cat gcc | 101 |
| Gly Tyr Leu Thr Phe Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala | |
| 15 20 25 | |
| tac agc aaa gtg tat aca tta gac atc cct ctt ctc atg gtt cgc ctg | 149 |
| Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu | |
| 30 35 40 | |
| gca gtc ctt gtg gca gta aca cta act gtg ccc att gtc ctc ttc cca | 197 |
| Ala Val Leu Val Ala Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro | |
| 45 50 55 | |
| att cgt aca tca gtg atc aca ctg tta ttt ccc aaa cga ccc ttc agc | 245 |
| Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser | |
| 60 65 70 75 | |
| tgg ata cga cat ttc ctg att gca gct gtg ctt att gca ctt aat aat | 293 |
| Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn | |
| 80 85 90 | |
| gtt ctg gtc atc ctt gtg cca act ata aaa tac atc ttc gga ttc ata | 341 |
| Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile | |
| 95 100 105 | |
| ggg gct tct tct gcc act atg ctg att ttt att ctt cca gca gtt ttt | 389 |
| Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe | |
| 110 115 120 | |
| tat ctt aaa ctt gtc aag aaa gaa act ttt agg tca ccc caa aag gtc | 437 |
| Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val | |
| 125 130 135 | |
| ggg gct tta att ttc ctt gtg gtt gga ata ttc ttc atg att gga agc | 485 |
| Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser | |
| 140 145 150 155 | |
| atg gca ctc att ata att gac tgg att tat gat cct cca aat tcc aag | 533 |
| Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys | |
| 160 165 170 | |
| cat cac taacacaagg aaaaatactt tcttttttcta ttggaaatgg ttacaagtta | 589 |

His His
tactccaaaa gatatttgaa ttatcttgat tggaatgtta ttcataaggaa ataacaggaa 649
gattccaaaag acgtttacca gtmatatcac caggcacctg cagaagagga aaatcactgt 709
ttttgtcaag gatggttggtg tatgtgttta aaataaaacc tgtggtgcac aaaaaaaaaa 769
aaaaaaa 776

<210> 215
<211> 1412
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 34..1143

<400> 215
atgcggtgaa gggcgagcgg cgcgcgcggt gcg atg agt gcc tct gcg gcc acc 54
Met Ser Ala Ser Ala Thr
1 5
ggg gtc ttc gtg ctg tcc ctc tcg gcc atc ccg gtc acc tat gtc ttc 102
Gly Val Phe Val Leu Ser Leu Ser Ala Ile Pro Val Thr Tyr Val Phe
10 15 20
aac cac ctg gcg gcc cag cat gat tcc tgg act att gta ggg gtt gct 150
Asn His Leu Ala Ala Gln His Asp Ser Trp Thr Ile Val Gly Val Ala
25 30 35
gcc ctc atc ctg ttc ctg gta gca ctg ctg gct cgt gtc ctc gtc aaa 198
Ala Leu Ile Leu Phe Leu Val Ala Leu Leu Ala Arg Val Leu Val Lys
40 45 50 55
aga aaa cca ccc cgg gac cca ctg ttc tat gtg tat gca gtt ttt gga 246
Arg Lys Pro Pro Arg Asp Pro Leu Phe Tyr Val Tyr Ala Val Phe Gly
60 65 70
ttt acc agc gtg gtg aac ctc atc ata gga ctg gag caa gat gga atc 294
Phe Thr Ser Val Val Asn Leu Ile Ile Gly Leu Glu Gln Asp Gly Ile
75 80 85
att gac ggg ttc atg aca cac tac ttg aga gag ggt gaa ccg tat ctg 342
Ile Asp Gly Phe Met Thr His Tyr Leu Arg Glu Gly Glu Pro Tyr Leu
90 95 100
aac acc gca tat ggg cac atg atc tgc tac tgg gat ggc tct gct cat 390
Asn Thr Ala Tyr Gly His Met Ile Cys Tyr Trp Asp Gly Ser Ala His
105 110 115
tat ctg atg tac ctg gtg atg gtg gca gcc ata gca tgg gag gaa act 438
Tyr Leu Met Tyr Leu Val Met Val Ala Ala Ile Ala Trp Glu Glu Thr
120 125 130 135
tat aga acc att ggc cta tat tgg gtt gga tct att att atg agt gtt 486
Tyr Arg Thr Ile Gly Leu Tyr Trp Val Gly Ser Ile Ile Met Ser Val
140 145 150
gtt gtt ttt gtg cca gga aac att gta ggg aag tat gga aca cga att 534
Val Val Phe Val Pro Gly Asn Ile Val Gly Lys Tyr Gly Thr Arg Ile
155 160 165
tgc cct gct ttt ttc tta agc ata cca tat act tgt ctt cct gtc tgg 582
Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp
170 175 180
gct ggt ttc aga atc tat aat cag cca tca gaa aat tat aat tac ccc 630
Ala Gly Phe Arg Ile Tyr Asn Gln Pro Ser Glu Asn Tyr Asn Tyr Pro
185 190 195
tca aag gtt att caa gaa gcc caa gcg aaa gac ctg aga aga cca 678
Ser Lys Val Ile Gln Glu Ala Gln Ala Lys Asp Leu Leu Arg Arg Pro
200 205 210 215

| | |
|--|------|
| ttt gat tta atg ttg gtt gtg tgt ctc ctc ctg gca act gga ttt tgc | 726 |
| Phe Asp Leu Met Leu Val Val Cys Leu Leu Leu Ala Thr Gly Phe Cys | |
| 220 225 230 | |
| ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga | 774 |
| Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg | |
| 235 240 245 | |
| tta tat acg caa ttt caa gag ccc tat cta aag gat cct gct gct tat | 822 |
| Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr | |
| 250 255 260 | |
| cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt | 870 |
| Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe | |
| 265 270 275 | |
| gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct | 918 |
| Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro | |
| 280 285 290 295 | |
| gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct | 966 |
| Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser | |
| 300 305 310 | |
| cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc | 1014 |
| His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val | |
| 315 320 325 | |
| cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga | 1062 |
| Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly | |
| 330 335 340 | |
| gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc | 1110 |
| Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe | |
| 345 350 355 | |
| ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taataaatatt acttcatgtt | 1163 |
| Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu | |
| 360 365 370 | |
| cctccttttct aaattactaa cttttgttat actgggtactg atattttgtc ccattttcact | 1223 |
| ctctttctcat acgtgagtac ttaagaatat gtacattctt gctctgcact gtatgtgtga | 1283 |
| gctatatggt attgtgtaaa ttttttttga agggaaatgg aaattcttga gaaacagttt | 1343 |
| gtttaaagaa atatattcaa aatcatttgt gaataaactt gatcatccat ctcaaaaaaa | 1403 |
| aaaaaaaa | 1412 |

<210> 216

<211> 1773

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 6..1184

<400> 216

| | |
|---|-----|
| ccaac atg acc tac agg tgg ggg aca ctg ctc atg aag aga aag ttt gag | 50 |
| Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu | |
| 1 5 10 15 | |
| gag ccc cgg cca gga ttt cat ggt gtc ttg ggt atc aat tcc atc act | 98 |
| Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr | |
| 20 25 30 | |
| ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att | 146 |
| Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile | |
| 35 40 45 | |
| tac ctg gtc tcc ctg cca ttc gtg tgc ctc tgc ctc tat ttc tca ctg | 194 |
| Tyr Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu | |
| 50 55 60 | |

Leu Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu
 370 375 380
 cca atg gaa agc ggg aag gag aag gca acc tgagtgccca gcgtgcccag 1204
 Pro Met Glu Ser Gly Lys Glu Lys Ala Thr
 385 390
 ctgccctgtt ggcagaggcc tgtgtctgtg ccacacctgc cacggtggca gggggggtac 1264
 ccgggggcagc atcgtggctc ctgaaccacag acccaatgct tagccaaacg aagtggctcc 1324
 catgtggcaa gcacccttct cagtttcgca gtggcttggc tcgggatcct tggcagttcc 1384
 cccagcccca cctgtctgc tccttcccag ttcttcccgc ggccccacac gctgctccag 1444
 ctgccaactt tgctgcagag ccactgccgc ccttgagcct ctcaccatga gtgagccacc 1504
 agctctccac gttccctca tagcagtgtc actcccaacc ccaccatggc ccagggaccc 1564
 gtggacaggt tggggatggg gtgtgtgtccc actgtgtctca tcacaggagc ctcagttgag 1624
 agtgagcggg gtacagtaag gcagtgtctc ccacactgga cctctttcct gggtctcttt 1684
 tgcaatacat taacagaccc tttatcaaca taaacaatag taactgagct attaaaggca 1744
 aaaaaaaaaa taaaaaaaaa aaaaaaaaaa 1773

<210> 217
 <211> 1251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..376

<400> 217
 tatccggtcc tcggtgcgg cgggcacc atg gtc ggt ggc gag gcg gct gcc 52
 Met Val Gly Gly Glu Ala Ala Ala
 1 5
 gca gtg gag gag ctg gtt tcg ggg gtg cgg cag gcg gcc gac ttc gcg 100
 Ala Val Glu Glu Leu Val Ser Gly Val Arg Gln Ala Ala Asp Phe Ala
 10 15 20
 gag cag ttc cgc tcc tac tca gag agc gag aag caa tgg aag gcc cgc 148
 Glu Gln Phe Arg Ser Tyr Ser Glu Ser Glu Lys Gln Trp Lys Ala Arg
 25 30 35 40
 atg gaa ttc atc ctg cgc cac ctg ccc gac tac cgc gac ccg ccc gac 196
 Met Glu Phe Ile Leu Arg His Leu Pro Asp Tyr Arg Asp Pro Pro Asp
 45 50 55
 ggc agt ggc cgc ctg gac cag ctg ctc tcc ctc tcc atg gtc tgg gcc 244
 Gly Ser Gly Arg Leu Asp Gln Leu Leu Ser Leu Ser Met Val Trp Ala
 60 65 70
 aac cat ctc ttc cta ggc tgc agt tac aat aaa gac ctt tta gac aag 292
 Asn His Leu Phe Leu Gly Cys Ser Tyr Asn Lys Asp Leu Leu Asp Lys
 75 80 85
 gtg atg gaa atg gcc gat ggg att gaa gtg gaa gac ctg cca caa ttt 340
 Val Met Glu Met Ala Asp Gly Ile Glu Val Glu Asp Leu Pro Gln Phe
 90 95 100
 act acc aga agt gaa tta atg aaa aag cat caa agc taagccagaa 386
 Thr Thr Arg Ser Glu Leu Met Lys Lys His Gln Ser
 105 110 115
 gatttatcac attttcatca tcagctacag gattagaaag gaggtctggga tgaatgtgac 446
 atagaccaca gcagctctct taagactcct ggtattacca acataaagag gcaggtggaa 506
 tgagaaggac tctgtctaga ttggcttttt taacattctc attttcccag gagttatcac 566
 tgtaaaagta tgcattggata tttatgtatt tataaatcat gcaactctaag atgagttcat 626
 caacattgta aaagccctct tttctgtttt caggtttttt tttttcttat cgacaaggtc 686
 tcaactgtgc gccaggcag aatcacaaag gtgcattatt ggctcattgc agcctcgaac 746
 tcctgggctc atattttcag ggttttttgt tttttgtttt gtttttttga gacagagtct 806
 tgctctgttg cccaggcagt agtgcmagtg gcgcgatata ttttcagttt ttaaactgca 866


```

gaatttttgt ttaaaatgcc tttttgggct gggccacagt ggccttatgc ccataataat 926
cccagcactt tgggaggccg aggtgagcag atcacctgag gttaggagtt tgagaccagc 986
ctggccaaca cgatgaaacc ccgctctctac taaaaataca aacaaaatta gctggggcatg 1046
gtggcggaaca tctgtaatcc cagctactca ggaggctgaa gcagaagaac tgcttgaacc 1106
tgggaggtgg aggttgcagt gagccaagat cgcaccattg cactccatcc tgggcgacaa 1166
aaatgaaaca ccgctctcaa aaaaaaataa aaataataaa ataaaatgcc tttttgttgt 1226
tgatgtgaaa aaaaaaaaaa aaaaaa 1251

```

```

<210> 218
<211> 894
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 78..566

```

```

<400> 218
gcgcgccatc ttggctccgg atcgtgcgtg aggcggcttc gtgggcagcg agagtcacag 60
acaagacagc aagcagg atg gag cac tac cgg aaa gct ggc tct gta gag 110
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu
1 5 10
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag 158
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu
15 20 25
atg cgg gtc cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct 206
Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala
30 35 40
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt 254
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly
45 50 55
tct ggc agg gct gca gga aag gct gtc agc tgc gct gag att gtc aag 302
Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys
60 65 70 75
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag 350
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln
80 85 90
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc 398
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro
95 100 105
ctc aca gtg cgc cgc cat gtg cct gca gtg tgg gtg ctg ctc agc cgg 446
Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg
110 115 120
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc 494
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro
125 130 135
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga 542
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg
140 145 150 155
aga agg gct cga gac acc cga tcg tgaagacctg ctgagccagc ctgttctccg 596
Arg Arg Ala Arg Asp Thr Arg Ser
160
ggcctgaatg tctgggggtgc ttgtgccttt tctgagaagc gttgtgactg ctcaacatcc 656
ccatcaaggt ttgagtccac aaaagtggac ctccctatca tgcttcccct tccctctagc 716
atgtgggaag ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt 776
gctaaataag ggcttctctt gccttctacc tacagtgcac ttgaactgcc ttctgaaaga 836
ggtccagggga gggatttagg aaataaagtt tctacctatt taiaaaaaaa aaaaaaaa 894

```

<210> 219
 <211> 910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..705

<400> 219
 acatgagcca ccaaa atg gtg gtg ttc ggg tat gag gct ggg act aag cca 51
 Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro
 1 5 10
 agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag gtt 99
 Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val
 15 20 25
 ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta gaa 147
 Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu
 30 35 40
 gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa aat 195
 Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn
 45 50 55 60
 ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg gcg 243
 Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala
 65 70 75
 aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc ctg 291
 Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu
 80 85 90
 ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat gca 339
 Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala
 95 100 105
 tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag ctt 387
 Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu
 110 115 120
 ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac tgt 435
 Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys
 125 130 135 140
 gtt ttc aga agc tca ctg att ggc ata gtt tgt ggt gtt ttc tat ccc 483
 Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro
 145 150 155
 agt tct ttg gct ttt act aaa aat gga cgc ctg gca acc aag tat cat 531
 Ser Ser Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His
 160 165 170
 acc gtt cca ctg cca cca aaa gga agg gtt tta atc cat tgg atg acg 579
 Thr Val Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr
 175 180 185
 ctt tgt caa aca caa atg aaa tta atg gcg att cct cta gtc ttt cag 627
 Leu Cys Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln
 190 195 200
 att atg ttt gga ata tta aat ggt cta tac cat tat gca gta ttt gaa 675
 Ile Met Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu
 205 210 215 220
 gag aca ctt gag aaa act ata cat gaa gag taacacaaaaa aatgaatggt 725
 Glu Thr Leu Glu Lys Thr Ile His Glu Glu
 225 230
 tgctaactta gcaaaatgaa gtttctataa agaggactca ggcatgtgctg aaagagttaa 785
 aagtaactgt gaacaaataa tttgttctgt gccttttggc tggtatatag caaataactca 845
 aaaaatattc aataattcaa tcaataaata taagtttcat cttacaccaa aaaaaaaaaa 905

aaaaa 910

<210> 220
<211> 519
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..405

<400> 220
acttccggtg cgaaccgcct cggccgttcc ctccgaggagc ttactgagcg cggccgccga 60
gccagctcc gccgcccagc gctgtgccc gcacgbhaca cc atg gag cgc ccg 114
Met Glu Arg Pro
1
gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa 162
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu
5 10 15 20
agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta 210
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe Phe Thr Ala Leu
25 30 35
atg atc act gtt cct att ggg tta tat ttc aca act aaa tct tac ata 258
Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile
40 45 50
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct 306
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala
55 60 65
gct att gtt gca gtg gtc gcc gtc cat gtg gtg ctg gcc ctc ttt gtg 354
Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val
70 75 80
tat gtg gcc tgg aat gaa ggc tca cga cag tgb cgt gaa ggc aaa cag 402
Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln
85 90 95 100
gat taaagtgaac atcacctttt tatagcatta aattcatttt ttaaaatgat 455
Asp
aatgctggag ggggccatct gatttgaata aagttgaaag aacatgtaaa aaaaaaaaaa 515
aaaa 519

<210> 221
<211> 632
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..350

<400> 221
agtgaaccg cgccgcaaca gcttgcggct gcggtagtc cgtgggagct ccgctggctg 60
tgcaggcggc c atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca atg 110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met
1 5 10
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc 158
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr
15 20 25
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag 206
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln

| | | | | |
|--|----|----|----|-----|
| 30 | 35 | 40 | 45 | |
| gac cca agg agc aga gag gag gcg gcc agg acc cag cag cta ttg ctg | | | | 254 |
| Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu | | | | |
| | 50 | 55 | 60 | |
| gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg | | | | 302 |
| Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg | | | | |
| | 65 | 70 | 75 | |
| aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc ggc ggg agg tca ccg | | | | 350 |
| Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro | | | | |
| | 80 | 85 | 90 | |
| tgagaccgga cttgcctccg tgggcgcggg accttggtt gggcgcagga atccgaggca | | | | 410 |
| gcctttctcc ttcggtgggc cagcggagag tccggaccga gataccatgc caggactctc | | | | 470 |
| cggtgtctctg tgagctgccg tcgggtgagc acgtttcccc caaaccttg actgactgct | | | | 530 |
| ttaagggtccg caaggcgggc cagggccgag acgcgagtcg gatgtggtga actgaaagaa | | | | 590 |
| ccaataaaat catgttcctc cacccaaaaa aaaaaaaaaa aa | | | | 632 |

<210> 222
 <211> 652
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..436

| | |
|---|-------------------------|
| <400> 222 | |
| actgctgtcc cccgagctgc tctacgcgct ggcgcg atg ggg cac ggg gac gag | 55 |
| | Met Gly His Gly Asp Glu |
| | 1 5 |
| atc gtt ctt gcg gac ttg aac ttc ccg gcc tcc tcc atc tgc cag tgt | 103 |
| Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys | |
| | 10 15 20 |
| ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg | 151 |
| Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu | |
| | 25 30 35 |
| gag gcc gtg ctg aag ctg ctg ccc ctg gac acc tat gtg gag agt ccg | 199 |
| Glu Ala Val Leu Lys Leu Pro Leu Asp Thr Tyr Val Glu Ser Pro | |
| | 40 45 50 |
| gct gca gtc atg gag ctg gtg ccc agc gac aag gag agg ggc ctg cag | 247 |
| Ala Ala Val Met Glu Leu Val Pro Ser Asp Lys Glu Arg Gly Leu Gln | |
| | 55 60 65 70 |
| acc cca gtg tgg acg gag tac gag tcc atc cta cgc agg gcc ggc tgt | 295 |
| Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile Leu Arg Arg Ala Gly Cys | |
| | 75 80 85 |
| gtg aga gcc ctg gca aag ata gag agg ttt gag ttt tat gaa cgg gct | 343 |
| Val Arg Ala Leu Ala Lys Ile Glu Arg Phe Glu Phe Tyr Glu Arg Ala | |
| | 90 95 100 |
| aag aag gct ttt gct gtt gtg gca acg ggg gag acg gcc ctc tac gga | 391 |
| Lys Lys Ala Phe Ala Val Val Ala Thr Gly Glu Thr Ala Leu Tyr Gly | |
| | 105 110 115 |
| aac ctc atc ctc agg aag ggg gtg ctt gcc ctc aac ccc ctg ctg | 436 |
| Asn Leu Ile Leu Arg Lys Gly Val Leu Ala Leu Asn Pro Leu Leu | |
| | 120 125 130 |
| taggcctggt gaagaccacc tgggcgggaa gaggaactgg gggcaccctg agctccagta | 496 |
| ccaccactca caacaggcct cccagtggca gctcccagac ctggggcctg gccagggtc | 556 |
| taggggccgg cagtcttggg gtgggcctg ccaattggga cgagtatccc tgatttgtga | 616 |
| aaatgatgga aaaacgttca aaaaaaaaaa aaaaaa | 652 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ser | Tyr | Cys | Lys | Arg | Gly | Asn | Gly | Tyr | Arg | Ser | Arg | Val | Pro | Lys | | |
| | | | 30 | | | | | 35 | | | | | 40 | | | | |
| gaa | tgc | gaa | tgc | aac | tgg | ctt | cat | ctt | gaa | agc | gac | act | ctg | aag | aaa | 375 | |
| Glu | Cys | Glu | Cys | Asn | Trp | Leu | His | Leu | Glu | Ser | Asp | Thr | Leu | Lys | Lys | | |
| | | 45 | | | | | 50 | | | | | 55 | | | | | |
| tta | ccc | ata | att | tct | ccc | tct | tgg | aca | tgc | aga | att | atc | ctg | ttc | ttg | 423 | |
| Leu | Pro | Ile | Ile | Ser | Pro | Ser | Trp | Thr | Cys | Arg | Ile | Ile | Leu | Phe | Leu | | |
| | | 60 | | | | 65 | | | | | 70 | | | | | | |
| tat | ttt | tct | ggc | cag | ctt | ctc | caa | ctt | tcc | ctt | tct | tgt | ttg | caa | cta | 471 | |
| Tyr | Phe | Ser | Gly | Gln | Leu | Leu | Gln | Leu | Ser | Leu | Ser | Cys | Leu | Gln | Leu | | |
| | | 75 | | | 80 | | | | 85 | | | 90 | | | | | |
| att | aaa | ctt | taaggataaaa | aaaaaaaaaa | aa | | | | | | | | | | | 502 | |
| Ile | Lys | Leu | | | | | | | | | | | | | | | |

<210> 225
 <211> 1739
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 171..1670

| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 225 | | | | | | | | | | | | | | | | | |
| actctggcct | tgetgcttct | ctccagctcc | tgaacttttc | tttcttccat | catgctctga | 60 | | | | | | | | | | | |
| gcccattcct | tgaaaactaa | aaggtccctg | actcccagtc | tgcagccatc | ctgggcctgc | 120 | | | | | | | | | | | |
| tgagctctga | ttcaagtgcc | tgcctctgcc | ccttggtggg | ctgaagcttc | atg gag | 176 | | | | | | | | | | | |
| | | | | | Met Glu | | | | | | | | | | | | |
| | | | | | 1 | | | | | | | | | | | | |
| gta | tcc | acc | aac | ccc | tcc | tcc | aac | atc | gat | cca | ggc | aac | tat | gtt | gaa | 224 | |
| Val | Ser | Thr | Asn | Pro | Ser | Ser | Asn | Ile | Asp | Pro | Gly | Asn | Tyr | Val | Glu | | |
| | | 5 | | | | | 10 | | | | | 15 | | | | | |
| atg | aat | gat | tca | atc | acc | cac | cta | ccc | tct | aaa | gtg | gtg | ata | caa | gat | 272 | |
| Met | Asn | Asp | Ser | Ile | Thr | His | Leu | Pro | Ser | Lys | Val | Val | Ile | Gln | Asp | | |
| | | 20 | | | | 25 | | | | 30 | | | | | | | |
| att | act | atg | gag | cta | cac | tgc | cct | ctg | tgc | aat | gat | tgg | ttc | cga | gac | 320 | |
| Ile | Thr | Met | Glu | Leu | His | Cys | Pro | Leu | Cys | Asn | Asp | Trp | Phe | Arg | Asp | | |
| | | 35 | | | 40 | | | | 45 | | | | | 50 | | | |
| cca | ctg | atg | cta | agc | tgt | ggc | cac | aac | ttc | tgt | gaa | gcc | tgt | atc | caa | 368 | |
| Pro | Leu | Met | Leu | Ser | Cys | Gly | His | Asn | Phe | Cys | Glu | Ala | Cys | Ile | Gln | | |
| | | | | 55 | | | | 60 | | | | | | 65 | | | |
| gac | ttt | tgg | agg | ctg | caa | gca | aag | gaa | aca | ttc | tgt | cct | gag | tgt | aag | 416 | |
| Asp | Phe | Trp | Arg | Leu | Gln | Ala | Lys | Glu | Thr | Phe | Cys | Pro | Glu | Cys | Lys | | |
| | | 70 | | | | | 75 | | | | | 80 | | | | | |
| atg | cta | tgt | cag | tat | aac | aac | tgt | aca | ttc | aac | cct | gta | ctg | gac | aag | 464 | |
| Met | Leu | Cys | Gln | Tyr | Asn | Asn | Cys | Thr | Phe | Asn | Pro | Val | Leu | Asp | Lys | | |
| | | 85 | | | | 90 | | | | | 95 | | | | | | |
| ttg | gta | gag | aag | att | aag | aag | tta | ccc | tta | ctc | aag | ggc | cat | cca | cag | 512 | |
| Leu | Val | Glu | Lys | Ile | Lys | Lys | Leu | Pro | Leu | Leu | Lys | Gly | His | Pro | Gln | | |
| | | 100 | | | | 105 | | | | | 110 | | | | | | |
| tgc | cca | gag | cat | gga | gag | aac | ctg | aaa | ctg | ttc | agt | aaa | cca | gat | ggg | 560 | |
| Cys | Pro | Glu | His | Gly | Glu | Asn | Leu | Lys | Leu | Phe | Ser | Lys | Pro | Asp | Gly | | |
| | | 115 | | | 120 | | | | 125 | | | | | 130 | | | |
| aaa | ctg | atc | tgc | ttt | caa | tgc | aag | gat | gct | cgg | ttg | tct | gtg | ggg | cag | 608 | |
| Lys | Leu | Ile | Cys | Phe | Gln | Cys | Lys | Asp | Ala | Arg | Leu | Ser | Val | Gly | Gln | | |
| | | | | 135 | | | | | 140 | | | | | 145 | | | |
| tct | aag | gag | ttc | ctg | caa | atc | tct | gat | gct | gtc | cat | ttc | ttc | atg | gag | 656 | |
| Ser | Lys | Glu | Phe | Leu | Gln | Ile | Ser | Asp | Ala | Val | His | Phe | Phe | Met | Glu | | |


```

acc ttc agt aac act ttc atg gag aaa ctt tat ccc tac ttc tgc ccc 1616
Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe Cys Pro
      470                      475                      480
tgc ctt aat gat ggt aga gag aat aaa gaa cca ttg cac atc tta cat 1664
Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
      485                      490                      495
cca cag taatgagtca taatattata caaattcaga gtgttattaa agagggttttg 1720
Pro Gln
      500
aaataaaaaa aaaaaaaaaa 1739

```

```

<210> 226
<211> 657
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 199..618

```

```

<400> 226
aactggatag agtactgccc ccttcagccc atggagaaaag gcaaatgcct ccttcagagt 60
ctacctaatag ctttctcaga taaataagca tgaagaaaag tcaaagtcca ttctagctct 120
aaaataagga atgaaatggt ttcctgatat gattttttgt tttcatctga taataatttt 180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc 231
                        Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
                        1                      5                      10
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg 279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
      15                      20                      25
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac 327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
      30                      35                      40
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag 375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
      45                      50                      55
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct 423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
      60                      65                      70                      75
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa 471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
      80                      85                      90
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac 519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
      95                      100                      105
cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc 567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
      110                      115                      120
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata 615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile
      125                      130                      135
tgc tagtactaat aaaaccaaca tgttaaaaaa aaaaaaaaaa 657
Cys
140

```

```

<210> 227
<211> 888
<212> DNA

```


<213> Homo sapiens

<220>

<221> CDS

<222> 182..481

<400> 227

```
attttgcctc tcagtgttca agcttgagcc cacgcatcca actcctgaga tcttactggg      60
aagctgctga tcatcagttt caggaagtca gcatggatca gccttacgtt catggcctcc      120
aggccctatt ctctgcctc acagggaccg gccaggatct ctatccttac agcacgttgg      180
a atg tat atg ctc ctc tcc cca cat cgc ctt agg gag cag gca ggt gtc      229
  Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
    1           5           10          15
agg ggc agc ata agg acg gcc aac agg aca gaa gac ggg ttg aag atc      277
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
           20           25           30
cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc      325
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
           35           40           45
ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga      373
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
           50           55           60
cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca      421
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
           65           70           75           80
tct gca cct cct ctc aga gaa agc ctg atg cct act aaa gga ctt ggg      469
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
           85           90           95
tgg tgg acg cag tgaccctcag tctggagctt gttcactgaa cattggagac      521
Trp Trp Thr Gln
           100
tatcatttgc gcagatgggc ttgggcctct atgagcagca ggctgcaccc cacagtgacc      581
tcctcattct actctgaggg atcttcatga aagcagatgt ccattgaaaa gcacccaagt      641
gcagtctcag ctgatgaact tcagaggcga ttgagacaaa ggctctcggc cccctctgcc      701
cttggatggg gcctctggta tgcacttggc ctctgtgtct ttatttagac tggtcacttc      761
acaacccatc atgtcacccc acccctaacc gtgcccactc tgggtcctcc cctcaactgc      821
ctgacttccc actttgagct cagcaaaggc aatagatggt ttgtctgctt cgaaaaaaaa      881
aaaaaaaaa      888
```

<210> 228

<211> 716

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 161..517

<400> 228

```
acctgtcatt atgcttacta acgttcggga cgtctcccgg gctgcttggg cgaggagagg      60
caggggtgtg tgaccccggt gggtactgtg ctgcgctaga gcacctaggg cctgctgaag      120
ccctccctcg cccgcgcctc tccttagtcc ttgagatgag atg gca agt tac agc      175
                               Met Ala Ser Tyr Ser
                               1           5
ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc      223
Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly Pro Gly His Arg Ser
           10           15           20
tgc ctt ccc caa ttc gct ttc ttt ccg cag ccg ccg ctg ccc cga ccc      271
```

Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro Pro Leu Pro Arg Pro
 25 30 35
 cgg atc tgc atg tgg gtg ctg gct gag ctg ctg gag cta ggg tgt cct 319
 Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu Glu Leu Gly Cys Pro
 40 45 50
 gag cag agc ctg agg gac gcc atc acc ctg gac ctc ttc tgc cac gcg 367
 Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp Leu Phe Cys His Ala
 55 60 65
 ctc att ttc tgc cgc cag cag ggc ttc tca ctg gag cag acg tca gcg 415
 Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu Glu Gln Thr Ser Ala
 70 75 80 85
 gct tgt gcc ctg ctc cag gat ctt cac aag gct tgt att ggt gag agg 463
 Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala Cys Ile Gly Glu Arg
 90 95 100
 ggg cag cta cca ggt ttg agc ccc agg gag aag agg aac cgg gcc tgg 511
 Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys Arg Asn Arg Ala Trp
 105 110 115
 cac aag tgaccatggg aagcagaagc aggggatttc tgcctggaat atgtcattat 567
 His Lys
 tagtagcatc atcatacaca agccatcagc tttccaatcc actgcttcct tatctagaaa 627
 ttaaggatac agcacacatt ttacaggact gttctgagaa ataatatatg caaatatatg 687
 catagtgcac aataaaaaaaaa aaaaaaaaaa 716

 <210> 229
 <211> 654
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 86..505

 <400> 229
 agttcgcggt gtcagcctcc gcctccgagc ctcagttgtc ttctctgtga ggtgggaatg 60
 ccggtgaatc ctgccgctgg cgtgg atg aga agt gaa tgc gtg ctc gga gct 112
 Met Arg Ser Glu Cys Val Leu Gly Ala
 1 5
 gcg agt gac agc ggg cag gag gcg ccc agg gac act tgg ttt ctc cag 160
 Ala Ser Asp Ser Gly Gln Glu Ala Pro Arg Asp Thr Trp Phe Leu Gln
 10 15 20 25
 ggc tgg aag gct tct aga agg ttc ctc atc aag gga agt gtg gct ggg 208
 Gly Trp Lys Ala Ser Arg Arg Phe Leu Ile Lys Gly Ser Val Ala Gly
 30 35 40
 ggc gcc gtc tac ctg gtg tac gac cag gag ctg ctg ggg ccc agc gac 256
 Gly Ala Val Tyr Leu Val Tyr Asp Gln Glu Leu Leu Gly Pro Ser Asp
 45 50 55
 aag agc cag gca gcc cta cag aag gct ggg gag gtg gtc ccc ccc gcc 304
 Lys Ser Gln Ala Ala Leu Gln Lys Ala Gly Glu Val Val Pro Pro Ala
 60 65 70
 atg tac cag ttc agc cag tac gtg tgt cag cag aca ggc ctg cag ata 352
 Met Tyr Gln Phe Ser Gln Tyr Val Cys Gln Gln Thr Gly Leu Gln Ile
 75 80 85
 ccc cag ctc cca gcc cct cca aag att tac ttt ccc atc cgt gac tcc 400
 Pro Gln Leu Pro Ala Pro Pro Lys Ile Tyr Phe Pro Ile Arg Asp Ser
 90 95 100 105
 tgg aat gca ggc atc atg acg gtg atg tca gct ctg tcg gtg gcc ccc 448
 Trp Asn Ala Gly Ile Met Thr Val Met Ser Ala Leu Ser Val Ala Pro
 110 115 120

| | |
|---|-----|
| tcc aag gcc cgc gag tac tcc aag gag ggc tgg gag tat gtg aag gcg | 496 |
| Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala | |
| 125 130 135 | |
| cgc acc aag tagcgagtca gcaggggccc cctgccccgg ccagaacggg | 545 |
| Arg Thr Lys | |
| 140 | |
| cagggctgcc actgacctga agactccgga ctgggacccc actccgaggg cagctcccgg | 605 |
| ccttgccggc ccaataaagg acttcagaag tcaaaaaaaaa aaaaaaaaaa | 654 |

<210> 230
 <211> 635
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..382

| | |
|---|-----|
| <400> 230 | |
| aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aacttcagga caaaa atg | 58 |
| Met | |
| 1 | |
| ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc | 106 |
| Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser | |
| 5 10 15 | |
| cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca | 154 |
| Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr | |
| 20 25 30 | |
| ttt caa cag att cgg tgc tat tct gca cct gtt gct gct gag ccc ttt | 202 |
| Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro Phe | |
| 35 40 45 | |
| ctc agt ggg act agt tcg aac tat gtg gag gag atg tac tgt gct tgg | 250 |
| Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala Trp | |
| 50 55 60 65 | |
| ctg gaa aac ccc aaa agt gta cat aag aca ggg tcc cac tgt tgt cca | 298 |
| Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys Pro | |
| 70 75 80 | |
| ggc tgg agt gca gtg gcg gga tct cgg ctt gct gca acc tcc gac tcc | 346 |
| Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp Ser | |
| 85 90 95 | |
| tgg gtt caa gtg att ctt atg cct cag cct ccc gag taactgggac | 392 |
| Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu | |
| 100 105 | |
| tacaggtgca cgtcaccacg cctgactagt ttttgtatatt ttagtagaga tgggatttta | 452 |
| ctttgtttggc caggctgggc ttgaaccctt ggccctcaagt gatccaccca ccttggcctc | 512 |
| ccaaagtgct gggattacag gtatgatcaa ccacgcctgg ccatgtcatg ccttgtgaca | 572 |
| gaattccttt attctgtttt gagccaataa atatttatag gtttcgaaaa aaaaaaaaaa | 632 |
| aaa | 635 |

<210> 231
 <211> 634
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..355

<400> 231

```
aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aacttcagga caaaa atg      58
                                         Met
                                         1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc      106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
                    5                10                15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca      154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
                20                25                30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc      202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Ser Pro Phe
                35                40                45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc      250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly
                50                55                60                65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag      298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln
                70                75                80
gct gga gtg cag tgg cgg gat ctc ggc ttg ctg caa cct ccg act cct      346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro
                85                90                95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca      395
Gly Phe Lys
                100
ggtgcacgtc accacgcctg actagttttt gtatttttag tagagatggg attttacttt      455
ggtggccagg ctggtcttga acccctggcc tcaagtgatc caccacactt ggccctcccaa      515
agtgtctgga ttacaggtat gatcaaccac gcctggccat gtcatgcctt gtgacagaat      575
tcctttattc tgttttgagc caataaatat ttataggttt cgaaaaaaaa aaaaaaaaaa      634
```

<210> 232

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..498

<400> 232

```
aatatagcca gccgcggctg cccttgcgct tcccgagctg gcgggggtccg tgggtgcggga      60
tcgagattgc gggct atg gcg ccg aag gtt ttt cgt cag tac tgg gat atc      111
                                         Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
                                         1                5                10
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att      159
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
                15                20                25
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat      207
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
                30                35                40
cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg      255
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
                45                50                55                60
ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc      303
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile
                65                70                75
agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc      351
Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu
```

```

      80      85      90
ggg ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac      399
Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr
      95      100      105
ggg att ggc gcc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg      447
Gly Ile Gly Ala Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu
      110      115      120
gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag      495
Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys
      125      130      135      140
gtg tgagccctgt gcctgccggg acctccagcc tgcagaatgc gtccagaaat      548
Val
aaattctgtg tctgtgtgaa aaaaaaaaaa aaaaa      583

<210> 233
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..600

<400> 233
atttttccga tgccaggcac cctcaaggca cagaggctgg ggctcatgtt ggggggcactt      60
ggcctctcca ggcctcgaag gcttctcttg gctgatgcga gctggggaac gggagggacg      120
gacgtgggag cgagaacgtc aacttgagg cagctggtgg cacgatgggg gacagagtga      180
aagagccttc gtgtcacc atg gcc aca cac ccc gat ggc ttc cgg ctt gag      231
                Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu
                1                5                10
gga ccc ctg gct gca gcc cac agc cct ggg cct tgc act gtg ctc tac      279
Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr
                15                20                25
gaa ggc cct gtc cgt ggg ctc tgc ccy ttt gcc ccg cga aat tcc aac      327
Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn
                30                35                40
acc atg gcg gcg gct gcc ctg gct gcc ccc agc ctg ggc ttc gat ggg      375
Thr Met Ala Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly
                45                50                55
gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac atg cac gtg      423
Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp Met His Val
        60                65                70                75
gtg gat gta gag ctg agc gga ccc cgg ggc ccc act ggc cga agc ttt      471
Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe
                80                85                90
gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc gcg gtc acc      519
Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr
                95                100                105
ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg gcc tgc tgc      567
Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys
                110                115                120
cag ctc ccc tcc agg ccg ggg atc cat ctc tgc tgagaagcct cctccctccc      620
Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
                125                130
gagacaagat catctgcctg gcctctcacc accaccatcc caccctgcc ctgccccact      680
tcccagggt ctcccttctg actcagtaaa gatcaccgct gcctccccc gcaaataaaa      740
aaaaaaaaa aaa      753

```

<210> 234
 <211> 762
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 211..612

<400> 234
 atttccgatg ccaggcaccc tcaaggcaca gaggctgggg ctcatgttgg gggcacttgg 60
 cctctccagg cctcgaaggc ttctcctggg ctgatgcgag ctggggaacg ggagggacgg 120
 acgtgggagc gagaacgtca cactggaggc agctggtggc acgatggggg acagagtga 180
 aggtagcaag tcaagagcct tcgtgtcacc atg gcc aca cac ccc gat ggc ttc 234
 Met Ala Thr His Pro Asp Gly Phe
 1 5
 cgg ctt gag gga ccc ctg gct gca gcg cac agc cct ggg cct tgc act 282
 Arg Leu Glu Gly Pro Leu Ala Ala His Ser Pro Gly Pro Cys Thr
 10 15 20
 gtg ctc tac gaa ggc cct gtc cgt ggg ctc tgc ccc ttt gcc ccg cga 330
 Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg
 25 30 35 40
 aat tcc aac acc atg tgc gcg gct gcc ctg gct gcc ccc agc ctg ggc 378
 Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly
 45 50 55
 ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac 426
 Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp
 60 65 70
 atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc 474
 Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys
 75 80 85
 cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc 522
 Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly
 90 95 100
 gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg 570
 Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu
 105 110 115 120
 gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc 612
 Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
 125 130
 tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc accaccatcc 672
 caccctgcc ctgccccact tccccagggt ctcccttctg actcagtaaa gatcaccgct 732
 gcctccccc gccaaaaaaa aaaaaaaaaa 762

<210> 235
 <211> 537
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..259

<400> 235
 aaaa atg cta aag gta gaa gca act ggt agt ccc gag gaa ggg tgg gcg 49
 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala
 1 5 10 15
 ggt gga gag ccc cgg act gga gct cct gcg aac tcc cct tcc tgc cct 97

| | |
|--|-----|
| Gly Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro | |
| 20 25 30 | |
| cag gag atg cca ctg cag gac cca agg agc agg gag gag gcg gcc agg | 145 |
| Gln Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg | |
| 35 40 45 | |
| acc cag cag cta ttg ctg gcc act ctg cag gag gca gcg acc acg cag | 193 |
| Thr Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln | |
| 50 55 60 | |
| gag aac gtg gcc tgg agg aag aac tgg atg gtt ggc ggc gaa ggc ggc | 241 |
| Glu Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly | |
| 65 70 75 | |
| gcc agc ggg agg tca ccg tgagaccgga cttgcctccg tgggcgcggg | 289 |
| Ala Ser Gly Arg Ser Pro | |
| 80 85 | |
| accttggctt gggcgcagga atccgaggca gcctttctcc ttcgtgggcc cagcggagag | 349 |
| tccggaccga gataccatgc caggactctc cggggtcctg tgagctgccg tccgggtgagc | 409 |
| acgtttcccc caaaccttg actgactgct ttaagggtccg caaggcgggc cagggccgag | 469 |
| acgcgagtcg gatgtggtga actgaaagaa ccaataaaat catgttcttc caaaaaaaaa | 529 |
| aaaaaaaa | 537 |
| <210> 236 | |
| <211> 994 | |
| <212> DNA | |
| <213> Homo sapiens | |
| <220> | |
| <221> CDS | |
| <222> 23..370 | |
| <400> 236 | |
| gattgctgtt tgctgtaaag tg atg ggg agg ccc tgg atg gtg atg ata ttg | 52 |
| Met Gly Arg Pro Trp Met Val Met Ile Leu | |
| 1 5 10 | |
| gag tca aaa tct gaa gaa aag atg tgg tat ggt gta ttc ctg tgg gca | 100 |
| Glu Ser Lys Ser Glu Glu Lys Met Trp Tyr Gly Val Phe Leu Trp Ala | |
| 15 20 25 | |
| ctg gtg tct tct ctg ttc ttt cat gtc cct gct gga tta ctg gcc ctg | 148 |
| Leu Val Ser Ser Leu Phe Phe His Val Pro Ala Gly Leu Leu Ala Leu | |
| 30 35 40 | |
| ttc acc ctg aga cat cac aaa tat ggt agg ttc atg tct gta agc atc | 196 |
| Phe Thr Leu Arg His His Lys Tyr Gly Arg Phe Met Ser Val Ser Ile | |
| 45 50 55 | |
| ctg ttg atg ggc atc gtg gga cca att act gct gga atc ttg aca agt | 244 |
| Leu Leu Met Gly Ile Val Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser | |
| 60 65 70 | |
| gca gct att gct gga gtt tac cga gca gca ggg aag gaa atg ata cca | 292 |
| Ala Ala Ile Ala Gly Val Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro | |
| 75 80 85 90 | |
| ttt gaa gcc ctg aca ctg ggc act gga cag aca ttt tgc gtc ttg gtg | 340 |
| Phe Glu Ala Leu Thr Leu Gly Thr Gly Gln Thr Phe Cys Val Leu Val | |
| 95 100 105 | |
| gtc tcc ttt tta cgg att tta gct act cta tagcatacat ccttatgctg | 390 |
| Val Ser Phe Leu Arg Ile Leu Ala Thr Leu | |
| 110 115 | |
| agatgttgaa cttaaacttt atggaatcct ccaaaagaat acattatgga gtgtagtgtt | 450 |
| ttcttagttc ttcaaaggga agcaacttgg atgaacagga acatgaagga caacacatct | 510 |
| cagccttttc ttcatTTtga agctcctaga attgaagact tatgtggact cctattgttc | 570 |
| tcaacaaaa caagtctttt ggctttcttt tttgtagata tttaatttaa gcagttttca | 630 |

| | | | |
|---|--------------|-----|------|
| 305 | 310 | 315 | |
| atg cgg gag aag gag gag cag cgg ggg ctg cgc aag tac aac tac acg | | | 1007 |
| Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr | | | |
| 320 | 325 | 330 | 335 |
| ctg ctg cgc gtg cgc ctc ccc gat ggc tgc ctc ctg cag ggc act ttc | | | 1055 |
| Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe | | | |
| 340 | 345 | 350 | |
| tac gct cgg gag cgg ctg ggg gcg gtg tac ggg ttc gtc cgg gag gcc | | | 1103 |
| Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala | | | |
| 355 | 360 | 365 | |
| ctg cag agc gac tgg ctg cct ttt gag ctg ctg gcc tcg gga ggg cag | | | 1151 |
| Leu Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln | | | |
| 370 | 375 | 380 | |
| aag ctg tcc gag gac gag aac ctg gcc ttg aac gag tgc ggg ctg gtg | | | 1199 |
| Lys Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val | | | |
| 385 | 390 | 395 | |
| ccc tct gcc ctc ctg acc ttc tcg tgg gac atg gct gtg ctg gag gac | | | 1247 |
| Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp | | | |
| 400 | 405 | 410 | 415 |
| atc aag gcc gcg ggg gcc gag ccg gac tcc atc ctg aaa ccc gag ctc | | | 1295 |
| Ile Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu | | | |
| 420 | 425 | 430 | |
| ctg tca gcc atc gag aag ctc ttg tgaaataaaaa gcagggttgg cctcagccct | | | 1349 |
| Leu Ser Ala Ile Glu Lys Leu Leu | | | |
| 435 | | | |
| gtgggtctgt ctcatgctct cctgttctct ctccccgcca cccaggggcc tccaagccac | | | 1409 |
| ctctggaaat acttggtctt gccccatggg caggggaggg gcgccagccg tggagctgtg | | | 1469 |
| gaattggggc ccgtggcaga gccccatcc cttgggggct gtggggatgc gcccaagccc | | | 1529 |
| ccgagggaga ggcttgggga caccaacaaa tctaagccct cctagctct tggtaactgt | | | 1589 |
| gtcatgaagc tgccggacag acacacgtgg catctccctg gcaggagag caggcctgca | | | 1649 |
| gcatgggtcc cgttcccgctg tgccgtgggt ggacgtggct gcacctggca ctagggtgc | | | 1709 |
| tctgtggatg tgggtgacaa cggcaggagg ggacgtggc cttcctgcac atagacctgc | | | 1769 |
| agttagtaaa tcataagccc aaataaacag gttgtttgaa tataaaaaaa aaaaaaaaaa | | | 1829 |
| | | | |
| <210> | 239 | | |
| <211> | 1083 | | |
| <212> | DNA | | |
| <213> | Homo sapiens | | |
| | | | |
| <220> | | | |
| <221> | CDS | | |
| <222> | 421..768 | | |
| | | | |
| <400> | 239 | | |
| aaggatgtgc tctttcccaa ggagagggag ctctgttgcc tccttccac agaactcactc | | | 60 |
| tgtgcaaacc tcttcccctc ctgggcccc gtctcccaa ttctaaaatc ggatactgga | | | 120 |
| taaaatgcca cggaagaacc tagggatgca ccaggaacca cgcgcctgaa tgccacaggt | | | 180 |
| ttgatttgat tcatgaccct catctggaca caagctctaa aatacttgag ccttggcaga | | | 240 |
| aatggctgat agagtccaca gaacacgtg tctcatctc agagaggaga actctgaacc | | | 300 |
| cagaggggaa ggatttacct gcagttgtat ggcaagccag aggtaggcgc tgcactggaa | | | 360 |
| cgcagcctaa ccagcctaaa gaaaccatgg gaggagaggc tcttaccctc tcctttgcag | | | 420 |
| atg tgg gcc cgg ctg cct cac act cca gag cag atg ggc cac agg ctt | | | 468 |
| Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu | | | |
| 1 | 5 | 10 | 15 |
| ata ggt ccc aag gaa gct tca ctt cat gtg gta ccc agc tgg cca gcc | | | 516 |
| Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala | | | |
| 20 | 25 | 30 | |
| agg aag atg gag ggg ctt ctg gct ggc ctc tct tcc tct cct aga aag | | | 564 |

Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys
 35 40 45
 tca tgc tgg ccc ttt tgg gtc cat ggg cca aag gtt cat gaa ggt ggc 612
 Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly
 50 55 60
 tct gcc tgt gag aca tca agc tcc tgg gtt gaa gga ctt gga tta aga 660
 Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg
 65 70 75 80
 aga gtg aca tca gtg cac agt tta tgc caa ggg ctt ggg gcc tca gtc 708
 Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val
 85 90 95
 cag ctt ctt cct gga cca cca cca aca aca acc agt gat aaa aat aat 756
 Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Thr Ser Asp Lys Asn Asn
 100 105 110
 tat act agt ggc tgacatttat ggattcttcc tacacactag gctataccac 808
 Tyr Thr Ser Gly
 115
 agcgagtgcc tcgaaaggaa atatagtata gcactgtgcc gtccaacatg gcggccacta 868
 gccacatgca ctactgagca cttgaaatgt ggctagccca cattgagatg tgctgtaa 928
 aaagaataga caccagattt ccaagactta gtacccaaaa aagaatgtaa aatttctcat 988
 taacaatttt ttttcttaca tttattacat gttaacatga cgctatttgg agtttaaata 1048
 aatgcattat taaaattcaa aaaaaaaaaa aaaaa 1083

 <210> 240
 <211> 1831
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 78..590

 <400> 240
 aaggacttaa gcgccccgga gccgggagggc gaacttggga cccgctggcc tcgctcggtg 60
 cgcgctcccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg 110
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
 1 5 10
 atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc 158
 Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
 15 20 25
 tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg 206
 Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
 30 35 40
 atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg 254
 Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
 45 50 55
 aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc 302
 Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
 60 65 70 75
 cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat 350
 Arg Val Trp Met Val Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn
 80 85 90
 ccc ggc tac tac cac cag ctt ctc cag gga gag aga aac ccc agg ctg 398
 Pro Gly Tyr Tyr His Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu
 95 100 105
 gag gac gcc atc agg aca gac ctg aac cgg acc ttc ccc gac aac gtg 446
 Glu Asp Ala Ile Arg Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val
 110 115 120

```

aag ttc cgg aag acc acg gac ccc tgc tta cag agg acc ctg tac aat      494
Lys Phe Arg Lys Thr Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn
      125                      130                      135
gtg ctg ctg gca tat ggg cac cat aac cag gga gtg ggc tac tgc cag      542
Val Leu Leu Ala Tyr Gly His His Asn Gln Gly Val Gly Tyr Cys Gln
      140                      145                      150                      155
gga atg aat ttt ata gca gga tat ctg att ctt ata aca aat aat gaa      590
Gly Met Asn Phe Ile Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
      160                      165                      170
taagaatctt tttggctgtt agatgctctt gttggaagaa tactaccaga ttactacagc      650
ccggccatgc tgggcctgaa gaccgaccag gaggtcctcg gggagctggt gcgggcgaag      710
ctgccggctg tgggggccct gatggagcgt ctccgtgtgc tgtggacgct gctggtgtcc      770
cgctggttca tctgcctgtt tgtggacatc ttgccctgtg agacagtgtc tcggatctgg      830
gactgtttgt ttaacgaagg ctccaagatt atcttccggt tggccctgac ctttaattaag      890
cagcaccagg agttgatttt ggaagccacc agcgttccag acatttgca taagttaaag      950
cagataacca aagggagttt cgtgatggag tgtcacacgt ttatgcagggt gtgtggggct 1010
gcacgtggct cagtcccctc ccagggggcc ccgcctcacc tgcagcccg gggctgtctc 1070
gaccaccgag aggatgcaca ggatgggcac cagtgggcat agggcacagg atgagcctcc 1130
agetctgttc tgcacgtgcc ccctgcgcct ggctcccgag ggctttcctg tctatggcgg 1190
ccctgtcttc ttggccctgg cactgcggac gctgctcctg gtcctaattg ctgtactcat 1250
ctgctgtgtg tggtgccaga agtgtggctt ccgaggccc ggctcccca ctgggtcctg 1310
gacctggcgc aggcctgata gactcaggtc ctgatgaggg cgttgtggga gctgtacctg 1370
acaggccttc tgaggaagcc aagacgccag gagaggctca ggctgggag tcagtagttt 1430
cctaagaggg agtggaggct cggggccact ctgggtgcag catggcaaac gtgggcggta 1490
tttcagcagc tgggccttca tcaaagagaa gaccatgttg gccgggcgcg gtggctcacg 1550
cctgcagtc cagcactttg ggaggccaag gcgtgtggat cacctgaggt caggagttca 1610
agaccagcct ggccaacacg gtgaaacccc gtctctacta aaaaatacaa aaattagcca 1670
ggtgtggtgg ctacgcctta tgtagtccca gttactcggg aggctgaggc acgagaatca 1730
cttgaacctg ggaggcggag gttgcagtga gccgagatcg cgccactgca ctccagcctg 1790
ggcaacagag tgagactctg tctcaaaaaa aaaaaaaaaa a      1831

<210> 241
<211> 1830
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..608

<400> 241
aaggacttaa gcgccccgga gccgggaggc gaacttggga cccgctggcc tcgctcgggtg      60
cgcgccctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg      110
Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
      1                      5                      10
atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc      158
Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
      15                      20                      25
tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg      206
Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
      30                      35                      40
atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg      254
Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
      45                      50                      55
aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc      302
Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
      60                      65                      70                      75
cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat      350

```

| | | | | | | | | | | | | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|------|--|
| Arg | Val | Trp | Met | Val | Leu | Ser | Gly | Ala | Gln | Ala | Gln | Met | Asp | Gln | Asn | | |
| | | | | 80 | | | | | 85 | | | | | 90 | | | |
| ccc | ggc | tac | tac | cac | cag | ctt | ctc | cag | gga | gag | aga | aac | ccc | agg | ctg | 398 | |
| Pro | Gly | Tyr | Tyr | His | Gln | Leu | Leu | Gln | Gly | Glu | Arg | Asn | Pro | Arg | Leu | | |
| | | | | 95 | | | | 100 | | | | | 105 | | | | |
| gag | gac | gcc | atc | agg | aca | gac | ctg | aac | cgg | acc | ttc | ccc | gac | aac | gtg | 446 | |
| Glu | Asp | Ala | Ile | Arg | Thr | Asp | Leu | Asn | Arg | Thr | Phe | Pro | Asp | Asn | Val | | |
| | | | | 110 | | | 115 | | | | | 120 | | | | | |
| aag | ttc | cgg | aag | acc | acg | gac | ccc | tgc | tta | cag | agg | acc | ctg | tac | aat | 494 | |
| Lys | Phe | Arg | Lys | Thr | Thr | Asp | Pro | Cys | Leu | Gln | Arg | Thr | Leu | Tyr | Asn | | |
| | | | | 125 | | | 130 | | | | | 135 | | | | | |
| gtg | ctg | ctg | gca | tat | ggg | cac | cat | aac | cag | gga | gtg | ggc | tac | tgc | cag | 542 | |
| Val | Leu | Leu | Ala | Tyr | Gly | His | His | Asn | Gln | Gly | Val | Gly | Tyr | Cys | Gln | | |
| | | | | 140 | | | 145 | | | 150 | | | | | 155 | | |
| gga | atg | aat | ttt | ata | gca | gga | tat | ctg | att | ctt | ata | aca | aat | aat | gat | 590 | |
| Gly | Met | Asn | Phe | Ile | Ala | Gly | Tyr | Leu | Ile | Leu | Ile | Thr | Asn | Asn | Asp | | |
| | | | | 160 | | | | 165 | | | | | 170 | | | | |
| aag | aat | ctt | ttt | ggc | tgt | tagatgctct | tggttgaaga | atactaccag | | | | | | | | 638 | |
| Lys | Asn | Leu | Phe | Gly | Cys | | | | | | | | | | | | |
| | | | | 175 | | | | | | | | | | | | | |
| attactacag | cccgcccatg | ctgggcctga | agaccgacca | ggaggtcctc | ggggagctgg | | | | | | | | | | | 698 | |
| tgcgggcgaa | gctgccggct | gtggggggccc | tgatggagcg | tctcgggtgtg | ctgtggacgc | | | | | | | | | | | 758 | |
| tgctggtgtc | ccgctggttc | atctgcctgt | ttgtggacat | cttgcccgtg | gagacagtgc | | | | | | | | | | | 818 | |
| ttcggatctg | ggactgtttg | tttaacgaag | gctcgaagat | tatcttccgg | ttggccctga | | | | | | | | | | | 878 | |
| ccttaattaa | gcagcaccag | gagttgattt | tggaagccac | cagcgttcca | gacatttgcg | | | | | | | | | | | 938 | |
| ataagtttaa | gcagataacc | aaagggagtt | tcgtgatgga | gtgtcacacg | tttatgcagg | | | | | | | | | | | 998 | |
| tgtgtggggc | tgacagtggc | tcagtcacct | cccagggggc | cccgcctcac | ctgcagcccg | | | | | | | | | | | 1058 | |
| ggggctgctc | tgaccaccgc | gaggatgcac | aggatgggca | ccagtgggca | tagggcacag | | | | | | | | | | | 1118 | |
| gatgagcctc | cagctctgtc | ctgcacctgc | cccctgcgcc | tggcctccga | gggctttcct | | | | | | | | | | | 1178 | |
| gtctatggcg | gcctgtgctt | cttggccctg | gcactgcgga | cgtgctcct | ggtcctaattg | | | | | | | | | | | 1238 | |
| gctgtactca | tctgctgtgt | gtgggtgccag | aagtgtggct | tcccagaggcc | cggcctcccc | | | | | | | | | | | 1298 | |
| actgggtcct | ggacctggcg | caggccgtat | agactcaggt | cctgatgagg | gcgttgtggg | | | | | | | | | | | 1358 | |
| agctgtacct | gacaggcctt | ctgaggaagc | caagacgcc | ggagaggctc | aggcctggga | | | | | | | | | | | 1418 | |
| gtcagtagtt | tcctaagagg | gagtgagggc | tcggggccac | tctgggtgca | gcatggcaaa | | | | | | | | | | | 1478 | |
| cgtgggcggg | atttcagcag | ctgggccttc | atcaaagaga | agaccatgtt | ggccgggcgc | | | | | | | | | | | 1538 | |
| ggtggctcac | gcctgcagtc | ccagcacttt | gggaggccaa | ggcgtgtgga | tcacctgagg | | | | | | | | | | | 1598 | |
| tcaggagttc | aagaccagcc | tggccaacac | ggtgaaaccc | cgtctctact | aaaaaataca | | | | | | | | | | | 1658 | |
| aaaattagcc | aggtgtggtg | gctcacgctt | atgtagtccc | agttactcgg | gaggctgagg | | | | | | | | | | | 1718 | |
| cacgagaatc | acttgaacct | gggaggcgga | ggttgagctg | agccgagatc | gcgccactgc | | | | | | | | | | | 1778 | |
| actccagcct | gggcaacaga | gtgagactct | gtctcaaaaa | aaaaaaaaaa | aa | | | | | | | | | | | 1830 | |

<210> 242
 <211> 508
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 242
 Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu
 -25 -20 -15
 Leu Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro
 -10 -5 1 5
 Pro Ala Leu Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp
 10 15 20
 Glu Phe Val Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser

<210> 243
 <211> 331
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 243
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
 50 55 60 65
 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
 70 75 80
 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
 85 90 95
 Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
 100 105 110
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Met Glu Ala
 115 120 125
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
 130 135 140 145
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
 150 155 160
 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
 165 170 175
 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu
 180 185 190
 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
 195 200 205
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
 210 215 220 225
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
 230 235 240
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
 245 250 255
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
 260 265 270
 Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
 275 280 285
 Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 290 295 300

<210> 244
 <211> 274
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 244

```

Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
      -15              -10              -5
Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
  1          5          10          15
Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
      20          25          30
Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Ala
      35          40          45
Ala Ala Phe Phe Ile Thr Tyr Glu Tyr Val Lys Trp Phe Leu His Ala
      50          55          60
Asp Ser Ser Ser Tyr Leu Thr Pro Met Lys His Met Leu Ala Ala Ser
      65          70          75
Ala Gly Glu Val Val Ala Cys Leu Ile Arg Val Pro Ser Glu Val Val
  80          85          90          95
Lys Gln Arg Ala Gln Val Ser Ala Ser Thr Arg Thr Phe Gln Ile Phe
      100          105          110
Ser Asn Ile Leu Tyr Glu Glu Gly Ile Gln Gly Leu Tyr Arg Gly Tyr
      115          120          125
Lys Ser Thr Val Leu Arg Glu Ile Pro Phe Ser Leu Val Gln Phe Pro
      130          135          140
Leu Trp Glu Ser Leu Lys Ala Leu Trp Ser Trp Arg Gln Asp His Val
      145          150          155
Val Asp Ser Trp Gln Ser Ala Val Cys Gly Ala Phe Ala Gly Gly Phe
  160          165          170          175
Ala Ala Ala Val Thr Thr Pro Leu Asp Val Ala Lys Thr Arg Ile Met
      180          185          190
Leu Ala Lys Ala Gly Ser Ser Thr Ala Asp Gly Asn Val Leu Ser Val
      195          200          205
Leu His Gly Val Trp Arg Ser Gln Gly Leu Ala Gly Leu Phe Ala Gly
      210          215          220
Val Phe Pro Arg Met Ala Ala Ile Ser Leu Gly Gly Phe Ile Phe Leu
      225          230          235
Gly Ala Tyr Asp Arg Thr His Ser Leu Leu Leu Glu Val Gly Arg Lys
  240          245          250          255
Ser Pro

```

<210> 245
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 245

```

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro
-35          -30          -25          -20
Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
      -15          -10          -5
Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
  1          5          10
Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

```


Pro Ser Ala Ser Val Ile Arg Thr
1 5

<210> 247
<211> 348
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29...-1

<400> 247
Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met
-25 -20 -15
Leu Leu Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His
-10 -5 1
Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr
5 10 15
Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala
20 25 30 35
Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln
40 45 50
Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln
55 60 65
Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn
70 75 80
Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser
85 90 95
Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met
100 105 110 115
Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu
120 125 130
Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val
135 140 145
Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe
150 155 160
Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp
165 170 175
Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser
180 185 190 195
Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
200 205 210
Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser
215 220 225
Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys
230 235 240
Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys
245 250 255
Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln
260 265 270 275
Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val
280 285 290
Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu
295 300 305
Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
310 315

<210> 248
 <211> 397
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 248
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
 15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
 95 100 105
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
 110 115 120
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
 125 130 135 140
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
 145 150 155
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
 160 165 170
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val
 175 180 185
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser Pro
 190 195 200
 Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp Glu
 205 210 215 220
 Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser Val
 225 230 235
 Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr Leu
 240 245 250
 Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr Glu
 255 260 265
 Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala Arg
 270 275 280
 Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile Lys
 285 290 295 300
 Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys Ile
 305 310 315
 Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg Glu
 320 325 330
 Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile Lys
 335 340 345

Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
 350 355 360

<210> 249
 <211> 403
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 249
 Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
 -20 -15 -10
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly
 -5 1 5 10
 Val Leu Phe Cys Thr Ile Leu Leu Leu Trp Val Ser Val Phe Leu
 15 20 25
 Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
 30 35 40
 Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
 45 50 55
 Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
 60 65 70 75
 Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
 80 85 90
 Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
 95 100 105
 Thr Ile Ser Cys Tyr Thr Arg Gly Arg Ile Ile Ser Thr Ser Ser
 110 115 120
 Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
 125 130 135
 Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
 140 145 150 155
 Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Val
 160 165 170
 Ser Glu Tyr Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys
 175 180 185
 Arg Ile Gln Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr
 190 195 200
 Gly Leu Arg Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile
 205 210 215
 Gly Val Ala Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser
 220 225 230 235
 Tyr Met Gln Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser
 240 245 250
 Leu Gln Val Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln
 255 260 265
 Arg Arg Ile Ser Ala His Gln Pro Gly Ala Gly Pro Glu Gly Gln Glu
 270 275 280
 Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu
 285 290 295
 Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu Glu Lys Pro Asp
 300 305 310 315
 Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu Pro Glu Ala Ser Asp
 320 325 330
 Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu Thr Glu Ala Asn Leu

335 340 345
 Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu
 350 355 360
 Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys
 365 370 375
 Ser Ser Ser
 380

<210> 250
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 250
 Met Pro His Leu Met Glu Arg Met Val Gly Ser Gly Leu Leu Trp Leu
 -25 -20 -15
 Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser Ala Val Gln Arg Gly
 -10 -5 1 5
 Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly Leu Asp Leu Asp Cys
 10 15 20
 Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys Phe Asp Pro Cys Gln
 25 30 35
 Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr Arg Arg Gly Ala Gln
 40 45 50
 Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr Ala Gly Phe Leu Val
 55 60 65 70
 Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu Ala Trp Leu Phe
 75 80 85

<210> 251
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 251
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
 -15 -10 -5
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1 5 10 15
 Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys Ala Gly Gly Phe His Gly
 20 25 30
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Gly
 35 40 45
 Cys Leu Pro Asp Ser Ser Ser Ile
 50 55

<210> 252
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 252
 Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu
 -15 -10 -5 1
 Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala
 5 10 15
 Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala
 20 25 30
 Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser
 35 40 45
 Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu
 50 55 60 65
 Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu
 70 75 80
 Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly
 85 90 95
 Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu
 100 105 110
 Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala
 115 120

<210> 253
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<220>
 <221> UNSURE
 <222> 45
 <223> Xaa = Glu,Gln

<220>
 <221> UNSURE
 <222> 44
 <223> Xaa = Lys,Asn

<400> 253
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser Xaa Xaa Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Leu Arg Met Glu Gln Gln Ala Trp Ser
 50 55 60 65
 Trp Thr Leu Ser Leu Leu Leu Thr Gly Phe Leu Ser

70

75

<210> 254
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 254
 Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
 -20 -15 -10
 Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
 -5 1 5
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
 10 15 20
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
 25 30 35 40
 Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile
 45 50 55
 Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser
 60 65 70
 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro
 75 80 85
 Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val
 90 95 100
 Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe
 105 110 115 120
 Arg Arg Pro

<210> 255
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 255
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met
 65 70 75
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys
 80 85 90 95

Ser Lys Asp Tyr Phe Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr
 100 105 110
 Ala Gly Ala Arg Gln Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln
 115 120 125
 Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr
 130 135 140
 Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu
 145 150 155
 Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile
 160 165 170 175
 Gly Ser Gly Cys Asn Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly
 180 185 190
 Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly Trp Ile Leu Gly
 195 200 205
 Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala
 210 215 220
 Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp
 225 230 235
 Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr
 240 245 250 255
 Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser
 260 265 270
 Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His
 275 280 285
 Pro Val Ser Thr Ile Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val
 290 295 300
 Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu
 305 310 315
 Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser
 320 325 330 335
 Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu
 340 345

<210> 256
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 256
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met
 65 70 75
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val

<400> 258

Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
-20 -15 -10 -5
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
1 5 10
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
15 20 25
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
30 35 40
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
45 50 55 60
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
65 70 75
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
80 85 90
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
95 100 105
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
110 115 120
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
125 130 135 140
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
145 150 155
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
160 165 170
Asp Cys Asp Cys Glu Gln Cys Cys
175 180

<210> 259

<211> 394

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39..-1

<400> 259

Met Ala Thr Ala Gln Leu Gln Arg Thr Pro Met Ser Ala Leu Val Phe
-35 -30 -25
Pro Asn Lys Ile Ser Thr Glu His Gln Ser Leu Val Leu Val Lys Arg
-20 -15 -10
Leu Leu Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe
-5 1 5
Pro Glu Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys
10 15 20 25
Ile Leu Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys
30 35 40
Trp Ile Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met
45 50 55
Val Val Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser
60 65 70
Glu Cys Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met
75 80 85
Asp Phe Ile Ser Lys Asn Gln Ser Asn Glu Ser Ser Met Leu Ser Thr
90 95 100 105
Asp Thr Lys Lys Ala Ser Ile Leu Leu Ile Arg Lys Ile Tyr Ile Leu
110 115 120

```

Met Gln Asn Leu Gly Pro Leu Pro Asn Asp Val Cys Leu Thr Met Lys
      125                      130                      135
Leu Phe Tyr Tyr Asp Glu Val Thr Pro Pro Asp Tyr Gln Pro Pro Gly
      140                      145                      150
Phe Lys Asp Gly Asp Cys Glu Gly Val Ile Phe Glu Gly Glu Pro Met
      155                      160                      165
Tyr Leu Asn Val Gly Glu Val Ser Thr Pro Phe His Ile Phe Lys Val
      170                      175                      180                      185
Lys Val Thr Thr Glu Arg Glu Arg Met Glu Asn Ile Asp Ser Thr Ile
      190                      195                      200
Leu Ser Pro Lys Gln Ile Lys Thr Pro Phe Gln Lys Ile Leu Arg Asp
      205                      210                      215
Lys Asp Val Glu Asp Glu Gln Glu His Tyr Thr Ser Asp Asp Leu Asp
      220                      225                      230
Ile Glu Thr Lys Met Glu Glu Gln Glu Lys Asn Pro Ala Ser Ser Glu
      235                      240                      245
Leu Glu Glu Pro Ser Leu Val Cys Glu Glu Asp Glu Ile Met Arg Ser
      250                      255                      260                      265
Lys Glu Ser Pro Asp Leu Ser Ile Ser His Ser Gln Val Glu Gln Leu
      270                      275                      280
Val Asn Lys Thr Ser Glu Leu Asp Met Ser Glu Ser Lys Thr Arg Ser
      285                      290                      295
Gly Lys Val Phe Gln Asn Lys Met Ala Asn Gly Asn Gln Pro Val Lys
      300                      305                      310
Ser Ser Lys Glu Asn Arg Lys Arg Ser Gln His Glu Ser Gly Arg Ile
      315                      320                      325
Val Leu His His Phe Asp Ser Ser Ser Gln Glu Ser Val Pro Lys Arg
      330                      335                      340                      345
Arg Lys Phe Ser Glu Pro Lys Glu His Ile
      350                      355

```

```

<210> 260
<211> 158
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -17..-1

```

```

<400> 260
Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly
      -15                      -10                      -5
Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met
      1                      5                      10                      15
Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala
      20                      25                      30
Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr
      35                      40                      45
Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr
      50                      55                      60
Arg Val Val Ser Glu Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe
      65                      70                      75
Thr Pro Arg Asn Ile Asp His Asp Pro Gln Glu Ile His Leu Glu Cys
      80                      85                      90                      95
Ser Thr Ser Arg Lys Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn
      100                      105                      110
Glu Ile Lys Leu Asp Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr

```


1 5 10
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 15 20 25
 Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu
 30 35 40
 Glu Pro Ser
 45

<210> 263
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 263
 Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser
 -25 -20 -15 -10
 His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro
 -5 1 5
 Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg
 10 15 20
 Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser
 25 30 35
 Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro
 40 45 50 55
 Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
 60 65

<210> 264
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 264
 Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys
 -15 -10 -5
 Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg
 1 5 10
 Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln
 15 20 25
 Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn
 30 35 40 45
 Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys
 50 55 60
 Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu
 65 70 75
 Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln
 80 85 90
 Leu Leu Arg Gln Glu His Glu Arg Leu Gln Lys Ile Ser Leu Glu
 95 100 105
 His Leu Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val

110 115 120 125
 Glu Pro Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser
 130 135 140
 Ser Cys Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155

<210> 265
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 265
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly
 -15 -10 -5
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met
 1 5 10 15
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala
 20 25 30
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr
 35 40 45
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr
 50 55 60
 Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys Met Phe Cys Gln
 65 70 75
 Thr Phe Met Pro Ser Ile Lys Ile Val Phe
 80 85

<210> 266
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 266
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
 -15 -10 -5
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 1 5 10
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 15 20 25 30
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 35 40 45
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 50 55 60
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
 65 70 75
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Ser Leu Ala
 80 85 90
 Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
 95 100 105

<210> 267
 <211> 261
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 267
 Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly Pro Pro Ile Ser Ser
 -15 -10 -5
 Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe Ser Arg Ala Thr Ser
 1 5 10 15
 Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr Glu Ala Ser Ser Pro
 20 25 30
 Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile Ile Val Arg Gln Gly
 35 40 45
 Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser Leu Gly Asp Thr Gln
 50 55 60
 His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile Tyr Arg Pro Trp Phe
 65 70 75 80
 Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys Glu Ser Gln Leu Glu
 85 90 95
 Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu Gly Lys Trp Asp Asn
 100 105 110
 Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys Ser Ser Ser Ser
 115 120 125
 Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys Lys Ser Arg His Gly
 130 135 140
 Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met Ala Ser Arg Trp His
 145 150 155 160
 Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala Cys Cys Arg Met Tyr
 165 170 175
 Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys Arg Gly Phe Arg Glu
 180 185 190
 Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu Lys Ala Leu Trp Ser
 195 200 205
 Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu Ser Ser Gly Ser Cys
 210 215 220
 Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg Gln Ile Gly Gly Glu
 225 230 235 240
 Ala Tyr Leu Cys Leu
 245

<210> 268
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 268
 Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu
 -25 -20 -15 -10
 Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | -5 | | | | | 1 | | | | 5 | | | | |
| Ser | Phe | Phe | Arg | Ala | Asp | Tyr | Asp | Leu | Ala | Ser | Arg | Ser | Ala | Asp | Gln | | |
| | | 10 | | | | | 15 | | | | | 20 | | | | | |
| Ser | Ser | Gln | Lys | Val | Lys | Leu | Arg | Met | Phe | Thr | Gly | Arg | Leu | Pro | Ile | | |
| | 25 | | | | | 30 | | | | | 35 | | | | | | |
| Gly | Pro | Phe | Ala | Ser | Val | Gly | Asn | Ala | Ala | Glu | Leu | | | | | | |
| 40 | | | | | 45 | | | | | 50 | | | | | | | |

<210> 269
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 269

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Glu | Thr | Phe | Pro | Leu | Leu | Leu | Ser | Leu | Gly | Leu | Val | Leu | Ala | | | |
| | -15 | | | | | -10 | | | | -5 | | | | | | | |
| Glu | Ala | Ser | Glu | Ser | Thr | Met | Lys | Ile | Ile | Lys | Glu | Glu | Phe | Thr | Asp | | |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | | | |
| Glu | Glu | Met | Gln | Tyr | Asp | Met | Ala | Lys | Ser | Gly | Gln | Glu | Lys | Gln | Thr | | |
| | | | 20 | | | | 25 | | | | | 30 | | | | | |
| Ile | Glu | Ile | Leu | Met | Asn | Pro | Ile | Leu | Leu | Val | Lys | Asn | Thr | Ser | Leu | | |
| | 35 | | | | | 40 | | | | | 45 | | | | | | |
| Ser | Met | Ser | Lys | Asp | Asp | Met | Ser | Ser | Thr | Leu | Leu | Thr | Phe | Arg | Ser | | |
| | 50 | | | | 55 | | | | | 60 | | | | | | | |
| Leu | His | Tyr | Asn | Asp | Pro | Lys | Gly | Asn | Ser | Ser | Gly | Asn | Asp | Lys | Glu | | |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | | | |
| Cys | Cys | Asn | Asp | Met | Thr | Val | Trp | Arg | Lys | Val | Ser | Glu | Ala | Asn | Gly | | |
| | | | 85 | | | | | 90 | | | | | 95 | | | | |
| Ser | Cys | Lys | Trp | Ser | Asn | Asn | Phe | Ile | Arg | Ser | Ser | Thr | Glu | Val | Met | | |
| | | | 100 | | | | 105 | | | | | | 110 | | | | |
| Arg | Arg | Val | His | Arg | Ala | Pro | Ser | Cys | Lys | Phe | Val | Gln | Asn | Pro | Gly | | |
| | 115 | | | | | 120 | | | | | | 125 | | | | | |
| Ile | Ser | Cys | Cys | Glu | Ser | Leu | Glu | Leu | Glu | Asn | Thr | Val | Cys | Gln | Phe | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| Thr | Thr | Gly | Lys | Gln | Phe | Pro | Arg | Cys | Gln | Tyr | His | Ser | Val | Thr | Ser | | |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | | | |
| Leu | Glu | Lys | Ile | Leu | Thr | Val | Leu | Thr | Gly | His | Ser | Leu | Met | Ser | Trp | | |
| | | | 165 | | | | | 170 | | | | | 175 | | | | |
| Leu | Val | Cys | Gly | Ser | Lys | Leu | | | | | | | | | | | |
| | | | 180 | | | | | | | | | | | | | | |

<210> 270
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 270

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ala | Ser | Val | Val | Pro | Val | Lys | Asp | Lys | Lys | Leu | Leu | Glu | Val | Lys | | |
| | -35 | | | | | -30 | | | | | -25 | | | | | | |
| Leu | Gly | Glu | Leu | Pro | Ser | Trp | Ile | Leu | Met | Arg | Asp | Phe | Ser | Pro | Ser | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| -20 | | | | | -15 | | | | | -10 | | | | | -5 |
| Gly | Ile | Phe | Gly | Ala | Phe | Gln | Arg | Gly | Tyr | Tyr | Arg | Tyr | Tyr | Asn | Lys |
| | | | | 1 | | | | 5 | | | | | 10 | | |
| Tyr | Ile | Asn | Val | Lys | Lys | Gly | Ser | Ile | Ser | Gly | Ile | Thr | Met | Val | Leu |
| | | 15 | | | | | 20 | | | | | 25 | | | |
| Ala | Cys | Tyr | Val | Leu | Phe | Ser | Tyr | Ser | Phe | Ser | Tyr | Lys | His | Leu | Lys |
| | 30 | | | | | 35 | | | | | 40 | | | | |
| His | Glu | Arg | Leu | Arg | Lys | Tyr | His | | | | | | | | |
| 45 | | | | | 50 | | | | | | | | | | |

<210> 271
 <211> 481
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 271

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Leu | Ala | Arg | Ala | Leu | Pro | Ser | Ile | Leu | Leu | Ala | Leu | Leu |
| -25 | | | | | -20 | | | | | -15 | | | | | -10 |
| Leu | Thr | Ser | Thr | Pro | Glu | Ala | Leu | Gly | Ala | Asn | Pro | Gly | Leu | Val | Ala |
| | | | | -5 | | | | 1 | | | | 5 | | | |
| Arg | Ile | Thr | Asp | Lys | Gly | Leu | Gln | Tyr | Ala | Ala | Gln | Glu | Gly | Leu | Leu |
| | 10 | | | | | 15 | | | | | 20 | | | | |
| Ala | Leu | Gln | Ser | Glu | Leu | Leu | Arg | Ile | Thr | Leu | Pro | Asp | Phe | Thr | Gly |
| | 25 | | | | 30 | | | | | 35 | | | | | |
| Asp | Leu | Arg | Ile | Pro | His | Val | Gly | Arg | Gly | Arg | Tyr | Glu | Phe | His | Ser |
| 40 | | | | | 45 | | | | | 50 | | | | | 55 |
| Leu | Asn | Ile | His | Ser | Cys | Glu | Leu | Leu | His | Ser | Ala | Leu | Arg | Pro | Val |
| | | | | 60 | | | | | 65 | | | | | 70 | |
| Pro | Gly | Gln | Gly | Leu | Ser | Leu | Ser | Ile | Ser | Asp | Ser | Ser | Ile | Arg | Val |
| | | 75 | | | | | 80 | | | | | | 85 | | |
| Gln | Gly | Arg | Trp | Lys | Val | Arg | Lys | Ser | Phe | Phe | Lys | Leu | Gln | Gly | Ser |
| | 90 | | | | | 95 | | | | | | 100 | | | |
| Phe | Asp | Val | Ser | Val | Lys | Gly | Ile | Ser | Ile | Ser | Val | Asn | Leu | Leu | Leu |
| | 105 | | | | | 110 | | | | | 115 | | | | |
| Gly | Ser | Asp | Ser | Ser | Gly | Arg | Pro | Thr | Val | Thr | Ala | Ser | Ser | Cys | Ser |
| 120 | | | | | 125 | | | | | 130 | | | | | 135 |
| Ser | Asp | Ile | Ala | Asp | Val | Glu | Val | Asp | Met | Ser | Gly | Asp | Leu | Gly | Trp |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Leu | Leu | Asn | Leu | Phe | His | Asn | Gln | Ile | Glu | Ser | Lys | Phe | Gln | Lys | Val |
| | | 155 | | | | | 160 | | | | | | 165 | | |
| Leu | Glu | Ser | Arg | Ile | Cys | Glu | Met | Ile | Gln | Lys | Ser | Val | Ser | Ser | Asp |
| | 170 | | | | | | 175 | | | | | 180 | | | |
| Leu | Gln | Pro | Tyr | Leu | Gln | Thr | Leu | Thr | Val | Thr | Thr | Glu | Ile | Asp | Ser |
| | 185 | | | | | 190 | | | | | 195 | | | | |
| Phe | Ala | Asp | Ile | Asp | Tyr | Ser | Leu | Val | Glu | Ala | Pro | Arg | Ala | Thr | Ala |
| 200 | | | | | 205 | | | | | 210 | | | | | 215 |
| Gln | Met | Leu | Glu | Val | Met | Phe | Lys | Gly | Glu | Ile | Phe | His | Arg | Asn | His |
| | | | | 220 | | | | | 225 | | | | | 230 | |
| Arg | Ser | Pro | Val | Thr | Leu | Leu | Ala | Ala | Val | Met | Ser | Leu | Pro | Glu | Glu |
| | | 235 | | | | | 240 | | | | | | 245 | | |
| His | Asn | Lys | Met | Val | Tyr | Phe | Ala | Ile | Ser | Asp | Tyr | Val | Phe | Asn | Thr |
| | 250 | | | | | | 255 | | | | | 260 | | | |
| Ala | Ser | Leu | Val | Tyr | His | Glu | Glu | Gly | Tyr | Leu | Asn | Phe | Ser | Ile | Thr |
| 265 | | | | | | 270 | | | | | 275 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asp | Met | Ile | Pro | Pro | Asp | Ser | Asn | Ile | Arg | Leu | Thr | Thr | Lys | Ser |
| 280 | | | | | 285 | | | | | 290 | | | | | 295 |
| Phe | Arg | Pro | Phe | Val | Pro | Arg | Leu | Ala | Arg | Leu | Tyr | Pro | Asn | Met | Asn |
| | | | 300 | | | | | | 305 | | | | | 310 | |
| Leu | Glu | Leu | Gln | Gly | Ser | Val | Pro | Ser | Ala | Pro | Leu | Leu | Asn | Phe | Ser |
| | | | 315 | | | | | 320 | | | | | 325 | | |
| Pro | Gly | Asn | Leu | Ser | Val | Asp | Pro | Tyr | Met | Glu | Ile | Asp | Ala | Phe | Val |
| | 330 | | | | | 335 | | | | | | 340 | | | |
| Leu | Leu | Pro | Ser | Ser | Ser | Lys | Glu | Pro | Val | Phe | Arg | Leu | Ser | Val | Ala |
| | 345 | | | | | 350 | | | | | 355 | | | | |
| Thr | Asn | Val | Ser | Ala | Thr | Leu | Thr | Phe | Asn | Thr | Ser | Lys | Ile | Thr | Gly |
| 360 | | | | | 365 | | | | | 370 | | | | | 375 |
| Phe | Leu | Lys | Pro | Gly | Lys | Val | Lys | Val | Glu | Leu | Lys | Glu | Ser | Lys | Val |
| | | | | 380 | | | | | 385 | | | | | 390 | |
| Gly | Leu | Phe | Asn | Ala | Glu | Leu | Leu | Glu | Ala | Leu | Leu | Asn | Tyr | Tyr | Ile |
| | | | 395 | | | | | 400 | | | | 405 | | | |
| Leu | Asn | Thr | Phe | Tyr | Pro | Lys | Phe | Asn | Asp | Lys | Leu | Ala | Glu | Gly | Phe |
| | 410 | | | | | | 415 | | | | | 420 | | | |
| Pro | Leu | Pro | Leu | Leu | Lys | Arg | Val | Gln | Leu | Tyr | Asp | Leu | Gly | Leu | Gln |
| | 425 | | | | | 430 | | | | | 435 | | | | |
| Ile | His | Lys | Asp | Phe | Leu | Phe | Leu | Gly | Ala | Asn | Val | Gln | Tyr | Met | Arg |
| 440 | | | | | 445 | | | | | 450 | | | | | 455 |
| Val | | | | | | | | | | | | | | | |

<210> 272
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43..-1

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Tyr | Gln | Gly | Glu | Val | Gln | Ser | Leu | Lys | Leu | Asp | Asp | Asp |
| | | | -40 | | | | | -35 | | | | | -30 | | |
| Ser | Val | Ile | Glu | Gly | Val | Ser | Asp | Gln | Val | Leu | Val | Ala | Val | Val | Val |
| | | -25 | | | | | -20 | | | | | -15 | | | |
| Ser | Phe | Ala | Leu | Ile | Ala | Thr | Leu | Val | Tyr | Ala | Leu | Phe | Arg | Asn | Val |
| | -10 | | | | -5 | | | | | 1 | | | | 5 | |
| His | Gln | Asn | Ile | His | Pro | Glu | Asn | Gln | Glu | Leu | Val | Arg | Val | Leu | Arg |
| | | | 10 | | | | | 15 | | | | | | 20 | |
| Glu | Gln | Leu | Gln | Thr | Glu | Gln | Asp | Ala | Pro | Ala | Ala | Thr | Arg | Gln | Gln |
| | | 25 | | | | | 30 | | | | | 35 | | | |
| Phe | Tyr | Thr | Asp | Met | Tyr | Cys | Pro | Ile | Cys | Leu | His | Gln | Ala | Ser | Phe |
| | 40 | | | | | 45 | | | | | 50 | | | | |
| Pro | Val | Glu | Thr | Asn | Cys | Gly | His | Leu | Phe | Cys | Gly | Ala | Cys | Ile | Ile |
| | 55 | | | | 60 | | | | | 65 | | | | | |
| Ala | Tyr | Trp | Arg | Tyr | Gly | Ser | Trp | Leu | Gly | Ala | Ile | Ser | Cys | Pro | Ile |
| 70 | | | | 75 | | | | | 80 | | | | | 85 | |
| Cys | Arg | Gln | Thr | Arg | His | Gly | His | Ile | Ala | Leu | Ser | Arg | Thr | Ala | |
| | | | 90 | | | | | 95 | | | | | | 100 | |

<210> 273
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 273

```
Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
1          5          10          15
Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
          20          25          30
Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
          35          40          45
His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
          50          55          60
Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val
65          70          75          80
Leu His
```

<210> 274

<211> 373

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 274

```
Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu
          -25          -20          -15
Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile
          -10          -5          1          5
Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro Gly Leu Arg Asp Phe Glu
          10          15          20
Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile Thr Asn Gly Ser Arg Ile
          25          30          35
Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr Tyr Gln Pro Gly Leu Leu
          40          45          50
Tyr Gly Gly Ser Val Glu His Asp Cys Ser Val Leu Arg Gly Ile Gly
          55          60          65
Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala Pro Phe Met Lys His Pro
70          75          80          85
Leu Lys Ile Val Leu Arg Gly Val Thr Asn Asp Gln Ile Asp Pro Ser
          90          95          100
Val Asp Val Leu Lys Ala Thr Ala Leu Pro Leu Leu Lys Gln Phe Gly
          105          110          115
Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile Val Arg Arg Gly Met Pro
          120          125          130
Pro Gly Gly Gly Gly Glu Val Val Phe Ser Cys Pro Val Arg Lys Val
          135          140          145
Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly Lys Ile Lys Arg Ile Arg
150          155          160          165
Gly Met Ala Tyr Ser Val Arg Val Ser Pro Gln Met Ala Asn Arg Ile
          170          175          180
Val Asp Ser Ala Arg Ser Ile Leu Asn Lys Phe Ile Pro Asp Ile Tyr
          185          190          195
Ile Tyr Thr Asp His Ile Lys Gly Val Asn Ser Gly Lys Ser Pro Gly
          200          205          210
Phe Gly Leu Ser Leu Val Ala Glu Thr Thr Ser Gly Thr Phe Leu Ser
          215          220          225
Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln Gly Ala Ala Val Leu Pro
230          235          240          245
Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu Leu Leu Glu Glu Ile Tyr
```

250 255 260
 Arg Gly Gly Cys Val Asp Ser Thr Asn Gln Ser Leu Ala Leu Leu Leu
 265 270 275
 Met Thr Leu Gly Gln Gln Asp Val Ser Lys Val Leu Leu Gly Pro Leu
 280 285 290
 Ser Pro Tyr Thr Ile Glu Phe Leu Arg His Leu Lys Ser Phe Phe Gln
 295 300 305
 Ile Met Phe Lys Ile Glu Thr Lys Pro Cys Gly Glu Glu Leu Lys Gly
 310 315 320 325
 Gly Asp Lys Val Leu Met Thr Cys Val Gly Ile Gly Phe Ser Asn Leu
 330 335 340
 Ser Arg Thr Leu Lys
 345

<210> 275
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 275
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly
 60 65

<210> 276
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 276
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
 -20 -15 -10 -5
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 1 5 10
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40
 Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55 60
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | 65 | | | | | 70 | | | | | 75 | | | |
| Lys | Cys | Leu | Gln | Thr | Thr | Glu | Glu | Pro | Pro | Ser | Arg | Thr | Ala | Gly | Ala | | |
| | | | 80 | | | | | 85 | | | | | 90 | | | | |
| Met | Met | Gln | Phe | Thr | Ala | Pro | Ile | Pro | Gly | Ala | Thr | Gly | Pro | Ile | Lys | | |
| | | 95 | | | | | 100 | | | | | 105 | | | | | |
| Leu | Ser | Gln | Lys | Thr | Ile | Val | Gln | Thr | Leu | Gly | Pro | Ile | Val | Gln | Tyr | | |
| | 110 | | | | 115 | | | | | | 120 | | | | | | |
| Pro | Gly | Ser | Asn | Gly | Arg | Ile | Asn | Ile | Ser | Gln | Leu | Thr | Ser | Glu | Asp | | |
| 125 | | | | 130 | | | | | | 135 | | | | | 140 | | |
| Leu | Thr | Gly | Ala | Lys | Gly | Arg | Val | Thr | Ser | Gly | Pro | Gln | Phe | Pro | Asn | | |
| | | | | 145 | | | | | | 150 | | | | | 155 | | |
| Ser | His | His | Val | Pro | Glu | Asn | Leu | His | Gly | Tyr | Met | Asn | Ser | Leu | Ser | | |
| | | | 160 | | | | | 165 | | | | | | 170 | | | |
| Leu | Phe | Ser | Pro | Ala | | | | | | | | | | | | | |
| | | | 175 | | | | | | | | | | | | | | |

<210> 277
 <211> 344
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 277

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Asp | Phe | Leu | Val | Leu | Phe | Leu | Phe | Tyr | Leu | Ala | Ser | Val | Leu | Met | | |
| | | | | -25 | | | | | -20 | | | | | | -15 | | |
| Gly | Leu | Val | Leu | Ile | Cys | Val | Cys | Ser | Lys | Thr | His | Ser | Leu | Lys | Gly | | |
| | | | -10 | | | | | -5 | | | | | 1 | | | | |
| Leu | Ala | Arg | Gly | Gly | Ala | Gln | Ile | Phe | Ser | Cys | Ile | Ile | Pro | Glu | Cys | | |
| | 5 | | | | 10 | | | | | 15 | | | | | | | |
| Leu | Gln | Arg | Ala | Val | His | Gly | Leu | Leu | His | Tyr | Leu | Phe | His | Thr | Arg | | |
| 20 | | | | 25 | | | | | 30 | | | | | 35 | | | |
| Asn | His | Thr | Phe | Ile | Val | Leu | His | Leu | Val | Leu | Gln | Gly | Met | Val | Tyr | | |
| | | | 40 | | | | | 45 | | | | | | 50 | | | |
| Thr | Glu | Tyr | Thr | Trp | Glu | Val | Phe | Gly | Tyr | Cys | Gln | Glu | Leu | Glu | Leu | | |
| | | | 55 | | | | | 60 | | | | | 65 | | | | |
| Ser | Leu | His | Tyr | Leu | Leu | Leu | Pro | Tyr | Leu | Leu | Leu | Gly | Val | Asn | Leu | | |
| | 70 | | | | 75 | | | | | | 80 | | | | | | |
| Phe | Phe | Phe | Thr | Leu | Thr | Cys | Gly | Thr | Asn | Pro | Gly | Ile | Ile | Thr | Lys | | |
| | 85 | | | | 90 | | | | | 95 | | | | | | | |
| Ala | Asn | Glu | Leu | Leu | Phe | Leu | His | Val | Tyr | Glu | Phe | Asp | Glu | Val | Met | | |
| 100 | | | | 105 | | | | | | 110 | | | | | 115 | | |
| Phe | Pro | Lys | Asn | Val | Arg | Cys | Ser | Thr | Cys | Asp | Leu | Arg | Lys | Pro | Ala | | |
| | | | 120 | | | | | | 125 | | | | | 130 | | | |
| Arg | Ser | Lys | His | Cys | Ser | Val | Cys | Asn | Trp | Cys | Val | His | Arg | Phe | Asp | | |
| | | | 135 | | | | | 140 | | | | | 145 | | | | |
| His | His | Cys | Val | Trp | Val | Asn | Asn | Cys | Ile | Gly | Ala | Trp | Asn | Ile | Arg | | |
| | 150 | | | | | 155 | | | | | | 160 | | | | | |
| Tyr | Phe | Leu | Ile | Tyr | Val | Leu | Thr | Leu | Thr | Ala | Ser | Ala | Ala | Thr | Val | | |
| | 165 | | | | 170 | | | | | 175 | | | | | | | |
| Ala | Ile | Val | Ser | Thr | Thr | Phe | Leu | Val | His | Leu | Val | Val | Met | Ser | Asp | | |
| 180 | | | | | 185 | | | | | 190 | | | | | 195 | | |
| Leu | Tyr | Gln | Glu | Thr | Tyr | Ile | Asp | Asp | Leu | Gly | His | Leu | His | Val | Met | | |
| | | | 200 | | | | | 205 | | | | | | 210 | | | |
| Asp | Thr | Val | Phe | Leu | Ile | Gln | Tyr | Leu | Phe | Leu | Thr | Phe | Pro | Arg | Ile | | |
| | | | 215 | | | | | 220 | | | | | | 225 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Met | Leu | Gly | Phe | Val | Val | Val | Leu | Ser | Phe | Leu | Leu | Gly | Gly |
| | | 230 | | | | | 235 | | | | | 240 | | | |
| Tyr | Leu | Leu | Phe | Val | Leu | Tyr | Leu | Ala | Ala | Thr | Asn | Gln | Thr | Thr | Asn |
| | 245 | | | | | 250 | | | | | 255 | | | | |
| Glu | Trp | Tyr | Arg | Gly | Asp | Trp | Ala | Trp | Cys | Gln | Arg | Cys | Pro | Leu | Val |
| 260 | | | | | 265 | | | | | 270 | | | | | 275 |
| Ala | Trp | Pro | Pro | Ser | Ala | Glu | Pro | Gln | Val | His | Arg | Asn | Ile | His | Ser |
| | | | | 280 | | | | | 285 | | | | | 290 | |
| His | Gly | Leu | Arg | Ser | Asn | Leu | Gln | Glu | Ile | Phe | Leu | Pro | Ala | Phe | Pro |
| | | 295 | | | | | | 300 | | | | | 305 | | |
| Cys | His | Glu | Arg | Lys | Lys | Gln | Glu | | | | | | | | |
| | | 310 | | | | | 315 | | | | | | | | |

<210> 278
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

| | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> | 278 | | | | | | | | | | | | | | |
| Met | Gly | Ser | Gln | Glu | Val | Leu | Gly | His | Ala | Ala | Arg | Leu | Ser | Ser | Ser |
| | | | -25 | | | | -20 | | | | | -15 | | | |
| Gly | Leu | Leu | Leu | Gln | Val | Leu | Phe | Arg | Leu | Ile | Thr | Phe | Val | Leu | Asn |
| | | -10 | | | | | -5 | | | | | 1 | | | |
| Ala | Phe | Ile | Leu | Arg | Phe | Leu | Ser | Lys | Glu | Ile | Val | Gly | Val | Val | Asn |
| 5 | | | | 10 | | | | | 15 | | | | | | 20 |
| Val | Arg | Leu | Thr | Leu | Leu | Tyr | Ser | Thr | Thr | Leu | Phe | Leu | Ala | Arg | Glu |
| | | | 25 | | | | | 30 | | | | | | 35 | |
| Ala | Phe | Arg | Arg | Ala | Cys | Leu | Ser | Gly | Gly | Thr | Gln | Arg | Asp | Trp | Ser |
| | | | 40 | | | | | 45 | | | | 50 | | | |
| Gln | Thr | Leu | Asn | Leu | Leu | Trp | Leu | Thr | Val | Pro | Leu | Gly | Val | Phe | Trp |
| | 55 | | | | | 60 | | | | | | 65 | | | |
| Ser | Leu | Phe | Leu | Gly | Trp | Ile | Trp | Leu | Gln | Leu | Leu | Glu | Val | Pro | Asp |
| | 70 | | | | | 75 | | | | 80 | | | | | |
| Pro | Asn | Val | Val | Pro | His | Tyr | Ala | Thr | Gly | Val | Val | Leu | Phe | Gly | Leu |
| 85 | | | | | 90 | | | | 95 | | | | | | 100 |
| Ser | Ala | Val | Val | Glu | Leu | Leu | Gly | Glu | Pro | Phe | Trp | Val | Leu | Ala | Gln |
| | | | | 105 | | | | 110 | | | | | | 115 | |
| Ala | His | Met | Phe | Val | Lys | Leu | Lys | Val | Ile | Ala | Glu | Ser | Leu | Ser | Val |
| | | | 120 | | | | | 125 | | | | | 130 | | |
| Ile | Leu | Lys | Thr | Val | Leu | Thr | Ala | Phe | Leu | Val | Leu | Trp | Leu | Pro | His |
| | 135 | | | | | | 140 | | | | | 145 | | | |
| Trp | Gly | Leu | Tyr | Ile | Phe | Ser | Leu | Ala | Gln | Leu | Phe | Tyr | Thr | Thr | Val |
| | 150 | | | | | 155 | | | | | 160 | | | | |
| Leu | Val | Leu | Cys | Tyr | Val | Ile | Tyr | Phe | Thr | Lys | Leu | Leu | Gly | Ser | Pro |
| 165 | | | | | 170 | | | | | 175 | | | | | 180 |
| Glu | Ser | Thr | Lys | Leu | Gln | Thr | Leu | Pro | Val | Ser | Arg | Ile | Thr | Asp | Leu |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Leu | Pro | Asn | Ile | Thr | Arg | Asn | Gly | Ala | Phe | Ile | Asn | Trp | Lys | Glu | Ala |
| | | 200 | | | | | 205 | | | | | | 210 | | |
| Lys | Leu | Thr | Trp | Ser | Phe | Phe | Lys | Gln | Ser | Phe | Leu | Lys | Gln | Ile | Leu |
| | 215 | | | | | | 220 | | | | | 225 | | | |
| Thr | Glu | Gly | Glu | Arg | Tyr | Val | Met | Thr | Phe | Leu | Asn | Val | Leu | Asn | Phe |
| | 230 | | | | | 235 | | | | | 240 | | | | |
| Gly | Asp | Gln | Gly | Val | Tyr | Asp | Ile | Val | Asn | Asn | Leu | Gly | Ser | Leu | Val |

```

245          250          255          260
Ala Arg Leu Ile Phe Gln Pro Ile Glu Glu Ser Phe Tyr Ile Phe Phe
          265          270          275
Ala Lys Val Leu Glu Arg Gly Lys Asp Ala Thr Leu Gln Lys Gln Glu
          280          285          290
Asp Val Ala Val Ala Ala Ala Val Leu Glu Ser Leu Leu Lys Leu Ala
          295          300          305
Leu Leu Ala Gly Leu Thr Ile Thr Val Phe Gly Phe Ala Tyr Ser Gln
          310          315          320
Leu Ala Leu Asp Ile Tyr Gly Gly Thr Met Leu Ser Ser Gly Ser Gly
          325          330          335          340
Pro Val Leu Leu Arg Ser Tyr Cys Leu Tyr Val Leu Leu Leu Ala Ile
          345          350          355
Asn Gly Val Thr Glu Cys Phe Thr Phe Ala Ala Met Ser Lys Glu Glu
          360          365          370
Val Asp Arg Tyr Asn Phe Val Met Leu Ala Leu Ser Ser Ser Phe Leu
          375          380          385
Val Leu Ser Tyr Leu Leu Thr Arg Trp Cys Gly Ser Val Gly Phe Ile
          390          395          400
Leu Ala Asn Cys Phe Asn Met Gly Ile Arg Ile Thr Gln Ser Leu Cys
          405          410          415          420
Phe Ile His Arg Tyr Tyr Arg Arg Ser Pro His Arg Pro Leu Ala Gly
          425          430          435
Leu His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly
          440          445          450
Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
          455          460          465
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
          470          475          480
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
          485          490          495          500
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
          505          510

```

```

<210> 279
<211> 267
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -24...-1

```

```

<400> 279
Met Ala Arg Phe Leu Thr Leu Cys Thr Trp Leu Leu Leu Leu Gly Pro
          -20          -15          -10
Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser Gln Asp Cys Ala Thr
          -5          1          5
Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile Asn Phe Leu Ala Cys
          10          15          20
Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu Lys Ile Trp Glu Thr
          25          30          35          40
Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp Leu Pro Gln Asp Gly
          45          50          55
Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu Glu Ser His Leu Leu
          60          65          70
Ala Lys Arg Tyr Gly Gly Phe Met Lys Arg Tyr Gly Gly Phe Met Lys
          75          80          85

```

Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu Glu Glu Ala Asn Gly
 90 95 100
 Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Lys Asp Ala
 105 110 115 120
 Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp Leu Leu Lys Glu Leu
 125 130 135
 Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His His Gln Asp Gly Ser
 140 145 150
 Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly Gly Phe Met Arg Gly
 155 160 165
 Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala Lys Glu Leu Gln Lys
 170 175 180
 Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Trp Met
 185 190 195 200
 Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys Arg Phe Ala Glu Ala
 205 210 215
 Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser Lys Glu Val Pro Glu
 220 225 230
 Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe
 235 240

<210> 280
 <211> 362
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40...-1

<400> 280
 Met Pro Phe Ala Tyr Phe Phe Thr Glu Ser Glu Gly Phe Ala Gly Ser
 -40 -35 -30 -25
 Arg Lys Gly Val Leu Gly Arg Val Tyr Glu Thr Val Val Met Leu Met
 -20 -15 -10
 Leu Leu Thr Leu Leu Val Leu Gly Met Val Trp Val Ala Ser Ala Ile
 -5 1 5
 Val Asp Lys Asn Lys Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu
 10 15 20
 Tyr Tyr Leu Pro Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu
 25 30 35 40
 Leu Leu Leu Val Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val
 45 50 55
 Thr Gly Lys Leu Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu
 60 65 70
 Gln Leu Tyr Cys Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile
 75 80 85
 Cys Asn Pro Thr Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu His
 90 95 100
 Arg Gln Val Leu Ala Leu Gln Thr Gln Arg Val Leu Leu Glu Lys Arg
 105 110 115 120
 Arg Lys Ala Ser Ala Trp Gln Arg Asn Leu Gly Tyr Pro Leu Ala Met
 125 130 135
 Leu Cys Leu Leu Val Leu Thr Gly Leu Ser Val Leu Ile Val Ala Ile
 140 145 150
 His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met
 155 160 165
 Gln Gly Thr Ser Leu Gly Gln Val Ser Phe Ser Lys Leu Gly Ser Phe

| | | | | |
|---|-----|-----|-----|-----|
| 170 | | 175 | | 180 |
| Gly Ala Val Ile Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser | | | | |
| 185 | | 190 | | 200 |
| Val Val Gly Phe Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg | | | | |
| | 205 | | 210 | 215 |
| Trp His Asp Thr Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu | | | | |
| | 220 | | 225 | 230 |
| Leu Val Leu Ser Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu | | | | |
| | 235 | | 240 | 245 |
| Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly | | | | |
| | 250 | | 255 | 260 |
| Asn Phe Tyr Ile Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr | | | | |
| 265 | | 270 | | 280 |
| Thr Leu Tyr Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu | | | | |
| | 285 | | 290 | 295 |
| Ile Arg Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe | | | | |
| | 300 | | 305 | 310 |
| Pro Gln Ala Ser Arg Lys Thr Gln His Gln | | | | |
| | 315 | | 320 | |

<210> 281
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

| |
|---|
| <400> 281 |
| Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr |
| -20 -15 -10 |
| Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln |
| -5 1 5 10 |
| Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys |
| 15 20 25 |
| Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln |
| 30 35 40 |
| Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys |
| 45 50 55 |
| Ser |
| 60 |

<210> 282
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

| |
|---|
| <400> 282 |
| Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser |
| -25 -20 -15 |
| Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn |
| -10 -5 1 |
| Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5 | | | | | 10 | | | | | 15 | | | | 20 | |
| Val | Arg | Leu | Thr | Leu | Leu | Tyr | Ser | Thr | Thr | Leu | Phe | Leu | Ala | Arg | Glu |
| | | | | 25 | | | | | 30 | | | | | 35 | |
| Ala | Phe | Arg | Arg | Ala | Cys | Leu | Ser | Gly | Gly | Thr | Gln | Arg | Asp | Trp | Ser |
| | | | 40 | | | | | 45 | | | | | 50 | | |
| Gln | Thr | Leu | Asn | Leu | Leu | Trp | Leu | Thr | Val | Pro | Leu | Gly | Val | Phe | Trp |
| | | 55 | | | | | 60 | | | | | 65 | | | |
| Ser | Leu | Phe | Leu | Gly | Trp | Ile | Trp | Leu | Gln | Leu | Leu | Glu | Val | Pro | Asp |
| | 70 | | | | | 75 | | | | 80 | | | | | |
| Pro | Asn | Val | Val | Pro | His | Tyr | Ala | Thr | Gly | Val | Val | Leu | Phe | Gly | Leu |
| 85 | | | | | 90 | | | | | 95 | | | | | 100 |
| Ser | Ala | Val | Val | Glu | Leu | Leu | Gly | Glu | Pro | Phe | Trp | Val | Leu | Ala | Gln |
| | | | | 105 | | | | 110 | | | | | | 115 | |
| Ala | His | Met | Phe | Val | Lys | Leu | Lys | Val | Ile | Ala | Glu | Ser | Leu | Ser | Val |
| | | | 120 | | | | | 125 | | | | | 130 | | |
| Ile | Leu | Lys | Ser | Val | Leu | Thr | Ala | Phe | Leu | Val | Leu | Trp | Leu | Pro | His |
| | | 135 | | | | | 140 | | | | | 145 | | | |
| Trp | Gly | Leu | Tyr | Ile | Phe | Ser | Leu | Ala | Gln | Leu | Phe | Tyr | Thr | Thr | Val |
| | 150 | | | | | 155 | | | | | 160 | | | | |
| Leu | Val | Leu | Cys | Tyr | Val | Ile | Tyr | Phe | Thr | Lys | Leu | Leu | Gly | Ser | Pro |
| 165 | | | | | 170 | | | | | 175 | | | | | 180 |
| Glu | Ser | Thr | Lys | Leu | Gln | Thr | Leu | Pro | Val | Ser | Arg | Ile | Thr | Asp | Leu |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Leu | Pro | Asn | Ile | Thr | Arg | Asn | Gly | Ala | Phe | Ile | Asn | Trp | Lys | Glu | Ala |
| | | 200 | | | | | 205 | | | | | | 210 | | |
| Lys | Leu | Thr | Trp | Ser | Phe | Phe | Lys | Gln | Ser | Phe | Leu | Lys | Gln | Ile | Leu |
| | 215 | | | | | | 220 | | | | | 225 | | | |
| Thr | Glu | Gly | Glu | Arg | Tyr | Val | Met | Thr | Phe | Leu | Asn | Val | Leu | Asn | Phe |
| | 230 | | | | | 235 | | | | | | 240 | | | |
| Gly | Asp | Gln | Gly | Val | Tyr | Asp | Ile | Val | Asn | Asn | Leu | Gly | Ser | Leu | Val |
| 245 | | | | | 250 | | | | | 255 | | | | | 260 |
| Ala | Arg | Leu | Ile | Phe | Gln | Pro | Ile | Glu | Glu | Ser | Phe | Tyr | Ile | Phe | Phe |
| | | | 265 | | | | | 270 | | | | | | 275 | |
| Ala | Lys | Val | Leu | Glu | Arg | Gly | Lys | Asp | Ala | Thr | Leu | Gln | Lys | Gln | Glu |
| | | 280 | | | | | | 285 | | | | | 290 | | |
| Asp | Val | Ala | Val | Ala | Ala | Ala | Val | Leu | Glu | Ser | Leu | Leu | Lys | Leu | Ala |
| | 295 | | | | | | 300 | | | | | 305 | | | |
| Leu | Leu | Ala | Gly | Leu | Thr | Ile | Thr | Val | Phe | Gly | Phe | Ala | Tyr | Ser | Gln |
| | 310 | | | | | 315 | | | | | 320 | | | | |
| Leu | Ala | Leu | Asp | Ile | Asn | Gly | Gly | Thr | Met | Leu | Ser | Ser | Gly | Ser | Gly |
| 325 | | | | | 330 | | | | | 335 | | | | | 340 |
| Pro | Val | Leu | Leu | Arg | Ser | Tyr | Cys | Leu | Tyr | Val | Leu | Leu | Leu | Ala | Ile |
| | | | | 345 | | | | | 350 | | | | | 355 | |
| Asn | Gly | Val | Thr | Glu | Cys | Phe | Thr | Phe | Ala | Ala | Met | Ser | Lys | Glu | Glu |
| | | 360 | | | | | | 365 | | | | | 370 | | |
| Val | Asp | Arg | Tyr | Asn | Phe | Val | Met | Leu | Ala | Leu | Ser | Ser | Ser | Phe | Leu |
| | 375 | | | | | | 380 | | | | | 385 | | | |
| Val | Leu | Ser | Tyr | Leu | Leu | Thr | Arg | Trp | Cys | Gly | Ser | Val | Gly | Phe | Ile |
| | 390 | | | | | 395 | | | | | 400 | | | | |
| Leu | Ala | Asn | Cys | Phe | Asn | Met | Gly | Ile | Arg | Ile | Thr | Gln | Ser | Leu | Cys |
| 405 | | | | | 410 | | | | | 415 | | | | | 420 |
| Phe | Ile | His | Arg | Tyr | Tyr | Arg | Arg | Ser | Pro | His | Arg | Pro | Leu | Ala | Gly |
| | | | 425 | | | | | 430 | | | | | | 435 | |
| Leu | His | Leu | Ser | Pro | Val | Leu | Leu | Gly | Thr | Phe | Ala | Leu | Ser | Gly | Gly |
| | | 440 | | | | | | 445 | | | | | 450 | | |
| Val | Thr | Ala | Val | Ser | Glu | Val | Phe | Leu | Cys | Cys | Glu | Gln | Gly | Trp | Pro |
| | 455 | | | | | 460 | | | | | 465 | | | | |
| Ala | Arg | Leu | Ala | His | Ile | Ala | Val | Gly | Ala | Phe | Cys | Leu | Gly | Ala | Thr |

| | | | | |
|---------------------|---------------------|-------------------------|--|-----|
| 470 | | 475 | | 480 |
| Leu Gly Thr Ala Phe | Leu Thr Glu Thr Lys | Leu Ile His Phe Leu Arg | | |
| 485 | 490 | 495 | | 500 |
| Thr Gln Leu Gly Val | Pro Arg Arg Thr Asp | Lys Met Thr | | |
| 505 | 510 | | | |

<210> 283
 <211> 468
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 283

| | |
|---|--|
| Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser | |
| -20 -15 -10 | |
| Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala | |
| -5 1 5 10 | |
| Val Asp Val Val Leu Asp Cys Phe Leu Val Lys Asp Gly Ala His Arg | |
| 15 20 25 | |
| Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu | |
| 30 35 40 | |
| Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp | |
| 45 50 55 | |
| Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu | |
| 60 65 70 75 | |
| Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His | |
| 80 85 90 | |
| Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe | |
| 95 100 105 | |
| Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala | |
| 110 115 120 | |
| Asn Val Gln Val Ser Gly Gly Gly Pro Ser Ile Ser Leu Val Met Lys | |
| 125 130 135 | |
| Thr Pro Arg Val Ala Lys Asn Glu Val Leu Trp His Pro Thr Leu Asn | |
| 140 145 150 155 | |
| Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln | |
| 160 165 170 | |
| Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala | |
| 175 180 185 | |
| Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser | |
| 190 195 200 | |
| Val Glu Trp Arg Leu Gln His Lys Gly Arg Gly Gln Leu Val Tyr Ser | |
| 205 210 215 | |
| Trp Thr Ala Gly Gln Gly Gln Ala Val Arg Lys Gly Ala Thr Leu Glu | |
| 220 225 230 235 | |
| Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly | |
| 240 245 250 | |
| Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser | |
| 255 260 265 | |
| Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro | |
| 270 275 280 | |
| Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile | |
| 285 290 295 | |
| Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr | |
| 300 305 310 315 | |

Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe
320 325 330
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser
335 340 345
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val
350 355 360
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val
365 370 375
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
380 385 390 395
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro
400 405 410
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
415 420 425
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val
430 435 440
Ser Gln Pro Ser
445

<210> 284
<211> 406
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 284
Met Val Arg Ile Gln Arg Arg Lys Leu Leu Ala Ser Cys Leu Cys Val
-30 -25 -20
Thr Ala Thr Val Phe Leu Leu Val Thr Leu Gln Ala Leu Asp Thr Val
-15 -10 -5 1
Glu Asn Leu Met Lys Val Thr Gly Pro Pro Gln Gly Val Thr Asp Ser
5 10 15
Met Gln Cys Phe Asn Asp Gln Trp Pro Leu Ser Asn Thr Arg Ser Ser
20 25 30
Glu His Ile Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys
35 40 45
Glu Phe Lys Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu
50 55 60 65
Ala Pro Thr His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe
70 75 80
Asn Arg Lys Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp
85 90 95
Trp Ser Pro Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala
100 105 110
Asp Ala Cys Phe Phe Thr Ile Asn Arg Thr Tyr Leu His His His Met
115 120 125
Thr Lys Ala Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu
130 135 140 145
Pro Leu Pro Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu
150 155 160
Ser Pro Lys Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu
165 170 175
Phe Asn Tyr Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr
180 185 190
Thr Gln Tyr Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu

| | | |
|-------------------------|---------------------|---------------------|
| 195 | 200 | 205 |
| Val Pro Leu Gln Ser Lys | Asn Lys Leu Arg Lys | Arg Leu Ala Pro Leu |
| 210 | 215 | 220 |
| Val Tyr Val Gln Ser Tyr | Cys Asp Pro Pro Ser | Asp Arg Asp Ser Tyr |
| | 230 | 235 |
| Val Arg Glu Leu Met Thr | Tyr Ile Glu Val Asp | Ser Tyr Gly Glu Cys |
| | 245 | 250 |
| Leu Arg Asn Lys Asp Leu | Pro Gln Gln Leu Lys | Asn Pro Ala Ser Met |
| | 260 | 265 |
| Asp Ala Asp Gly Phe Tyr | Arg Ile Ile Ala Gln | Tyr Lys Phe Ile Leu |
| | 275 | 280 |
| Ala Phe Glu Asn Ala Val | Cys Asp Asp Tyr Ile | Thr Glu Lys Phe Trp |
| 290 | 295 | 300 |
| Arg Pro Leu Lys Leu Gly | Val Val Pro Val Tyr | Tyr Gly Ser Pro Ser |
| | 310 | 315 |
| Ile Thr Asp Trp Leu Pro | Ser Asn Lys Ser Ala | Ile Leu Val Ser Glu |
| | 325 | 330 |
| Phe Ser His Pro Arg Glu | Leu Ala Ser Tyr Ile | Arg Arg Leu Asp Ser |
| | 340 | 345 |
| Asp Asp Arg Leu Tyr Glu | Ala Tyr Val Glu Trp | Lys Leu Lys Gly Arg |
| | 355 | 360 |
| Ser Leu Thr Ser Asp Phe | | |
| 370 | 375 | |

<210> 285
 <211> 305
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

| |
|---|
| <400> 285 |
| Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly |
| -25 -20 -15 |
| Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg |
| -10 -5 1 5 |
| Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu |
| 10 15 20 |
| Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe |
| 25 30 35 |
| Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly |
| 40 45 50 |
| Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg |
| 55 60 65 70 |
| Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu |
| 75 80 85 |
| Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly |
| 90 95 100 |
| Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val |
| 105 110 115 |
| Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His |
| 120 125 130 |
| Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala |
| 135 140 145 150 |
| Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu |
| 155 160 165 |

Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
 170 175 180
 Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
 185 190 195
 Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
 200 205 210
 Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
 215 220 225 230
 Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
 235 240 245
 Val Leu Val Leu Leu Cys Gly Pro Pro Met Val Gln Leu Ala Cys
 250 255 260
 His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
 265 270 275
 Tyr

<210> 286
 <211> 442
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<220>
 <221> UNSURE
 <222> 132
 <223> Xaa = Pro,Arg

<400> 286
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Met Gln Val Ser Gly Gly Gly Xaa Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Thr Lys Asn Glu Ala Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170
 Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala
 175 180 185
 Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Phe | Leu | Gly | Cys | Leu | Val | Asn | Leu | Gln | Ala | Gly | His | Tyr | Leu | Ala |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Met | Thr | Thr | Leu | Leu | Leu | Glu | Met | Ser | Thr | Pro | Phe | Thr | Cys | Val | Ser |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Trp | Met | Leu | Leu | Lys | Ala | Gly | Trp | Ser | Glu | Ser | Leu | Phe | Trp | Lys | Leu |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Asn | Gln | Trp | Leu | Met | Ile | His | Met | Phe | His | Cys | Arg | Met | Val | Leu | Thr |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Tyr | His | Met | Trp | Trp | Val | Cys | Phe | Trp | His | Trp | Asp | Gly | Leu | Val | Ser |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Ser | Leu | Tyr | Leu | Pro | His | Leu | Thr | Leu | Phe | Leu | Val | Gly | Leu | Ala | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Thr | Leu | Ile | Ile | Asn | Pro | Tyr | Trp | Thr | His | Lys | Lys | Thr | Gln | Gln |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Leu | Leu | Asn | Pro | Val | Asp | Trp | Asn | Phe | Ala | Gln | Pro | Glu | Ala | Lys | Ser |
| | | 210 | | | | 215 | | | | | 220 | | | | |
| Arg | Pro | Glu | Gly | Asn | Gly | Gln | Leu | Leu | Arg | Lys | Lys | Arg | Pro | | |
| 225 | | | | | 230 | | | | | 235 | | | | | |

<210> 288
 <211> 398
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 288

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asn | Asp | Pro | Pro | Val | Pro | Ala | Leu | Leu | Trp | Ala | Gln | Glu | Val |
| -20 | | | | | | -15 | | | | | -10 | | | | |
| Gly | Gln | Val | Leu | Ala | Gly | Arg | Ala | Arg | Arg | Leu | Leu | Leu | Gln | Phe | Gly |
| -5 | | | | | 1 | | | | 5 | | | | | 10 | |
| Val | Leu | Phe | Cys | Thr | Ile | Leu | Leu | Leu | Leu | Trp | Val | Ser | Val | Phe | Leu |
| | | | 15 | | | | | 20 | | | | | 25 | | |
| Tyr | Gly | Ser | Phe | Tyr | Tyr | Ser | Tyr | Met | Pro | Thr | Val | Ser | His | Leu | Ser |
| | | 30 | | | | 35 | | | | | | 40 | | | |
| Pro | Val | His | Phe | Tyr | Tyr | Arg | Thr | Asp | Cys | Asp | Ser | Ser | Thr | Thr | Ser |
| | | 45 | | | | 50 | | | | | 55 | | | | |
| Leu | Cys | Ser | Phe | Pro | Val | Ala | Asn | Val | Ser | Leu | Thr | Lys | Gly | Gly | Arg |
| 60 | | | | | 65 | | | | | 70 | | | | | 75 |
| Asp | Arg | Val | Leu | Met | Tyr | Gly | Gln | Pro | Tyr | Arg | Val | Thr | Leu | Glu | Leu |
| | | | 80 | | | | | 85 | | | | | | 90 | |
| Glu | Leu | Pro | Glu | Ser | Pro | Val | Asn | Gln | Asp | Leu | Gly | Met | Phe | Leu | Val |
| | | 95 | | | | | 100 | | | | | | 105 | | |
| Thr | Ile | Ser | Cys | Tyr | Thr | Arg | Gly | Gly | Arg | Ile | Ile | Ser | Thr | Ser | Ser |
| | | 110 | | | | | 115 | | | | | | 120 | | |
| Arg | Ser | Val | Met | Leu | His | Tyr | Arg | Ser | Asp | Leu | Leu | Gln | Met | Leu | Asp |
| | | 125 | | | | 130 | | | | | 135 | | | | |
| Thr | Leu | Val | Phe | Ser | Ser | Leu | Leu | Leu | Phe | Gly | Phe | Ala | Glu | Gln | Lys |
| 140 | | | | | 145 | | | | | 150 | | | | | 155 |
| Gln | Leu | Leu | Glu | Val | Glu | Leu | Tyr | Ala | Asp | Tyr | Arg | Glu | Asn | Ser | Tyr |
| | | | 160 | | | | | 165 | | | | | | 170 | |
| Val | Pro | Thr | Thr | Gly | Ala | Ile | Ile | Glu | Ile | His | Ser | Lys | Arg | Ile | Gln |
| | | 175 | | | | | 180 | | | | | | 185 | | |
| Leu | Tyr | Gly | Ala | Tyr | Leu | Arg | Ile | His | Ala | His | Phe | Thr | Gly | Leu | Arg |
| | | 190 | | | | 195 | | | | | | 200 | | | |
| Tyr | Leu | Leu | Tyr | Asn | Phe | Pro | Met | Thr | Cys | Ala | Phe | Ile | Gly | Val | Ala |

| | | | | |
|---|-----|-----|-----|-----|
| 205 | | 210 | | 215 |
| Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser Tyr Met Gln | | | | |
| 220 | | 225 | | 230 |
| Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser Leu Gln Val | | | | |
| | 240 | | 245 | 250 |
| Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln Arg Arg Ile | | | | |
| | 255 | | 260 | 265 |
| Ser Ala His Gln Pro Gly Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln | | | | |
| | 270 | | 275 | 280 |
| Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr | | | | |
| | 285 | | 290 | 295 |
| Glu Gly Gln Leu Ser Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser | | | | |
| 300 | | 305 | | 310 |
| Gly Glu Glu Glu Leu Glu Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp | | | | |
| | 320 | | 325 | 330 |
| Glu Asp Ala Ala Leu Leu Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro | | | | |
| | 335 | | 340 | 345 |
| Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu Gly Ser Ser Glu Pro | | | | |
| | 350 | | 355 | 360 |
| Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys Ser Ser Ser | | | | |
| 365 | | 370 | | 375 |

<210> 289
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

| |
|---|
| <400> 289 |
| Met Arg Gln Lys Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe |
| -20 -15 -10 -5 |
| Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser |
| 1 5 10 |
| Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly |
| 15 20 25 |
| Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala |
| 30 35 40 |
| Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala |
| 45 50 55 60 |
| Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu |
| 65 70 75 |
| Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly |
| 80 85 90 |
| Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp |
| 95 100 105 |
| Glu Glu |
| 110 |

<210> 290
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -20..-1

<400> 290

Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly
-20 -15 -10 -5
Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met
1 5 10
Ser Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu
15 20 25
Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile
30 35 40
Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp
45 50 55 60
Ser Glu Glu Asp Glu Glu
65

<210> 291

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23..-1

<400> 291

Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
-20 -15 -10
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
-5 1 5
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10 15 20 25
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
30 35 40
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
45 50 55
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
60 65 70
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
75 80 85
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90 95 100 105
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
110 115 120
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
125 130 135
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
140 145 150
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
155 160 165
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170 175 180

<210> 292

<211> 111

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 292
 Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser Phe Val Val Phe Ser
 -20 -15 -10
 Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val Val Tyr Ala Asp Ile
 -5 1 5
 Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala Phe Pro Leu Gln Arg
 10 15 20
 Ser Val Ser Phe Asn Phe Ser Thr Val His Lys Ser Cys Pro Ala Lys
 25 30 35 40
 Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp Ile Ala Glu Thr Lys
 45 50 55
 Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala Ile Asn Asn Ser Tyr
 60 65 70
 Leu Met Val Ile Gln Asp Ile Thr Ala Met Val Arg Phe Asn Ile
 75 80 85

<210> 293
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 293
 Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu
 -15 -10 -5 1
 Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys
 5 10 15
 Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val
 20 25 30
 Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met
 35 40 45
 Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp
 50 55 60 65
 Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe
 70 75 80
 Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys
 85 90 95
 Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr
 100 105 110
 Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
 115 120

<210> 294
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 294
Met Gln Arg Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu
-25 -20 -15
Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile
-10 -5 1 5
Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg
10 15 20
Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu
25 30 35
Ser Cys Val Glu Val Gln Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile
40 45 50
Ile Arg Phe Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile
55 60 65
Gly Leu Cys Leu Arg Val Lys Leu Gln Arg Cys Leu Pro Phe Lys His
70 75 80 85
Lys Leu Glu Ile Tyr Ile Ser Glu Gly Thr His Ser Thr Glu Glu Asp
90 95 100
Ile Asn Lys Gln Ile Asn Asp Lys Glu Arg Val Ala Ala Ala Met Glu
105 110 115
Asn Pro Asn Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp
120 125 130

<210> 295
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 295
Met Pro Pro Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser
-15 -10 -5
Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn
1 5 10 15
Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro
20 25 30
Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly
35 40 45
Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys
50 55 60
Gly Thr His Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly
65 70 75 80
Asp Gly Ile Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys
85 90 95
Cys Leu Trp Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr
100 105 110
Tyr Val Tyr Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys
115 120 125
Gly Arg Glu Tyr Leu Pro Cys Ala Leu Phe Leu His Gln Gln Gly His
130 135 140
Arg Trp Ser Pro Lys Val Pro Asn Tyr Arg Ile Cys Ser Tyr Ser Gly
145 150 155 160
Asn Tyr Ile Ser Ile
165

<210> 296

<211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 296
 Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser Ser
 -15 -10 -5
 Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser Ile Ala
 1 5 10
 Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val Leu Ile Thr
 15 20 25 30
 Cys Cys Ala Pro Gln Pro Pro Pro Pro Ile Thr Tyr Ser Leu Cys Gly
 35 40 45
 Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val Lys Thr His Glu Pro
 50 55 60
 Ala Ser Phe Asn Leu Asn Val Thr Leu Lys Ser Ser Pro Asp Leu Leu
 65 70 75
 Thr Tyr Phe Cys Arg Ala Ser Ser Thr Ser Gly Ala His Val Asp Ser
 80 85 90
 Ala Arg Leu Gln Met His Trp Glu Leu Trp Ser Lys Pro Val Ser Glu
 95 100 105 110
 Leu Arg Ala Asn Phe Thr Leu Gln Asp Arg Gly Ala Gly Pro Arg Val
 115 120 125
 Glu Met Ile Cys Gln Ala Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser
 130 135 140
 Leu Ile Gly Lys Asp Gly Gln Val His Leu Gln Gln Arg Pro Cys His
 145 150 155
 Arg Gln Pro Ala Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp
 160 165 170
 Phe Trp Cys Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu
 175 180 185 190
 Thr Val Val Pro Pro Gly Gly Leu Pro Arg Ala Pro Thr Ile Val Leu
 195 200 205
 Val Gly Ser Leu Ala Ser Thr Ala Ala Ile Thr Ser Arg Met Leu Gly
 210 215 220
 Trp Thr Thr Trp Ala Arg Trp
 225

<210> 297
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 297
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp
 -40 -35 -30
 Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser
 -25 -20 -15 -10
 Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly Tyr
 -5 1 5

Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg Asn
 10 15 20
 Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe Leu
 25 30 35
 Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile Ser
 40 45 50 55
 Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val Ser
 60 65 70
 Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu Gly
 75 80 85
 Cys Pro Gly Pro
 90

<210> 298
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 298
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
 -20 -15 -10
 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 -5 1 5
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 10 15 20
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 25 30 35 40
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 45 50 55
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 60 65 70
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 75 80 85
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 90 95 100
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 105 110 115 120
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 125 130 135
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 140 145 150
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 155 160 165
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 170 175 180
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 185 190 195 200
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 205 210 215
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 220 225

<210> 299
 <211> 137

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 299
 Met Leu Ser Gly Arg Leu Val Leu Gly Leu Val Ser Met Ala Gly Arg
 -20 -15 -10
 Val Cys Leu Cys Gln Gly Ser Ala Gly Ser Gly Ala Ile Gly Pro Val
 -5 1 5 10
 Glu Ala Ala Ile Arg Thr Lys Leu Glu Glu Ala Leu Ser Pro Glu Val
 15 20 25
 Leu Glu Leu Arg Asn Glu Ser Gly Gly His Ala Val Pro Pro Gly Ser
 30 35 40
 Glu Thr His Phe Arg Val Ala Val Val Ser Ser Arg Phe Glu Gly Leu
 45 50 55
 Ser Pro Leu Gln Arg His Arg Leu Val His Ala Ala Leu Ala Glu Glu
 60 65 70
 Leu Gly Gly Pro Val His Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala
 75 80 85 90
 Gln Trp Arg Glu Asn Ser Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly
 95 100 105
 Gly Asn Lys Lys Thr Leu Gly Thr Pro
 110 115

<210> 300
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 300
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
 -25 -20 -15
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
 -10 -5 1
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
 5 10 15 20
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
 25 30 35
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
 40 45 50
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 55 60 65
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
 70 75 80
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 85 90 95 100
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln
 105 110 115
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val
 120 125 130
 Ile Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His

Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln
 -15 -10 -5
 Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe
 1 5 10 15
 Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser
 20 25 30
 Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Tyr
 35 40 45
 Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Asp Met Met
 50 55 60
 Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn Lys Glu Asn Leu
 65 70 75
 Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro Ile Ser Pro Glu
 80 85 90 95
 Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr Arg Ser Ser Ala
 100 105 110
 Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly Ala Glu Glu Glu
 115 120 125
 Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe Pro Thr Cys Ser
 130 135 140
 Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg Gly Asp Leu Glu
 145 150 155
 Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu Gly Pro Ala Ala
 160 165 170 175
 Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu Arg Gly Pro Gln
 180 185 190
 Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr Met Met Val Asp
 195 200 205
 Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala Pro Lys Glu Ala
 210 215 220
 Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val Val Ser Thr Lys
 225 230 235
 Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala Glu Glu Met Lys
 240 245 250 255
 Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr Arg Phe His
 260 265 270

<210> 302
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 302
 Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro Pro His
 -35 -30 -25 -20
 Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro Pro Leu
 -15 -10 -5
 Ala Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr Gln Gly
 1 5 10
 Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg Gly Gly
 15 20 25
 Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala Cys Ala
 30 35 40 45
 Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val Trp Glu

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | | 50 | | | | | 55 | | | | 60 | | | |
| Ser | Leu | Gln | Gln | Glu | Ala | Arg | Gln | Ala | Pro | Arg | Pro | Asn | Asn | Leu | His | |
| | | | 65 | | | | | 70 | | | | | 75 | | | |
| Thr | Leu | Cys | Gly | Ala | Pro | Val | His | Val | Arg | Glu | Arg | Gly | Thr | Gly | Ser | |
| | | 80 | | | | | 85 | | | | | 90 | | | | |
| Glu | Thr | Asn | Gln | Glu | Thr | Leu | Arg | Ala | Thr | Ala | Pro | Ala | Leu | Pro | Met | |
| | 95 | | | | | 100 | | | | | 105 | | | | | |
| Ala | Pro | Ala | Pro | Pro | Leu | Leu | Ala | Ala | Ala | Leu | Ala | Leu | Ala | Tyr | Leu | |
| 110 | | | | | 115 | | | | | 120 | | | | | 125 | |
| Leu | Arg | Pro | Leu | Ala | | | | | | | | | | | | |
| | | | | 130 | | | | | | | | | | | | |

<210> 303
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 303 | | | | | | | | | | | | | | | | |
| Met | Ala | Ser | Val | Val | Leu | Ala | Leu | Arg | Thr | Arg | Thr | Ala | Val | Thr | Ser | |
| -25 | | | | | -20 | | | | -15 | | | | | | -10 | |
| Leu | Leu | Ser | Pro | Thr | Pro | Ala | Thr | Ala | Leu | Ala | Val | Arg | Tyr | Ala | Ser | |
| | | | -5 | | | | | 1 | | | | 5 | | | | |
| Lys | Lys | Ser | Gly | Gly | Ser | Ser | Lys | Asn | Leu | Gly | Gly | Lys | Ser | Ser | Gly | |
| | 10 | | | | | 15 | | | | | | 20 | | | | |
| Arg | Arg | Gln | Gly | Ile | Lys | Lys | Met | Glu | Gly | His | Tyr | Val | His | Ala | Gly | |
| | 25 | | | | 30 | | | | | | 35 | | | | | |
| Asn | Ile | Ile | Ala | Thr | Gln | Arg | His | Phe | Arg | Trp | His | Pro | Gly | Ala | His | |
| 40 | | | | 45 | | | | | 50 | | | | | | 55 | |
| Val | Gly | Val | Gly | Lys | Asn | Lys | Cys | Leu | Tyr | Ala | Leu | Glu | Glu | Gly | Ile | |
| | | | 60 | | | | | 65 | | | | | | 70 | | |
| Val | Arg | Tyr | Thr | Lys | Glu | Val | Tyr | Val | Pro | His | Pro | Arg | Asn | Thr | Glu | |
| | 75 | | | | | 80 | | | | | | 85 | | | | |
| Ala | Val | Asp | Leu | Ile | Thr | Arg | Leu | Pro | Lys | Gly | Ala | Val | Leu | Tyr | Lys | |
| | 90 | | | | | 95 | | | | | | 100 | | | | |
| Thr | Phe | Val | His | Val | Val | Pro | Ala | Lys | Pro | Glu | Gly | Thr | Phe | Lys | Leu | |
| | 105 | | | | 110 | | | | | | 115 | | | | | |
| Val | Ala | Met | Leu | | | | | | | | | | | | | |
| 120 | | | | | | | | | | | | | | | | |

<210> 304
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 304 | | | | | | | | | | | | | | | | |
| Met | Glu | Ser | Glu | Arg | Ser | Lys | Arg | Met | Gly | Asn | Ala | Cys | Ile | Pro | Leu | |
| | | | -30 | | | | | -25 | | | | | | -20 | | |
| Lys | Arg | Ile | Ala | Tyr | Phe | Leu | Cys | Leu | Leu | Ser | Ala | Leu | Leu | Leu | Thr | |
| | | -15 | | | | | -10 | | | | | | -5 | | | |
| Glu | Gly | Lys | Lys | Pro | Ala | Lys | Pro | Lys | Cys | Pro | Ala | Val | Cys | Thr | Cys | |

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 306
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp
 -10 -5 1
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val
 70 75 80
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly
 85 90 95
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala
 100 105 110
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile
 115 120 125 130
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu
 135 140 145
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu
 150 155 160
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu
 165 170 175
 Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu
 180 185 190
 Ile Asn Lys Ser Gly Glu Lys Ala Met
 195 200

<210> 307
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 307
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala

45 50 55 60
 Ile Leu Asn Gly Gly
 65

<210> 308
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 308
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys
 -40 -35 -30
 Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly
 -25 -20 -15
 Ser Leu Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr
 -10 -5 1 5
 Ser Ser Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys
 10 15 20
 Leu Gly Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys
 25 30 35
 Glu Asp Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro
 40 45 50
 Pro Leu Lys Ser Glu Lys His Glu Glu
 55 60

<210> 309
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 309
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
 -30 -25 -20
 Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr
 -15 -10 -5
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
 1 5 10
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
 15 20 25 30
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Val Phe Thr
 35 40 45
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
 50 55 60
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
 65 70 75
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
 80 85 90
 Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
 95 100 105 110
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Arg | Gln | His | Gly | Asp | Asp | Ala | Ser | Glu | Glu | Lys | Ala | Ala | Asn | Gln | |
| | | | 200 | | | | | 205 | | | | | | 210 | | |
| Ile | Arg | Lys | Cys | Gln | Gln | Ser | Thr | Ser | Ala | Val | Ile | Gly | Val | Arg | Val | |
| | | 215 | | | | | 220 | | | | | 225 | | | | |
| Cys | Gly | Met | Gln | Val | Tyr | Gln | Ala | Gly | Ser | Gly | Gln | Leu | Met | Phe | Met | |
| | | 230 | | | | 235 | | | | | 240 | | | | | |
| Asn | Lys | Tyr | His | Gly | Arg | Lys | Leu | Ser | Met | Gln | Gly | Phe | Lys | Glu | Ala | |
| 245 | | | | | 250 | | | | | 255 | | | | | 260 | |
| Leu | Phe | Gln | Phe | Phe | His | Asn | Gly | Arg | Tyr | Leu | Arg | Arg | Glu | Leu | Leu | |
| | | | 265 | | | | | | 270 | | | | | 275 | | |
| Gly | Pro | Val | Leu | Lys | Lys | Leu | Thr | Glu | Leu | Lys | Ala | Val | Leu | Glu | Arg | |
| | | 280 | | | | | | 285 | | | | | 290 | | | |
| Gln | Glu | Ser | Tyr | Arg | Phe | Tyr | Ser | Ser | Ser | Leu | Leu | Val | Ile | Tyr | Asp | |
| | | 295 | | | | | 300 | | | | | 305 | | | | |
| Gly | Lys | Glu | Arg | Pro | Glu | Val | Val | Leu | Asp | Ser | Asp | Ala | Glu | Asp | Leu | |
| | | 310 | | | | 315 | | | | | 320 | | | | | |
| Glu | Asp | Leu | Ser | Glu | Glu | Ser | Ala | Asp | Glu | Ser | Ala | Gly | Ala | Tyr | Ala | |
| 325 | | | | | 330 | | | | | 335 | | | | | 340 | |
| Tyr | Lys | Pro | Ile | Gly | Ala | Ser | Ser | Val | Asp | Val | Arg | Met | Ile | Asp | Phe | |
| | | | 345 | | | | | | 350 | | | | | 355 | | |
| Ala | His | Thr | Thr | Cys | Arg | Leu | Tyr | Gly | Glu | Asp | Thr | Val | Val | His | Glu | |
| | | | 360 | | | | | 365 | | | | | 370 | | | |
| Gly | Gln | Asp | Ala | Gly | Tyr | Ile | Phe | Gly | Leu | Gln | Ser | Leu | Ile | Asp | Ile | |
| | | 375 | | | | 380 | | | | | | 385 | | | | |
| Val | Thr | Glu | Ile | Ser | Glu | Glu | Ser | Gly | Glu | | | | | | | |
| | | 390 | | | | 395 | | | | | | | | | | |

<210> 311
 <211> 466
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 311

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Leu | Tyr | Ala | Ala | Ala | Ala | Gly | Val | Leu | Ala | Gly | Val | Glu | Ser | |
| | -15 | | | | | | -10 | | | | -5 | | | | | |
| Arg | Gln | Gly | Ser | Ile | Lys | Gly | Leu | Val | Tyr | Ser | Ser | Asn | Phe | Gln | Asn | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Val | Lys | Gln | Leu | Tyr | Ala | Leu | Val | Cys | Glu | Thr | Gln | Arg | Tyr | Ser | Ala | |
| | | 20 | | | | | | 25 | | | | 30 | | | | |
| Val | Leu | Asp | Ala | Val | Ile | Ala | Ser | Ala | Gly | Leu | Leu | Arg | Ala | Glu | Lys | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Lys | Leu | Arg | Pro | His | Leu | Ala | Lys | Val | Leu | Val | Tyr | Glu | Leu | Leu | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Gly | Lys | Gly | Phe | Arg | Gly | Gly | Gly | Gly | Arg | Trp | Lys | Ala | Leu | Leu | Gly | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | | |
| Arg | His | Gln | Ala | Arg | Leu | Lys | Ala | Glu | Leu | Ala | Arg | Leu | Lys | Val | His | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Arg | Gly | Val | Ser | Arg | Asn | Glu | Asp | Leu | Leu | Glu | Val | Gly | Ser | Arg | Pro | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Gly | Pro | Ala | Ser | Gln | Leu | Pro | Arg | Phe | Val | Arg | Val | Asn | Thr | Leu | Lys | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Thr | Cys | Ser | Asp | Asp | Val | Val | Asp | Tyr | Phe | Lys | Arg | Gln | Gly | Phe | Ser | |
| | 130 | | | | | 135 | | | | | | 140 | | | | |
| Tyr | Gln | Gly | Arg | Ala | Ser | Ser | Leu | Asp | Asp | Leu | Arg | Ala | Leu | Lys | Gly | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Lys | His | Phe | Leu | Leu | Asp | Pro | Leu | Met | Pro | Glu | Leu | Leu | Val | Phe | Pro |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Gln | Thr | Asp | Leu | His | Glu | His | Pro | Leu | Tyr | Arg | Ala | Gly | His | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ile | Leu | Gln | Asp | Arg | Ala | Ser | Cys | Leu | Pro | Ala | Met | Leu | Leu | Asp | Pro |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Pro | Pro | Gly | Ser | His | Val | Ile | Asp | Ala | Cys | Ala | Ala | Pro | Gly | Asn | Lys |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Ser | His | Leu | Ala | Ala | Leu | Leu | Lys | Asn | Gln | Gly | Lys | Ile | Phe | Ala |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Phe | Asp | Leu | Asp | Ala | Lys | Arg | Leu | Ala | Ser | Met | Ala | Thr | Leu | Leu | Ala |
| | | | 245 | | | | | | 250 | | | | 255 | | |
| Arg | Ala | Gly | Val | Ser | Cys | Cys | Glu | Leu | Ala | Glu | Glu | Asp | Phe | Leu | Ala |
| | | 260 | | | | | 265 | | | | | 270 | | | |
| Val | Ser | Pro | Ser | Asp | Pro | Arg | Tyr | His | Glu | Val | His | Tyr | Ile | Leu | Leu |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Asp | Pro | Ser | Cys | Ser | Gly | Ser | Gly | Met | Pro | Ser | Arg | Gln | Leu | Glu | Glu |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Pro | Gly | Ala | Gly | Thr | Pro | Ser | Pro | Val | Arg | Leu | His | Ala | Leu | Ala | Gly |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | |
| Phe | Gln | Gln | Arg | Ala | Leu | Cys | His | Ala | Leu | Thr | Phe | Pro | Ser | Leu | Gln |
| | | | 325 | | | | | | 330 | | | | | 335 | |
| Arg | Leu | Val | Tyr | Ser | Thr | Cys | Ser | Leu | Cys | Gln | Glu | Glu | Asn | Glu | Asp |
| | | 340 | | | | | | 345 | | | | | 350 | | |
| Val | Val | Arg | Asp | Ala | Leu | Gln | Gln | Asn | Pro | Gly | Ala | Phe | Arg | Leu | Ala |
| | 355 | | | | | | 360 | | | | | 365 | | | |
| Pro | Ala | Leu | Pro | Ala | Trp | Pro | His | Arg | Gly | Leu | Ser | Thr | Phe | Pro | Gly |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ala | Glu | His | Cys | Leu | Arg | Ala | Ser | Pro | Glu | Thr | Thr | Leu | Ser | Ser | Gly |
| 385 | | | | | 390 | | | | | 395 | | | | 400 | |
| Phe | Phe | Val | Ala | Val | Ile | Glu | Arg | Val | Glu | Val | Pro | Ser | Ser | Ala | Ser |
| | | | 405 | | | | | 410 | | | | | | 415 | |
| Gln | Ala | Lys | Ala | Ser | Ala | Pro | Glu | Arg | Thr | Pro | Ser | Pro | Ala | Pro | Lys |
| | | | 420 | | | | 425 | | | | | | 430 | | |
| Arg | Lys | Lys | Arg | Gln | Gln | Arg | Ala | Ala | Ala | Gly | Ala | Cys | Thr | Pro | Pro |
| | | 435 | | | | 440 | | | | | | 445 | | | |
| Cys | Thr | | | | | | | | | | | | | | |
| | 450 | | | | | | | | | | | | | | |

<210> 312
 <211> 382
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 312 | | | | | | | | | | | | | | | |
| Met | Gly | Leu | Tyr | Ala | Ala | Ala | Ala | Gly | Val | Leu | Ala | Gly | Val | Glu | Ser |
| -15 | | | | | | -10 | | | | | -5 | | | | |
| Arg | Gln | Gly | Ser | Ile | Lys | Gly | Leu | Val | Tyr | Ser | Ser | Asn | Phe | Gln | Asn |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| Val | Lys | Gln | Leu | Tyr | Ala | Leu | Val | Cys | Glu | Thr | Gln | Arg | Tyr | Ser | Ala |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Val | Leu | Asp | Ala | Val | Ile | Ala | Ser | Ala | Gly | Leu | Leu | Arg | Ala | Glu | Lys |
| | 35 | | | | | 40 | | | | | | 45 | | | |

Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 50 55 60
 Gly Lys Gly Phe Arg Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly
 65 70 75 80
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His
 85 90 95
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro
 100 105 110
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys
 115 120 125
 Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser
 130 135 140
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly
 145 150 155 160
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
 165 170 175
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
 180 185 190
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
 195 200 205
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
 210 215 220
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
 225 230 235 240
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
 245 250 255
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
 260 265 270
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
 275 280 285
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu
 290 295 300
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Ala
 305 310 315 320
 Ser Ser Ser Glu Pro Cys Ala Thr Arg Ser Leu Ser Leu Pro Cys Ser
 325 330 335
 Gly Ser Ser Thr Pro Arg Ala Pro Ser Ala Arg Arg Arg Met Lys Thr
 340 345 350
 Trp Cys Glu Met Arg Cys Ser Arg Thr Arg Ala Pro Ser Gly
 355 360 365

<210> 313

<211> 258

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36...-1

<400> 313

Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly

<400> 316
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ser Leu Val Leu
 -15 -10 -5
 Cys Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
 1 5 10 15
 Glu Leu Arg Thr Asp Phe Lys Ser Pro Ile Asp Gln Cys Asn Pro Val
 20 25 30
 His Ala Arg Glu Arg Leu Arg Asn Ile Glu Arg Ile Cys Phe Leu Leu
 35 40 45
 Arg Lys Leu Val Leu Pro Glu Tyr Ser Ile His Ser Leu Phe Cys Ile
 50 55 60
 Met Phe Leu Cys Ala Gln Glu Trp Leu Thr Leu Gly Leu Asn Val Pro
 65 70 75
 Leu Leu Phe Tyr His Phe Trp Arg Tyr Phe His Cys Pro Ala Asp Ser
 80 85 90 95
 Ser Glu Leu Ala Tyr Asp Pro Pro Val Val Met Asn Pro Asp Thr Leu
 100 105 110
 Ser Tyr Cys Gln Lys Glu Ala Trp Cys Lys Leu Ala Phe Tyr Leu Leu
 115 120 125
 Ser Phe Phe Tyr Tyr Leu Tyr Cys Met Ile Tyr Thr Leu Val Ser Ser
 130 135 140

<210> 317
 <211> 426
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 317
 Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
 -25 -20 -15
 Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
 -10 -5 1
 Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
 5 10 15 20
 His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys Phe Thr Pro
 25 30 35
 Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
 40 45 50
 Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
 55 60 65
 Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
 70 75 80
 Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
 85 90 95 100
 Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
 105 110 115
 Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
 120 125 130
 Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
 135 140 145
 Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
 150 155 160
 Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn
 165 170 175 180

Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly
 185 190 195
 Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln
 200 205 210
 Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val
 215 220 225
 Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met
 230 235 240
 Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala
 245 250 255 260
 Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu
 265 270 275
 Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg
 280 285 290
 Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp
 295 300 305
 Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu
 310 315 320
 Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala
 325 330 335 340
 Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe
 345 350 355
 Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu
 360 365 370
 Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
 375 380 385
 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
 390 395

<210> 318
 <211> 301
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 318
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 -20 -15 -10 -5
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 1 5 10
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 15 20 25
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
 30 35 40
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
 45 50 55 60
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe
 65 70 75
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
 80 85 90
 Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln
 95 100 105
 Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val
 110 115 120
 Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 125 | | | | | 130 | | | | | 135 | | | | 140 |
| Lys | Arg | Leu | Pro | Thr | Glu | Glu | Glu | Trp | Glu | Phe | Ala | Ala | Arg | Gly |
| | | | | 145 | | | | | 150 | | | | | 155 |
| Leu | Lys | Gly | Gln | Val | Tyr | Pro | Trp | Gly | Asn | Trp | Phe | Gln | Pro | Asn |
| | | | 160 | | | | | 165 | | | | | 170 | |
| Thr | Asn | Leu | Trp | Gln | Gly | Lys | Phe | Pro | Lys | Gly | Asp | Lys | Ala | Glu |
| | | 175 | | | | | 180 | | | | | 185 | | Asp |
| Gly | Phe | His | Gly | Val | Ser | Pro | Val | Asn | Ala | Phe | Pro | Ala | Gln | Asn |
| | 190 | | | | | 195 | | | | | 200 | | | Asn |
| Tyr | Gly | Leu | Tyr | Asp | Leu | Leu | Gly | Asn | Val | Trp | Glu | Trp | Thr | Ala |
| 205 | | | | | 210 | | | | | 215 | | | | 220 |
| Pro | Tyr | Gln | Ala | Ala | Glu | Gln | Asp | Met | Arg | Val | Leu | Arg | Gly | Ala |
| | | | 225 | | | | | 230 | | | | | 235 | Ser |
| Trp | Ile | Asp | Thr | Ala | Asp | Gly | Ser | Ala | Asn | His | Arg | Ala | Arg | Val |
| | | 240 | | | | | 245 | | | | | 250 | | Thr |
| Thr | Arg | Met | Gly | Asn | Thr | Pro | Asp | Ser | Ala | Ser | Asp | Asn | Leu | Gly |
| | 255 | | | | | 260 | | | | | 265 | | | Phe |
| Arg | Cys | Ala | Ala | Asp | Ala | Gly | Arg | Pro | Pro | Gly | Glu | Leu | | |
| 270 | | | | | 275 | | | | | | 280 | | | |

<210> 319
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

| | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 319 | | | | | | | | | | | | | | |
| Met | Gly | Ser | Gly | Trp | Leu | Thr | Ala | Val | Ala | Ser | Leu | Leu | Pro | Ser |
| | | -15 | | | | | -10 | | | | -5 | | | Pro |
| Gly | Asn | Ser | Glu | Leu | Pro | Val | Gln | Ala | Leu | Gly | Arg | Arg | Gly | Arg |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |
| Asp | Trp | Ala | Arg | Asn | Glu | Ala | Gly | Arg | Asp | Leu | Glu | Lys | Pro | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | Arg |
| Leu | His | Cys | Ser | Gly | Arg | Gly | Arg | Leu | Glu | Glu | Pro | Val | Pro | Asn |
| | | 35 | | | | | 40 | | | | | 45 | | |
| His | Leu | Pro | Val | Gly | Leu | Ser | Val | Arg | Gly | Ser | Gln | Val | Leu | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | Ser |
| Ala | Gly | Pro | Arg | Arg | Cys | Arg | Leu | Thr | Gly | Thr | Arg | Asn | Pro | Val |
| | 65 | | | | 70 | | | | 75 | | | | | Arg |
| Gly | Pro | Arg | Arg | Val | Glu | Gln | Ile | Ala | Arg | Gly | Gly | Pro | Glu | Ala |
| 80 | | | | | 85 | | | | 90 | | | | | 95 |
| Arg | Gln | Ala | Gly | Asp | Ser | Cys | | | | | | | | |
| | | | 100 | | | | | | | | | | | |

<210> 320
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 320
 Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | -35 | | | | | -30 | | | | | -25 | | | |
| Ala | Phe | Ala | Asp | Gly | Ala | Trp | Asp | Leu | Ser | Phe | Leu | Cys | Ala | Leu | Cys | | |
| | | | -20 | | | | | -15 | | | | | -10 | | | | |
| Ser | Phe | Cys | Pro | Ile | Ser | Ala | Ala | Ser | Gly | Arg | Pro | Tyr | Arg | Tyr | Leu | | |
| | | -5 | | | | | 1 | | | | 5 | | | | | | |
| Glu | Phe | Trp | Arg | Leu | Tyr | Leu | Ser | Pro | Ser | Ser | Met | Glu | Asn | Gly | Val | | |
| 10 | | | | | 15 | | | | | 20 | | | | | 25 | | |
| Gln | Lys | Phe | His | Glu | Thr | Phe | Phe | Ile | Val | Phe | Leu | Leu | Leu | Phe | Asp | | |
| | | | | 30 | | | | | 35 | | | | | 40 | | | |
| Ile | Glu | Arg | Lys | Gly | Lys | Ser | Ser | Val | Cys | Pro | Phe | Cys | Tyr | Arg | | | |
| | | | 45 | | | | | 50 | | | | | 55 | | | | |

<210> 321
 <211> 191
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39..-1

| | | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| <400> 321 | | | | | | | | | | | | | | | | | |
| Met | Met | Thr | Ile | Thr | Phe | Leu | Pro | Tyr | Thr | Phe | Ser | Leu | Met | Val | Thr | | |
| | | | | -35 | | | | -30 | | | | | | -25 | | | |
| Phe | Pro | Asp | Val | Pro | Leu | Gly | Ile | Phe | Leu | Phe | Cys | Val | Cys | Val | Ile | | |
| | | -20 | | | | | -15 | | | | -10 | | | | | | |
| Ala | Ile | Gly | Val | Val | Gln | Ala | Leu | Ile | Val | Gly | Tyr | Ala | Phe | His | Phe | | |
| | | -5 | | | | | 1 | | | | 5 | | | | | | |
| Pro | His | Leu | Leu | Ser | Pro | Gln | Ile | Gln | Arg | Ser | Ala | His | Arg | Ala | Leu | | |
| 10 | | | | 15 | | | | | 20 | | | | | | 25 | | |
| Tyr | Arg | Arg | His | Val | Leu | Gly | Ile | Val | Leu | Gln | Gly | Pro | Ala | Leu | Cys | | |
| | | | | 30 | | | | 35 | | | | | | 40 | | | |
| Phe | Ala | Ala | Ala | Ile | Phe | Ser | Leu | Phe | Phe | Val | Pro | Leu | Ser | Tyr | Leu | | |
| | | | 45 | | | | 50 | | | | | | 55 | | | | |
| Leu | Met | Val | Thr | Val | Ile | Leu | Leu | Pro | Tyr | Val | Ser | Lys | Val | Thr | Gly | | |
| | | 60 | | | | 65 | | | | | 70 | | | | | | |
| Trp | Cys | Arg | Asp | Arg | Leu | Leu | Gly | His | Arg | Glu | Pro | Ser | Ala | His | Pro | | |
| | 75 | | | | 80 | | | | | | 85 | | | | | | |
| Val | Glu | Val | Phe | Ser | Phe | Asp | Leu | His | Glu | Pro | Leu | Ser | Lys | Glu | Arg | | |
| 90 | | | | 95 | | | | | 100 | | | | | 105 | | | |
| Val | Glu | Ala | Phe | Ser | Asp | Gly | Val | Tyr | Ala | Ile | Val | Ala | Thr | Leu | Leu | | |
| | | | | 110 | | | | | 115 | | | | | 120 | | | |
| Ile | Leu | Asp | Ile | Cys | Pro | Ser | Cys | Ser | Leu | Trp | Leu | Ala | Val | Ala | Ser | | |
| | | | 125 | | | | 130 | | | | | | 135 | | | | |
| Phe | Gln | Arg | Leu | Leu | Leu | Arg | Gly | Leu | Ile | Cys | Leu | Phe | Val | Cys | | | |
| | | 140 | | | | 145 | | | | | | 150 | | | | | |

<210> 322
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41..-1

<400> 322
 Met Pro Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp

-40 -35 -30
 Asp Ser Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu
 -25 -20 -15 -10
 Ala Gln Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val
 -5 1 5
 Met Ser Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser
 10 15 20
 Gly Thr Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser
 25 30 35
 Ser Arg Leu Thr Phe Gln Arg Arg Phe
 40 45

<210> 323
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38..-1

<400> 323
 Met Ser Ser Pro Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu
 -35 -30 -25
 Thr Thr Ala Ile Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe
 -20 -15 -10
 Phe Thr Pro Leu Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys
 -5 1 5 10
 Val Thr Lys Asp Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys
 15 20 25
 Glu Ala Thr Trp Leu Pro
 30

<210> 324
 <211> 168
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 324
 Met Arg Gly Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu
 -25 -20 -15 -10
 Leu Val Val Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp
 -5 1 5
 Glu Arg Leu Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu
 10 15 20
 Val Leu Ala Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met
 25 30 35
 Leu Ala Ala Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe
 40 45 50 55
 Leu Ile Ala Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala
 60 65 70
 Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala
 75 80 85
 Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala


```

          90          95          100
Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro
    105          110          115
Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala
120          125          130          135
Cys Trp Ile Pro Ser Pro Pro Ala
          140

```

<210> 325
 <211> 166
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

```

<400> 325
Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys
-15          -10          -5          1
Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp
    5          10          15
Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln
    20          25          30
Asn Arg Asp His Leu Glu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val
    35          40          45
His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu
    50          55          60          65
Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile
    70          75          80
Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr
    85          90          95
Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr
    100          105          110
Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu
    115          120          125
Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly
    130          135          140          145
Lys Gly Arg Arg Arg Gln
          150

```

<210> 326
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

```

<400> 326
Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg
-15          -10          -5          1
Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val
    5          10          15
Gly His Cys Arg Arg Arg Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu
    20          25          30
Cys Arg Asn Lys Leu Ser Cys Cys Ile Ser Ile Ile Ser His Glu Tyr

```

35 40 45
 Thr Arg Arg Pro Ala Phe Pro Val Ile His Leu Glu Asp Ile Thr Leu
 50 55 60 65
 Asp Tyr Ser Asp Val Asp Ser Phe Thr Gly Ser Pro Val Ser Met Leu
 70 75 80
 Asn Asp Leu Ile Thr Phe Asp Thr Thr Lys Phe Gly Glu Thr Met Thr
 85 90 95
 Pro Glu Thr Asn Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Ala Thr
 100 105 110
 Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr
 115 120 125
 Met Pro Pro Pro Ser Gln Thr Ala Leu Thr His Asn
 130 135 140

<210> 327
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 327
 Met Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu
 -30 -25 -20
 Ser Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys
 -15 -10 -5
 Leu Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp
 1 5 10 15
 Ala Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr
 20 25 30
 Asn Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln
 35 40 45
 Cys Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro
 50 55 60
 Cys Cys Cys Asp Ile Asn Glu Gly Leu
 65 70

<210> 328
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 328
 Met Ser Asp Glu Asp Glu Ser Ser Asp Tyr Leu Cys Leu Ser Ile Leu
 -25 -20 -15
 Gly Leu Phe Cys Cys Leu Pro Leu Ala Ile Pro Ala Val Ile Phe Ser
 -10 -5 1 5
 Cys Leu Thr Lys Asn Tyr Asn Lys Ser Ser Asp Tyr Glu Leu Ala Ala
 10 15 20
 Lys Thr Ser Lys Gln Ala Tyr Tyr Trp Ala Ile Ala Ser Ile Thr Val
 25 30 35
 Gly Ile Leu Gly Thr Ile Leu Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg

40 45 50
 Leu
 <210> 329
 <211> 95
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -27..-1
 <400> 329
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly Ser Leu Thr
 -25 -20 -15
 Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val Phe Pro Gln
 -10 -5 1 5
 Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys Ile Ser Leu
 10 15 20
 Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln Gly Asp Leu
 25 30 35
 Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe Ser Ile Ile
 40 45 50
 Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val Gly Arg
 55 60 65
 <210> 330
 <211> 84
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -20..-1
 <400> 330
 Met Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His
 -20 -15 -10 -5
 Gln Gly Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly
 1 5 10
 Val Leu His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys
 15 20 25
 Ser Arg Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser
 30 35 40
 Leu Cys Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn
 45 50 55 60
 Thr Val Arg Thr
 <210> 331
 <211> 124
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32..-1
 <400> 331

Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro
-30 -25 -20
Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Leu Phe Ala
-15 -10 -5
Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe
1 5 10 15
Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys
20 25 30
Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro
35 40 45
Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn Gly Met
50 55 60
Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp
65 70 75 80
Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
85 90

<210> 332
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46..-1

<400> 332
Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp
-45 -40 -35
Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile
-30 -25 -20 -15
Thr Ala Val Leu Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu
-10 -5 1
Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu Glu
5 10 15

<210> 333
<211> 150
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 333
Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
-20 -15 -10
Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
-5 1 5
Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys
10 15 20 25
Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe
30 35 40
Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys
45 50 55
Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu
60 65 70

Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr
75 80 85
Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro
90 95 100 105
Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu
110 115 120
Glu Gly Ala Arg Arg Tyr
125

<210> 334
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 334
Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp
-10 -5 1
Ala Gly Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg
5 10 15
Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala
20 25 30 35
Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val
40 45 50
Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg
55 60 65
Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro
70 75 80
Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu
85 90 95
Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn
100 105 110 115
Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys
120 125 130
Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg
135 140 145
Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp
150 155 160
Leu Lys Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys
165 170 175
Ile Tyr Leu Arg Gly Lys
180 185

<210> 335
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 335
Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala Leu Glu
-20 -15 -10

Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly Leu Val
 -5 1 5
 Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe Leu Met
 10 15 20
 Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu Ser Asp
 25 30 35 40
 Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val Leu Ile
 45 50 55
 Ile Leu Glu Val Leu Gln Phe Gln
 60

<210> 336
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45...-1

<400> 336
 Met Val Leu Met Trp Thr Ser Gly Asp Ala Phe Lys Thr Ala Tyr Phe
 -45 -40 -35 -30
 Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser Val Cys Gly Leu Leu Gln
 -25 -20 -15
 Val Leu Val Asp Leu Ala Ile Leu Gly Gln Ala Tyr Ala Phe Ala Pro
 -10 -5 1
 Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala Pro His Trp His Gln Gly
 5 10 15
 Pro Leu Thr Val Gly Arg Thr Arg Met Trp Asp Arg Gln Pro Arg Ala
 20 25 30 35
 Leu Val Gly Pro Asp Leu Pro Ala Gly Arg Val Gly Ala Val Ala Pro
 40 45 50
 Ala Gly Val Ala Glu Met Gly His Gly His Trp Gly Leu His Gln Pro
 55 60 65
 Leu Trp Gly Val Ser Gly Trp Ala Val Gly Val Gly Leu Gly Arg Cys
 70 75 80
 Leu Cys Ser Ala Gly Thr Ala Arg Val Asp Leu Ala Pro Arg Val Leu
 85 90 95
 Asp Val Phe Arg Met Thr
 100 105

<210> 337
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 337
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr
 1 5 10
 Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu
 15 20 25

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Ser | Gln | Ile | Thr | Ser | Lys | Ser | Gln | Asp | Val | Arg | Gln | Ala | Leu |
| 30 | | | | | 35 | | | | 40 | | | | | 45 | |
| Val | Trp | Asn | Phe | Pro | Ile | Asp | Val | Thr | Phe | Lys | Ser | Thr | Asn | Pro | Tyr |
| | | | 50 | | | | | | 55 | | | | | 60 | |
| Gly | Trp | Pro | Gln | Ile | Val | Leu | Ser | Val | Tyr | Gly | Pro | Asp | Val | Phe | Gly |
| | | | 65 | | | | | | 70 | | | | | 75 | |
| Asn | Asp | Val | Val | Arg | Gly | Tyr | Gly | Ala | Val | His | Val | Pro | Phe | Ser | Pro |
| | | 80 | | | | | 85 | | | | | 90 | | | |
| Gly | Arg | His | Lys | Arg | Thr | Ile | Pro | Met | Phe | Val | Pro | Glu | Ser | Thr | Ser |
| | 95 | | | | 100 | | | | | | 105 | | | | |
| Lys | Leu | Gln | Lys | Phe | Thr | Arg | Ser | Ala | Ser | Cys | Ser | Thr | His | | |
| 110 | | | | | 115 | | | | | 120 | | | | | |

<210> 338
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<220>
 <221> UNSURE
 <222> 21
 <223> Xaa = Ala,Pro

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Glu | Glu | Arg | Thr | Ala | Met | Lys | Arg | Glu | Gly | Gly | Ala | Ala | His |
| | | -25 | | | | | -20 | | | | | -15 | | | |
| Leu | Cys | Ser | Asp | Ser | Leu | Pro | Glu | Ser | Gln | Gln | Gln | Asp | Gly | Asn | His |
| | -10 | | | | -5 | | | | | 1 | | | | 5 | |
| Ala | Pro | Asn | Phe | Ser | Ser | His | Gly | Ser | Cys | Arg | Arg | Arg | Gln | Arg | Xaa |
| | | | 10 | | | | | 15 | | | | | | 20 | |
| Asp | Met | Thr | Arg | Arg | Cys | Met | Pro | Ala | Arg | Pro | Gly | Phe | Pro | Ser | Ser |
| | | 25 | | | | | 30 | | | | | 35 | | | |
| Pro | Ala | Pro | Gly | Ser | Ser | Pro | Pro | Arg | Cys | His | Leu | Arg | Pro | Gly | Ser |
| | 40 | | | | | 45 | | | | | 50 | | | | |
| Thr | Ala | His | Ala | Ala | Ala | Gly | Lys | Arg | Thr | Glu | Ser | Pro | Gly | Asp | Arg |
| | 55 | | | | 60 | | | | | 65 | | | | | |
| Tyr | Arg | Ala | Glu | Gly | Leu | Arg | Arg | Gly | Arg | Val | Ala | Gly | Ala | Arg | Val |
| 70 | | | | | 75 | | | | | 80 | | | | | 85 |

<210> 339
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Cys | Leu | Asp | Gln | Gln | Leu | Thr | Val | His | Ala | Leu | Pro | Cys | Pro |
| | | -30 | | | | -25 | | | | | | -20 | | | |
| Ala | Gln | Pro | Ser | Ser | Leu | Ala | Phe | Cys | Gln | Val | Gly | Phe | Leu | Thr | Ala |
| | -15 | | | | -10 | | | | | | -5 | | | | |
| Gln | Pro | Ser | Pro | Pro | Arg | Arg | Arg | Asn | Gly | Lys | Asp | Arg | Tyr | Thr | Leu |

1 5 10 15
 Val Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu
 20 25 30
 Val Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His
 35 40 45
 Gln Ser Ile Thr Val Ala Asp Thr Asn Lys
 50 55

<210> 340
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 340
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
 -35 -30 -25 -20
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
 -15 -10 -5
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
 1 5 10
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
 15 20 25
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
 30 35 40 45

<210> 341
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 341
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly Phe Leu Tyr
 -15 -10 -5 1
 Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe Pro Pro Arg
 5 10 15
 Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly Glu Pro Thr
 20 25 30
 Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr Ile Glu Trp
 35 40 45
 Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp Pro Arg Ser
 50 55 60 65
 His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu Arg Ile Val
 70 75 80
 His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val Cys Val Ala
 85 90 95
 Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser Leu Glu Val
 100 105 110
 Ala Cys Lys
 115

<210> 342
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 342
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 Leu Leu Leu
 60

<210> 343
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 343
 Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile
 -40 -35 -30
 Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly
 -25 -20 -15
 Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val
 -10 -5 1 5
 Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu
 10 15 20
 Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser
 25 30 35
 Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys
 40 45 50
 Arg Tyr
 55

<210> 344
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<220>
 <221> UNSURE
 <222> 185
 <223> Xaa = Phe,Val

<400> 344
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
 -15 -10 -5
 Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser
 1 5 10
 Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala
 15 20 25
 Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His
 30 35 40 45
 Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu
 50 55 60
 Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu
 65 70 75
 Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp
 80 85 90
 Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser
 95 100 105
 Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly
 110 115 120 125
 Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His
 130 135 140
 Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu
 145 150 155
 Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser
 160 165 170
 Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys
 175 180 185
 Phe Gly Gly Asp Arg Leu Thr Leu His
 190 195

<210> 345
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 345
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 -20 -15 -10 -5
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 1 5 10
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 15 20 25
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 30 35 40
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 45 50 55 60
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 65 70 75

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
80 85 90
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
95 100 105
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
110 115 120
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
125 130 135 140
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
145 150 155
Asp Arg His Lys Met Leu Ser
160

<210> 346
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 346
Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
-10 -5 1
Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
5 10 15
Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
20 25 30 35
Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr
40 45 50
Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg
55 60 65
Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
70 75 80
Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
85 90 95
Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile
100 105 110 115
Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly
120 125 130
Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu
135 140 145
Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly
150 155 160
Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn
165 170 175
Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala
180 185 190 195
Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg
200 205 210
Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn Met Leu Leu Ile Pro
215 220 225
Thr Ser Phe Ser Pro Leu Lys
230

<210> 347
<211> 104

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 347
 Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro Leu His Ser Pro
 -45 -40 -35
 Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe Arg Ser Val Asp
 -30 -25 -20
 Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys Ile Phe Ala Asn
 -15 -10 -5 1
 Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu Gly Arg Tyr Thr
 5 10 15
 Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp Pro Thr Arg Asp
 20 25 30
 Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn Ser Pro Ala Glu
 35 40 45
 Gly Leu Ala Phe Gln Cys Arg Phe
 50 55

<210> 348
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 348
 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val
 -20 -15 -10
 Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser Arg
 -5 1 5 10
 Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala
 15 20 25
 Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn
 30 35 40
 Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu
 45 50 55
 Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser
 60 65 70 75
 Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln
 80 85 90
 Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
 95 100

<210> 349
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 349

Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu Ala Val Asn Val Val
-15 -10 -5
Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr Ala Thr Glu Glu Ala
1 5 10
Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly Leu Phe Ile Tyr Gln
15 20 25 30
Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg Arg Thr Asn Ser Cys
35 40 45
Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys Asp Ser Leu Ser Thr
50 55 60
Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala Arg Leu Gly Thr Tyr
65 70 75
Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly Met Phe Val Phe Tyr
80 85 90
Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met Leu Arg Phe Gly Lys
95 100 105 110
Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val Ile Val Phe Val Leu
115 120 125
Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr Thr Gly Thr Ser Val
130 135 140
Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile Ile Leu Ala Ile Met
145 150 155
Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu Lys His Pro Cys Leu
160 165 170
Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys Val Ser Gln Lys Leu
175 180 185 190
Val Val Ala His Met Thr Lys Ser Glu Leu Tyr Leu Gln Asp Thr Val
195 200 205
Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln Tyr Phe Asn Asn Phe
210 215 220
Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met Val Ile Ser Ser Phe
225 230 235
Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu Gln Ile Ser Arg His
240 245 250
Leu His Leu Asn Ile Phe Lys Thr Ala Cys His Gln Ala Pro Glu Gln
255 260 265 270
Val Gln Val Leu Ser Ser Lys Ser His Gln Asn Asn Met Asp
275 280

<210> 350

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 350

Met Ile Leu Val Thr Val Pro Gly Val Cys Pro Ala Gln Cys Cys Trp
-10 -5 1
Ala Glu Gln Arg Gly Arg Gly Ser Gly Met Tyr Phe Ile Asp Lys Trp
5 10 15
Ala Arg Pro Ser Trp Val Pro His Trp Leu Asn Asp Leu Phe Ile Val
20 25 30
Lys Ser Gly Tyr Leu Val Cys Ile Arg Thr Thr Val Ile Arg Gln Gly

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 35 | | | | 40 | | | | | 45 | | | | 50 | | |
| Ile | Val | Arg | Ile | Gly | Arg | Asn | Lys | Ile | Ser | Glu | Ser | Gly | Arg | Ser | Ala |
| | | | | 55 | | | | | 60 | | | | | 65 | |
| Leu | Tyr | Thr | Ile | Ala | Lys | Asn | Lys | Met | Val | Ile | Phe | Lys | Val | Pro | Asp |
| | | | 70 | | | | | 75 | | | | | 80 | | |
| Cys | Met | His | Leu | Asn | Ala | Asp | Tyr | Phe | Gly | Val | | | | | |
| | | 85 | | | | | 90 | | | | | | | | |

<210> 351
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 351 | | | | | | | | | | | | | | | |
| Met | Ser | Phe | Leu | Gln | Asp | Pro | Ser | Phe | Phe | Thr | Met | Gly | Met | Trp | Ser |
| | | | | -30 | | | | | -25 | | | | | -20 | |
| Ile | Gly | Ala | Gly | Ala | Leu | Gly | Ala | Ala | Ala | Leu | Ala | Leu | Leu | Leu | Ala |
| | | | -15 | | | | | -10 | | | | | -5 | | |
| Asn | Thr | Asp | Val | Phe | Leu | Ser | Lys | Pro | Gln | Lys | Ala | Ala | Leu | Glu | Tyr |
| | 1 | | | | 5 | | | | | | 10 | | | | |
| Leu | Glu | Asp | Ile | Asp | Leu | Lys | Thr | Leu | Glu | Lys | Glu | Pro | Arg | Thr | Phe |
| 15 | | | | | 20 | | | | 25 | | | | | 30 | |
| Lys | Ala | Lys | Glu | Leu | Trp | Glu | Lys | Asn | Gly | Ala | Val | Ile | Met | Ala | Val |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| Arg | Arg | Pro | Gly | Cys | Phe | Leu | Cys | Arg | Glu | Glu | Ala | Ala | Asp | Leu | Ser |
| | | | 50 | | | | 55 | | | | | | 60 | | |
| Ser | Leu | Lys | Ser | Met | Leu | Asp | Gln | Leu | Gly | Val | Pro | Leu | Tyr | Ala | Val |
| | 65 | | | | | 70 | | | | | 75 | | | | |
| Val | Lys | Glu | His | Ile | Arg | Thr | Glu | Val | Lys | Asp | Phe | Gln | Pro | Tyr | Phe |
| | 80 | | | | | 85 | | | | 90 | | | | | |
| Lys | Gly | Glu | Ile | Phe | Leu | Asp | Glu | Lys | Lys | Lys | Phe | Tyr | Gly | Pro | Gln |
| 95 | | | | | 100 | | | | 105 | | | | | 110 | |
| Arg | Arg | Lys | Met | Met | Phe | Met | Gly | Phe | Ile | Arg | Leu | Gly | Val | Trp | Tyr |
| | | | 115 | | | | | 120 | | | | | | 125 | |
| Asn | Phe | Phe | Arg | Ala | Trp | Asn | Gly | Gly | Phe | Ser | Gly | Asn | Leu | Glu | Gly |
| | | | 130 | | | | 135 | | | | | 140 | | | |
| Glu | Gly | Phe | Ile | Leu | Gly | Gly | Val | Phe | Val | Val | Gly | Ser | Gly | Lys | Gln |
| | | 145 | | | | 150 | | | | | 155 | | | | |
| Gly | Ile | Leu | Leu | Glu | His | Arg | Glu | Lys | Glu | Phe | Gly | Asp | Lys | Val | Asn |
| | 160 | | | | | 165 | | | | 170 | | | | | |
| Leu | Leu | Ser | Val | Leu | Glu | Ala | Ala | Lys | Met | Ile | Lys | Pro | Gln | Thr | Leu |
| 175 | | | | | 180 | | | | | 185 | | | | | 190 |
| Ala | Ser | Glu | Lys | Lys | | | | | | | | | | | |
| | | | | 195 | | | | | | | | | | | |

<210> 352
 <211> 206
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 352
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
-30 -25 -20
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
-15 -10 -5
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
1 5 10
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15 20 25 30
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
35 40 45
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
50 55 60
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
65 70 75
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
80 85 90
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
95 100 105 110
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
115 120 125
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
130 135 140
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
145 150 155
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
160 165 170

<210> 353
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44...-1

<400> 353
Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp Gly Arg Arg Cys
-40 -35 -30
Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro
-25 -20 -15
Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp
-10 -5 1
Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr
5 10 15 20
Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser Arg Ala Ala Leu
25 30 35
Cys Ser Arg Ala Ser Thr Tyr Val
40

<210> 354
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -32..-1

<400> 354

```
Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg
      -30                      -25                      -20
His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser
      -15                      -10                      -5
Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu
1          5          10          15
Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser
      20          25          30
Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp
      35          40          45
Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala
      50          55          60
Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile
65          70          75          80
Asp Gly Lys Ala Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr
      85          90          95
Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp
      100          105          110
Arg Leu Lys Gln Gly Lys Phe
      115
```

<210> 355

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 355

```
Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala
      -15                      -10                      -5
Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly
1          5          10          15
His Val Met Leu Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser
      20          25          30
Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr
      35          40          45
Leu
```

<210> 356

<211> 189

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<220>

<221> UNSURE

<222> 41

<223> Xaa = Ala,Gly

<400> 356
Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
-20 -15 -10
Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
-5 1 5
Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
10 15 20
Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
25 30 35 40
Xaa Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
45 50 55
Leu Thr Phe Trp Gly Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
60 65 70
Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
75 80 85
Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
90 95 100
Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
105 110 115 120
Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
125 130 135
His Gly Leu Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
140 145 150
Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
155 160 165

<210> 357
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

<400> 357
Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro Phe Ala Phe Glu
-45 -40 -35
Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser Leu Ser Asp Pro
-30 -25 -20
Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met Ala Leu Cys Ala
-15 -10 -5 1
Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys Lys Leu Ile Leu
5 10 15
Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile Val Ala Leu Leu
20 25 30
Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser Lys Glu Gln Gln
35 40 45
Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys Gly Gly Val
50 55 60 65
Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser Ser Asp Ser Ser
70 75 80
Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr Arg His His Ala
85 90 95
Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser Pro Tyr Trp Pro
100 105 110
Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu Pro Gln Pro Pro
115 120 125

Lys Val Leu Gly Leu Pro Ala
130 135

<210> 358
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 358
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
 20 25 30
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
35 40 45 50
Val Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
 55 60 65
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
 70 75 80
Val Thr Lys Lys Trp Ser
 85

<210> 359
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 359
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala Ile Tyr Ile Leu Thr
 -25 -20 -15
Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu Trp Ser Trp Ile Cys
 -10 -5 1
Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn
 5 10 15
Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe Ser Asn Leu Gln Glu
20 25 30 35
Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Glu Val Gly Cys Gly
 40 45 50
Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
 55 60 65
Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu Ile Lys Ser Ile Ala
 70 75 80
Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu
 85 90 95
Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Val Cys Thr
100 105 110 115
Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val
 120 125 130

Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr Phe Met Glu His Val
 135 140 145
 Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp Gln Gln Val Leu Asp
 150 155 160
 Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn Leu Thr Arg Glu Ser
 165 170 175
 Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys Leu Lys Leu Gln His
 180 185 190 195
 Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg Pro His Ile Tyr Gly
 200 205 210
 Tyr Ala Val Lys
 215

<210> 360
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 360
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
 -20 -15 -10
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
 -5 1 5
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val Lys
 10 15 20 25
 Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys Cys
 30 35 40
 Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile Tyr
 45 50 55
 Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val His
 60 65 70
 Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys Gln
 75 80 85
 Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile Asn
 90 95 100 105
 Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val Ile
 110 115 120
 Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys Ile
 125 130 135
 Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg Arg
 140 145 150
 Tyr

<210> 361
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 361
 Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| -20 | | | | | | -15 | | | | | | -10 | | | | |
| Pro | Pro | Thr | Val | Ala | Ala | Pro | Ala | Pro | Ser | Leu | Phe | Pro | Ala | Ala | Gln | |
| -5 | | | | | 1 | | | | 5 | | | | | 10 | | |
| Met | Met | Asn | Asn | Gly | Leu | Leu | Gln | Gln | Pro | Ser | Ala | Leu | Met | Leu | Leu | |
| | | 15 | | | | | | 20 | | | | | 25 | | | |
| Pro | Cys | Arg | Pro | Val | Leu | Thr | Ser | Val | Ala | Leu | Asn | Ala | Asn | Phe | Val | |
| | 30 | | | | | | 35 | | | | | 40 | | | | |
| Ser | Trp | Lys | Ser | Arg | Thr | Lys | Tyr | Thr | Ile | Thr | Pro | Val | Lys | Met | Arg | |
| 45 | | | | | | 50 | | | | | 55 | | | | | |
| Lys | Ser | Gly | Gly | Arg | Asp | His | Thr | Gly | Ala | Gly | Asn | Val | Arg | Arg | Thr | |
| 60 | | | | | 65 | | | | | 70 | | | | | 75 | |
| Val | Gly | Arg | Val | Ser | Asn | Val | Asp | His | Asn | Lys | Arg | Val | Ile | Gly | Lys | |
| | | | | 80 | | | | | 85 | | | | | 90 | | |
| Ala | Gly | Arg | Asn | Arg | Trp | Leu | Gly | Lys | Arg | Pro | Asn | Ser | Gly | Arg | Trp | |
| | | | 95 | | | | | 100 | | | | | 105 | | | |
| His | Arg | Lys | Gly | Gly | Trp | Ala | Gly | Arg | Lys | Ile | Arg | Pro | Leu | Pro | Pro | |
| | | 110 | | | | | 115 | | | | | 120 | | | | |
| Met | Lys | Ser | Tyr | Val | Lys | Leu | Pro | Ser | Ala | Ser | Ala | Gln | Ser | | | |
| 125 | | | | | | 130 | | | | | 135 | | | | | |

<210> 362
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 362 | | | | | | | | | | | | | | | | |
| Met | Ala | Thr | Ala | Ser | Pro | Ser | Val | Phe | Leu | Leu | Met | Val | Asn | Gly | Gln | |
| | | | | -15 | | | | -10 | | | | | -5 | | | |
| Val | Glu | Ser | Ala | Gln | Phe | Pro | Glu | Tyr | Asp | Asp | Leu | Tyr | Cys | Lys | Tyr | |
| | | 1 | | | | | 5 | | | | | 10 | | | | |
| Cys | Phe | Val | Tyr | Gly | Gln | Asp | Trp | Ala | Pro | Thr | Ala | Gly | Leu | Glu | Glu | |
| | 15 | | | | 20 | | | | | | 25 | | | | | |
| Gly | Ile | Ser | Gln | Ile | Thr | Ser | Lys | Ser | Gln | Asp | Val | Arg | Gln | Ala | Leu | |
| 30 | | | | 35 | | | | | 40 | | | | | 45 | | |
| Val | Trp | Asn | Phe | Pro | Ile | Asp | Val | Thr | Phe | Lys | Ser | Thr | Asn | Pro | Tyr | |
| | | 50 | | | | | | 55 | | | | | 60 | | | |
| Gly | Trp | Pro | Gln | Ile | Val | Leu | Ser | Val | Tyr | Gly | Pro | Asp | Val | Phe | Gly | |
| | | 65 | | | | | 70 | | | | | 75 | | | | |
| Asn | Asp | Val | Val | Arg | Gly | Tyr | Gly | Ala | Val | His | Val | Pro | Phe | Ser | Pro | |
| | 80 | | | | | 85 | | | | | 90 | | | | | |
| Gly | Arg | His | Lys | Arg | Thr | Ile | Pro | Met | Phe | Val | Pro | Glu | Ser | Thr | Ser | |
| | 95 | | | | 100 | | | | | | 105 | | | | | |
| Lys | Leu | Gln | Lys | Phe | Thr | Ser | Trp | Phe | Met | Gly | Arg | Arg | Pro | Glu | Tyr | |
| 110 | | | | 115 | | | | | | 120 | | | | 125 | | |
| Thr | Asp | Pro | Lys | Val | Val | Ala | Gln | Gly | Glu | Gly | Arg | Glu | Ala | Ile | Thr | |
| | | | 130 | | | | | 135 | | | | | | 140 | | |
| Ala | Pro | Arg | Lys | Ala | Val | Phe | Ser | Val | His | Gly | Leu | Thr | Ser | Pro | Arg | |
| | | 145 | | | | | 150 | | | | | 155 | | | | |
| Ala | Leu | Ala | Leu | Val | His | Ile | Lys | Gly | Thr | | | | | | | |
| 160 | | | | | | 165 | | | | | | | | | | |

<210> 363
 <211> 150
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47..-1

<400> 363

```
Met Gly Asp Arg Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro
      -45                      -40                      -35
Trp Pro His Thr Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln
      -30                      -25                      -20
Pro Thr Ala Leu Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val
      -15                      -10                      -5                      1
Gly Ser Ala Pro Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
      5                      10                      15
Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
      20                      25                      30
Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
      35                      40                      45
Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
      50                      55                      60                      65
Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
      70                      75                      80
Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
      85                      90                      95
Pro Gly Ile His Leu Cys
      100
```

<210> 364

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45..-1

<400> 364

```
Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu Leu His Leu
      -45                      -40                      -35                      -30
Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser Val Ser Ala
      -25                      -20                      -15
Phe Ile Leu Leu Leu Leu Leu Ser Gly Pro Ala Glu Met Ser Ala Ser
      -10                      -5                      1
Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala Ser Leu Ile
      5                      10                      15
Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser Thr Leu Leu
      20                      25                      30                      35
Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val Asn Leu
      40                      45                      50
```

<210> 365

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 365

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ile | Glu | Ile | Glu | Val | Lys | Pro | Asn | Gln | Gly | Phe | Cys | Gly |
| -25 | | | | | | -20 | | | | | -15 | | | | |
| Ser | Ala | Cys | Leu | Leu | Ala | Val | Ile | Arg | Ala | Phe | Phe | Phe | Lys | Lys | Asn |
| -10 | | | | | -5 | | | | 1 | | | | | 5 | |
| Ala | Cys | Leu | Leu | Arg | Glu | Ile | Leu | Gln | Ser | Lys | Leu | Gly | Gly | Met | Gly |
| | | 10 | | | | | 15 | | | | | | 20 | | |
| Pro | Val | Val | Phe | Ser | Tyr | Arg | Gly | Leu | Pro | Leu | Trp | Leu | Phe | Ala | Trp |
| | 25 | | | | | | 30 | | | | | 35 | | | |
| Leu | Phe | Pro | Arg | Cys | Thr | Val | Pro | Leu | Thr | Phe | Gly | Phe | Glu | Asn | Met |
| 40 | | | | | 45 | | | | | | 50 | | | | |
| Arg | Gly | Leu | Gly | Val | Val | Ala | Tyr | Ala | Cys | Asn | Pro | Ser | Thr | | |
| 55 | | | | | 60 | | | | | 65 | | | | | |

<210> 366

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -40...-1

<400> 366

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Met | Thr | Gln | Ser | Leu | Arg | Glu | Val | Ile | Lys | Ala | Met | Thr |
| -40 | | | | | -35 | | | | | -30 | | | | -25 | |
| Lys | Ala | Arg | Asn | Phe | Glu | Arg | Val | Leu | Gly | Lys | Ile | Thr | Leu | Val | Ser |
| | | | -20 | | | | | | -15 | | | | | -10 | |
| Ala | Ala | Pro | Gly | Lys | Val | Ile | Cys | Glu | Met | Lys | Val | Glu | Glu | Glu | His |
| | | | -5 | | | | 1 | | | | 5 | | | | |
| Thr | Asn | Ala | Ile | Gly | Thr | Leu | His | Gly | Gly | Leu | Thr | Ala | Thr | Leu | Val |
| 10 | | | | | 15 | | | | | 20 | | | | | |
| Asp | Asn | Ile | Ser | Thr | Met | Ala | Leu | Leu | Cys | Thr | Glu | Arg | Gly | Ala | Pro |
| 25 | | | | | 30 | | | | | 35 | | | | 40 | |
| Gly | Val | Ser | Val | Asp | Met | Asn | Ile | Thr | Tyr | Met | Ser | Pro | Ala | Lys | Leu |
| | | | 45 | | | | | | 50 | | | | | 55 | |
| Gly | Glu | Asp | Ile | Val | Ile | Thr | Ala | His | Val | Leu | Lys | Gln | Gly | Lys | Thr |
| | | 60 | | | | | 65 | | | | | 70 | | | |
| Leu | Ala | Phe | Thr | Ser | Val | Asp | Leu | Thr | Asn | Lys | Ala | Thr | Gly | Lys | Leu |
| | 75 | | | | | 80 | | | | | | 85 | | | |
| Ile | Ala | Gln | Gly | Arg | His | Thr | Lys | His | Leu | Gly | Asn | | | | |
| 90 | | | | | | 95 | | | | | 100 | | | | |

<210> 367

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 367

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Pro | Gly | Trp | Pro | His | Phe | Lys | Leu | Thr | His | Ser | Arg | Cys | Met |
| -35 | | | | | -30 | | | | | -25 | | | | -20 | |
| Ala | Val | Leu | Phe | Leu | Gly | Thr | Leu | Pro | Leu | Cys | Pro | Val | Thr | Ser | Pro |

Val Trp Gly Trp Ser Pro Gly
1

-15

-10

-5

<210> 368
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 368
Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
-40 -35 -30
Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
-25 -20 -15 -10
Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
-5 1 5
Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
10 15 20
Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
25 30 35

<210> 369
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 369
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
-40 -35 -30 -25
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
-20 -15 -10
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
-5 1 5
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
10 15 20
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
25 30 35 40
Lys Ser Lys

<210> 370
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 370
Met Ala Val Leu Ala Gly Ser Leu Leu Gly Pro Thr Ser Arg Ser Ala

```

-15          -10          -5          1
Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro Arg Ala Trp Leu Gly Phe
      5          10          15
Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln Gln Ala Arg Gly Lys Ala
      20          25          30
Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile Lys Arg Lys Asn Lys His
      35          40          45
Gly Trp Val Arg Arg Leu Ser Thr Pro Ala Gly Val Gln Val Ile Leu
50          55          60          65
Arg Arg Met Leu Lys Gly Arg Lys Ser Leu Ser His
      70          75

```

<210> 371
 <211> 279
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

```

<400> 371
Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly Gly Trp
      -40          -35          -30
Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg Ser Leu
      -25          -20          -15
Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg Leu Leu
-10          -5          1          5
Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys Pro Leu Thr
      10          15          20
Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu Ile Glu
      25          30          35
Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu Asn Gln
      40          45          50
Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp Glu Gln
55          60          65          70
Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln Lys Phe
      75          80          85
Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu Lys Asn
      90          95          100
Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val Leu Leu
      105          110          115
Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro Gln Ala
      120          125          130
Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg Thr Leu
135          140          145          150
Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly Asn Ala
      155          160          165
Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg Thr Glu
      170          175          180
Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu Leu Leu Thr
      185          190          195
Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp Val Ile
      200          205          210
Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala Gln Val
215          220          225          230
Arg Arg Phe Val Ser Asp Leu
      235

```


<210> 372
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 372
 Met Ala Cys Thr Thr Thr Ala Pro Ala Gln Glu His Met Leu Leu Thr
 -30 -25 -20
 Pro Leu Thr Ala Leu Met Val Gly Ala Ala Ser Leu Leu Glu Gly Arg
 -15 -10 -5 1
 Pro Gln Ile Ser Ala Pro Tyr Ser Arg Ala Ala Cys Cys Ser Pro Gly
 5 10 15
 Ala Leu Gly Cys Pro Ala Ala Arg Val Gly Ile Leu Asp Leu Met Tyr
 20 25 30
 Ser Trp Val Ala Arg Lys Val Leu Arg Cys Ser Asn Thr Gly Leu Gln
 35 40 45
 Gly Leu His Cys Ala Pro Ala Tyr Ala Ala Gln Leu Gly Met Asp Pro
 50 55 60 65
 Gly Arg Gly Gln Arg Ala Gly Gly Pro Val Glu Gln Thr Tyr Phe Ser
 70 75 80
 Pro Met Gly Lys Leu Pro Thr Leu Ser Trp Leu Glu Gly Cys Thr Ala
 85 90 95
 Val Met Thr Leu Ala Ser Ala Trp Leu Leu Gly Ser Pro Arg Glu Thr
 100 105 110
 Tyr Asn His Glu Lys Val Lys Glu Lys Gln Cys Pro Phe Ser Ser Met
 115 120 125
 Val Leu Gly Glu Tyr Gly Phe Leu Pro Thr Val Asp His Leu Ser Thr
 130 135 140 145
 Leu Gly Cys Asn Met Arg Glu Leu
 150

<210> 373
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 373
 Met Ala His Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys
 -40 -35 -30
 Ile Pro Gly Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys
 -25 -20 -15
 Phe His Leu Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr
 -10 -5 1 5
 Ala Pro Val Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu
 10 15 20
 Asp Leu Val Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val
 25 30 35
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala
 40 45 50

Cys Thr His Arg Asp
55

<210> 374
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 374
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser
-20 -15 -10 -5
Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu
1 5 10
Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln
15 20 25
Gln Pro Cys Lys Ser Gly Gly Gly Val Gly Glu Pro Asn Ala Gln
30 35 40
Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser
45 50 55 60
His Gly Gln Ala Phe
65

<210> 375
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 375
Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val
-25 -20 -15
Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys
-10 -5 1
Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val
5 10 15 20
Met Leu Val Ala Pro Phe Arg Gln Ser Ser Ser Leu Ser Arg Thr Phe
25 30 35
Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg
40 45 50
Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly
55 60

<210> 376
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<220>
 <221> UNSURE
 <222> 47
 <223> Xaa = Ala,Pro,Ser,Thr

<400> 376
 Met Ala Gln Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu
 -30 -25 -20
 Ala Pro Thr Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser
 -15 -10 -5
 Ser Ala Pro Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu
 1 5 10 15
 Leu Leu Leu Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala
 20 25 30
 Pro Ala Arg Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa
 35 40 45
 Gly Pro Leu Ile Pro Gly Gln Cys Pro
 50 55

<210> 377
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 377
 Met Asn Arg Val Leu Cys Ala Pro Ala Ala Gly Ala Val Arg Ala Leu
 -15 -10 -5 1
 Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu His Pro Leu Pro Gly Ser
 5 10 15
 Arg Asp Arg Ala His Pro Ala Ala Glu Glu Glu Asp Asp Pro Asp Arg
 20 25 30
 Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn Pro His Arg Trp Ser Val
 35 40 45
 Gly His Thr Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu
 50 55 60 65
 Pro Leu Ser Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg
 70 75 80
 Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val
 85 90 95
 Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr
 100 105 110
 Arg Ala Arg Thr
 115

<210> 378
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<220>

<221> UNSURE
 <222> 50
 <223> Xaa = Ala,Gly

<220>
 <221> UNSURE
 <222> 51
 <223> Xaa = Leu,Met,Val

<400> 378
 Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
 Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
 Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp
 20 25 30
 Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa
 35 40 45 50
 Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
 55 60 65
 Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
 70 75 80
 Val Thr Lys Lys Trp Ser
 85

<210> 379
 <211> 504
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 379
 Met Gly Ile Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser
 -20 -15 -10
 Leu Val Leu Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu
 -5 1 5
 Ala Ser Gln Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg
 10 15 20
 Pro Gly Trp Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu
 25 30 35 40
 Trp Val Met Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu
 45 50 55
 Ser Gly His Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys
 60 65 70
 Leu Arg Ser Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly
 75 80 85
 Thr Met Gly Pro Trp Tyr Leu Leu Leu Leu Leu Gly His Cys Val Gly
 90 95 100
 Leu Tyr Val Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu
 105 110 115 120
 Gly Leu Ala Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp
 125 130 135
 Gln Ser Gly Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe
 140 145 150
 His Gly Gly Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu

Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro
 25 30 35
 Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu
 40 45 50
 Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys
 55 60 65 70
 Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser
 75 80 85
 Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser
 90 95 100
 Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala
 105 110 115
 Thr Leu Leu Ile Leu Asp Ile Trp
 120 125

<210> 381
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 381
 Met Glu Met Leu Phe Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe
 -25 -20 -15
 Lys Phe Ser Leu Cys Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe
 -10 -5 1 5
 Gly Ser Val Ala Cys Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly
 10 15 20
 Ser Arg Leu
 25

<210> 382
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 382
 Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
 -20 -15 -10
 Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
 -5 1 5
 Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
 10 15 20 25
 Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
 30 35 40
 Val Tyr Lys Pro Ile Arg Arg Arg
 45

<210> 383
 <211> 95
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 383

```
Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
      -45                      -40                      -35
Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
      -30                      -25                      -20
Thr Ala Cys Phe Val Ile Leu Leu Phe Ile Phe Thr Val Val Ser
      -15                      -10                      -5
Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys
1          5          10          15
Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
      20          25          30
Arg Ser Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
      35          40          45
```

<210> 384

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 384

```
Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
-20                      -15                      -10                      -5
Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
      1          5          10
Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
      15          20          25
Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
      30          35          40
Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
      45          50          55          60
Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe
      65          70          75
Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
      80          85          90
Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala Pro
      95          100          105
Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met Ala
      110          115          120
Ser Met Glu Ser Pro Gln
125          130
```

<210> 385

<211> 354

<212> PRT

<213> Homo sapiens

<400> 385

Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | | |
| Met | Pro | Thr | Cys | Arg | Val | Tyr | Gly | Thr | Val | Ala | His | Gln | Asp | Gly | His | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Leu | Leu | Val | Leu | Gly | Gly | Cys | Gly | Arg | Ala | Gly | Leu | Pro | Leu | Asp | Thr | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Ala | Glu | Thr | Leu | Asp | Met | Ala | Ser | His | Thr | Trp | Leu | Ala | Leu | Ala | Pro | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Leu | Pro | Thr | Ala | Arg | Ala | Gly | Ala | Ala | Ala | Val | Val | Leu | Gly | Lys | Gln | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Val | Leu | Val | Val | Cys | Gly | Val | Asp | Glu | Val | Gln | Ser | Pro | Val | Ala | Ala | | |
| | | | | 85 | | | | 90 | | | | | | 95 | | | |
| Val | Glu | Ala | Phe | Leu | Met | Asp | Glu | Gly | Arg | Trp | Glu | Arg | Arg | Ala | Thr | | |
| | | 100 | | | | | | 105 | | | | | 110 | | | | |
| Leu | Pro | Gln | Ala | Ala | Met | Gly | Val | Ala | Thr | Val | Glu | Arg | Asp | Gly | Met | | |
| | 115 | | | | | | 120 | | | | | 125 | | | | | |
| Val | Tyr | Ala | Leu | Gly | Gly | Met | Gly | Pro | Asp | Thr | Ala | Pro | Gln | Ala | Gln | | |
| 130 | | | | | | 135 | | | | | 140 | | | | | | |
| Val | Arg | Val | Tyr | Asp | Pro | Arg | Arg | Asp | Cys | Trp | Leu | Ser | Leu | Pro | Ser | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| Met | Pro | Thr | Pro | Cys | Tyr | Gly | Ala | Ser | Thr | Phe | Leu | His | Gly | Asn | Lys | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| Ile | Tyr | Val | Leu | Gly | Gly | Arg | Gln | Gly | Lys | Leu | Pro | Val | Thr | Ala | Phe | | |
| | | 180 | | | | | | 185 | | | | | 190 | | | | |
| Glu | Ala | Phe | Asp | Leu | Glu | Ala | Arg | Thr | Trp | Thr | Arg | His | Pro | Ser | Leu | | |
| | 195 | | | | | | 200 | | | | | 205 | | | | | |
| Pro | Ser | Arg | Arg | Ala | Phe | Ala | Gly | Cys | Ala | Met | Ala | Glu | Gly | Ser | Val | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| Phe | Ser | Leu | Gly | Gly | Leu | Gln | Gln | Pro | Gly | Pro | His | Asn | Phe | Tyr | Ser | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Arg | Pro | His | Phe | Val | Asn | Thr | Val | Glu | Met | Phe | Asp | Leu | Glu | His | Gly | | |
| | | | | 245 | | | | 250 | | | | | | 255 | | | |
| Ser | Trp | Thr | Lys | Leu | Pro | Arg | Ser | Leu | Arg | Met | Arg | Asp | Lys | Arg | Ala | | |
| | | 260 | | | | | | 265 | | | | | 270 | | | | |
| Asp | Phe | Val | Val | Gly | Ser | Leu | Gly | Gly | His | Ile | Val | Ala | Ile | Gly | Gly | | |
| | 275 | | | | | | 280 | | | | | 285 | | | | | |
| Leu | Gly | Asn | Gln | Pro | Cys | Pro | Leu | Gly | Ser | Val | Glu | Ser | Phe | Ser | Leu | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| Ala | Arg | Arg | Arg | Trp | Glu | Ala | Leu | Pro | Ala | Met | Pro | Thr | Ala | Arg | Cys | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| Ser | Cys | Ser | Ser | Leu | Gln | Ala | Gly | Pro | Arg | Leu | Phe | Val | Ile | Gly | Gly | | |
| | | | | 325 | | | | 330 | | | | | | 335 | | | |
| Val | Ala | Gln | Gly | Pro | Ser | Gln | Ala | Val | Glu | Ala | Leu | Cys | Leu | Arg | Asp | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |

Gly Val

<210> 386

<211> 207

<212> PRT

<213> Homo sapiens

<400> 386

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ala | Leu | Leu | Phe | Ala | Arg | Ser | Leu | Arg | Leu | Cys | Arg | Trp | Gly | Ala | | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | | |
| Lys | Arg | Leu | Gly | Val | Ala | Ser | Thr | Glu | Ala | Gln | Arg | Gly | Val | Ser | Phe | | |
| | | 20 | | | | | | 25 | | | | | 30 | | | | |
| Lys | Leu | Glu | Lys | Thr | Ala | His | Ser | Ser | Leu | Ala | Leu | Phe | Arg | Asp | | | |
| | | 35 | | | | 40 | | | | | 45 | | | | | | |
| Asp | Thr | Gly | Val | Lys | Tyr | Gly | Leu | Val | Gly | Leu | Glu | Pro | Thr | Lys | Val | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50 | | 55 | | 60 | | | | | | | | | | | |
| Ala | Leu | Asn | Val | Glu | Arg | Phe | Arg | Glu | Trp | Ala | Val | Val | Leu | Ala | Asp |
| 65 | | | | 70 | | | | 75 | | | | | | | 80 |
| Thr | Ala | Val | Thr | Ser | Gly | Arg | His | Tyr | Trp | Glu | Val | Thr | Val | Lys | Arg |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Ser | Gln | Gln | Phe | Arg | Ile | Gly | Val | Ala | Asp | Val | Asp | Met | Ser | Arg | Asp |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Cys | Ile | Gly | Val | Asp | Asp | Arg | Ser | Trp | Val | Phe | Thr | Tyr | Ala | Gln |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Arg | Lys | Trp | Tyr | Thr | Met | Leu | Ala | Asn | Glu | Lys | Ala | Pro | Val | Glu | Gly |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Ile | Gly | Gln | Pro | Glu | Lys | Val | Gly | Leu | Leu | Leu | Glu | Tyr | Glu | Ala | Gln |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Lys | Leu | Ser | Leu | Val | Asp | Val | Ser | Gln | Val | Ser | Val | Val | His | Thr | Leu |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Gln | Thr | Asp | Phe | Arg | Gly | Pro | Val | Val | Pro | Ala | Phe | Ala | Leu | Trp | Asp |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gly | Glu | Leu | Leu | Thr | His | Ser | Gly | Leu | Glu | Val | Pro | Glu | Gly | Leu | |
| | | 195 | | | | | 200 | | | | | | 205 | | |

<210> 387
 <211> 210
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 387 | | | | | | | | | | | | | | | |
| Met | Ala | Ala | Ser | Val | Glu | Gln | Arg | Glu | Gly | Thr | Ile | Gln | Val | Gln | Gly |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Gln | Ala | Leu | Phe | Phe | Arg | Glu | Ala | Leu | Pro | Gly | Ser | Gly | Gln | Ala | Arg |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Phe | Ser | Val | Leu | Leu | Leu | His | Gly | Ile | Arg | Phe | Ser | Ser | Glu | Thr | Trp |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Gln | Asn | Leu | Gly | Thr | Leu | His | Arg | Leu | Ala | Gln | Ala | Gly | Tyr | Arg | Ala |
| | | 50 | | | | 55 | | | | 60 | | | | | |
| Val | Ala | Ile | Asp | Leu | Pro | Gly | Leu | Gly | His | Ser | Lys | Glu | Ala | Ala | Ala |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Pro | Ala | Pro | Ile | Gly | Glu | Leu | Ala | Pro | Gly | Ser | Phe | Leu | Ala | Ala | Val |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Val | Asp | Ala | Leu | Glu | Leu | Gly | Pro | Pro | Val | Val | Ile | Ser | Pro | Ser | Leu |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Ser | Gly | Met | Tyr | Ser | Leu | Pro | Phe | Leu | Thr | Ala | Pro | Gly | Ser | Gln | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Pro | Gly | Phe | Val | Pro | Val | Ala | Pro | Ile | Cys | Thr | Asp | Lys | Ile | Asn | Ala |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Ala | Asn | Tyr | Ala | Ser | Val | Lys | Thr | Pro | Ala | Leu | Ile | Val | Tyr | Gly | Asp |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | |
| Gln | Asp | Pro | Met | Gly | Gln | Thr | Ser | Phe | Glu | His | Leu | Lys | Gln | Leu | Pro |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Asn | His | Arg | Val | Leu | Ile | Met | Lys | Gly | Ala | Gly | His | Pro | Cys | Tyr | Leu |
| | | 180 | | | | | 185 | | | | | 190 | | | |
| Asp | Lys | Pro | Glu | Glu | Trp | His | Thr | Gly | Leu | Leu | Asp | Phe | Leu | Gln | Gly |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Leu | Gln | | | | | | | | | | | | | | |
| | | 210 | | | | | | | | | | | | | |

<210> 388
 <211> 375
 <212> PRT

<213> Homo sapiens

<400> 388

Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu
1 5 10 15
Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln
20 25 30
Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu
35 40 45
Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser
50 55 60
Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu
65 70 75 80
Met Ser Phe Met Met Glu Leu Lys Met Leu Leu Glu Val Ala Leu Lys
85 90 95
Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro Pro Gln Phe Tyr Ser
100 105 110
Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp Asp Lys Leu Val Tyr
115 120 125
Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys Ala Glu Asp Ala Ser
130 135 140
Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys Ala Lys Tyr Pro Ala
145 150 155 160
Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val Pro Phe Cys Ala Ser
165 170 175
Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr Ser Gln Phe Leu Ala
180 185 190
Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val Met Asp Glu Ile Asp
195 200 205
Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro Pro Arg Ser Ala Thr
210 215 220
Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser Ile Asn Ile Glu Val
225 230 235 240
Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys Phe Phe Leu Gly Ala
245 250 255
Asp His Val Val Lys Pro Leu Gly Ile Lys Leu Ser Arg Asn Ile His
260 265 270
Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn Leu Lys Asp Val Leu
275 280 285
Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu Lys Ser Asp Phe Thr
290 295 300
Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu Asp Gly Thr Ile Pro
305 310 315 320
Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln Pro Phe His Gln Ile
325 330 335
Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr Ser Arg Gln Ser Phe
340 345 350
Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser Lys Pro Ile Thr Leu
355 360 365
Lys Met Ser Gly Arg Lys His
370 375

<210> 389

<211> 509

<212> PRT

<213> Homo sapiens

<400> 389

Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu
 465 470 475 480
 Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu
 485 490 495
 Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser
 500 505

<210> 390
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 390
 Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His
 1 5 10 15
 Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu
 20 25 30
 Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His
 35 40 45
 Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu
 50 55 60
 Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
 65 70 75

<210> 391
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 391
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly

<210> 392
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 392

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu
1 5 10 15
Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala
20 25 30
Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro
35 40 45
Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr
50 55 60
Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro
65 70 75 80
His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val
85 90 95
Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys
100 105 110
Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu
115 120 125
Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu
130 135 140
Gly Phe
145

<210> 393
<211> 225
<212> PRT
<213> Homo sapiens

<400> 393
Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
1 5 10 15
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
20 25 30
Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
35 40 45
Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
50 55 60
Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
65 70 75 80
Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
85 90 95
Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
100 105 110
Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
115 120 125
Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
130 135 140
Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
145 150 155 160
Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
165 170 175
Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
180 185 190
Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
195 200 205
Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
210 215 220
Val
225

<210> 394
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 394
 Met Arg Leu Gln Asp Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met
 1 5 10 15
 Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile
 20 25 30
 Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp His
 35 40 45
 Met Ser Phe His Tyr Thr Val Leu Met Phe Ser Gln Val Ile Ser
 50 55 60
 Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn
 65 70 75 80
 Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val Ser
 85 90 95
 Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu
 100 105 110
 Gln Gly

<210> 395
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 395
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
 145 150 155 160
 Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
 165 170 175
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
 180 185 190
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
 195 200 205
 Ser Lys Gln Lys Lys Leu Met Val Lys Ile Leu Glu His Asp Asp Val
 210 215 220
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln
 225 230 235 240

Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys
 245 250 255
 Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu
 260 265 270
 Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys
 275 280 285
 Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg
 290 295 300
 Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr
 305 310 315 320
 Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg
 325 330 335
 Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly
 340 345 350
 Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile
 355 360 365

<210> 396
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 396
 Met Pro Val Cys Ala Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly
 1 5 10 15
 Met Pro Val Cys Ala Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr
 20 25 30
 Arg Ala Val Val Cys Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly
 35 40 45
 Cys Thr His Met Cys Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser
 50 55 60
 Pro Leu Ala Gly Gly Val Ile Leu Gly Val Ala Leu Trp Leu Arg His
 65 70 75 80
 Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro
 85 90 95
 Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly
 100 105 110
 Ala Val Met Met Phe Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln
 115 120 125
 Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu
 130 135 140
 Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp
 145 150 155 160
 Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln
 165 170 175
 Ala Val Val Asp Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr
 180 185 190
 Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu
 195 200 205
 Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile
 210 215 220
 Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu
 225 230 235 240
 Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala
 245 250 255
 Val Ile Met Ile Phe Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly
 260 265 270
 Ile Arg Asn Ser Ser Val Tyr

275

<210> 397
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
 1 5 10 15
 Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
 20 25 30
 Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
 35 40 45
 Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
 50 55 60
 Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
 65 70 75 80
 Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val Gln Leu
 85 90 95
 Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
 100 105 110
 Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu Glu Met
 115 120 125
 Lys Ser Leu Ile Arg Leu Pro Asp Ile Ile Ala Cys Ala Lys Gln Asn
 130 135 140
 Ile Thr Thr Ala Glu Ile Ser Ala Arg Glu Gly Thr Gly Leu Ala Gly
 145 150 155 160
 Val Leu Ala Trp Leu Gln Ala Thr His Arg Ala Asn Asp
 165 170

<210> 398
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 398
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Val Leu Phe Leu Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala
 20 25 30
 Tyr Phe Pro Gln Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala
 35 40 45
 Arg Leu Leu Glu Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly
 50 55 60
 Leu Gly Pro Thr Val Pro Glu Leu Gly Thr Glu Gly Leu Arg Pro Leu
 65 70 75 80
 Ala Lys Thr Cys Phe Ser Met Val Pro Ala Leu Gln Gln Glu Leu Asp
 85 90 95
 Ser Arg Pro Gln Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln
 100 105 110
 Ala Cys Ile Leu Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln
 115 120 125
 Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg
 130 135 140
 Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr
 145 150 155 160
 Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Lys | Glu | Ile | 165 | Gln | Lys | Leu | Ile | Lys | 170 | Glu | Pro | Ala | Pro | Asp | 175 | Ser | Gly |
| | | | 180 | | | | | | 185 | | | | | | 190 | | | |
| Leu | Leu | Gly | Leu | Phe | Gln | Gly | Gln | Asn | Ser | Leu | Leu | His | | | | | | |
| | | 195 | | | | | 200 | | | | | | 205 | | | | | |

<210> 399
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 399

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Leu | Tyr | Arg | Asn | Pro | Tyr | Val | Glu | Ala | Glu | Tyr | Phe | Pro | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Pro | Met | Phe | Val | Ile | Ala | Phe | Leu | Ser | Pro | Leu | Ser | Leu | Ile | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Ala | Lys | Phe | Leu | Lys | Lys | Ala | Asp | Thr | Arg | Asp | Ser | Arg | Gln | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Cys | Leu | Ala | Ala | Ser | Leu | Ala | Leu | Ala | Leu | Asn | Gly | Val | Phe | Thr | Asn |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Thr | Ile | Lys | Leu | Ile | Val | Gly | Arg | Pro | Arg | Pro | Asp | Phe | Phe | Tyr | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Cys | Phe | Pro | Asp | Gly | Leu | Ala | His | Ser | Asp | Leu | Met | Cys | Thr | Gly | Asp |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Lys | Asp | Val | Val | Asn | Glu | Gly | Arg | Lys | Ser | Phe | Pro | Ser | Gly | His | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Phe | Ala | Phe | Ala | Gly | Leu | Ala | Phe | Ala | Ser | Phe | Tyr | Leu | Ala | Gly |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Lys | Leu | His | Cys | Phe | Thr | Pro | Gln | Gly | Arg | Gly | Lys | Ser | Trp | Arg | Phe |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Cys | Ala | Phe | Leu | Ser | Pro | Leu | Leu | Phe | Ala | Ala | Val | Ile | Ala | Leu | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Arg | Thr | Cys | Asp | Tyr | Lys | His | His | Trp | Gln | Asp | Leu | Leu | Lys | Cys | Thr |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Asn | Thr | Ala | Lys | | | | | | | | | | | | |
| | | | 180 | | | | | | | | | | | | |

<210> 400
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 400

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Thr | Ala | Leu | Leu | Leu | Leu | Tyr | Leu | Arg | Trp | Cys | Phe | Asn | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Leu | Val | Asn | Val | Lys | Tyr | Glu | Pro | Lys | Asp | Ser | Leu | Gly | Pro | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Met | Thr | Phe | Val | Ala | Asp | Ala | Ala | Arg | Gly | Pro | Leu | Leu | Ser | Ser | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asp | Ser | Pro | Ala | Asn | Leu | Met | Ser | Thr | Ala | Ser | Val | Cys | Ile | Ser | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Glu | Gly | Cys | Ser | Gly | Gly | Arg | Ser | Pro | Cys | Tyr | Ser | Gln | Lys | Trp |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Pro | Pro | Glu | Val | Pro | Glu | Lys | Leu | Thr | Ser | Leu | Gly | Gln | Gln | Ser | Ser |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Thr | Ser | Ser | Leu | Thr | Asp | Thr | Asp | Val | Gln | Val | Ser | Pro | Met | Leu | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Gly | Val | Asn | His | Ser | Ser | Ser | Leu | Leu | Asp | Asn | Ile | Pro | Phe | Thr |

[illegible][illegible][illegible][illegible][illegible]

130 135 140
 Thr Glu Cys Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His
 145 150 155 160
 Tyr Ile Arg His Ala Arg Gly Glu Leu
 165

<210> 403
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 403
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
 145 150 155 160
 Cys Ile Leu His Leu Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
 165 170 175
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
 180 185 190
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
 195 200 205
 Ser Lys Gln Lys Lys Leu Met Ala Lys Ile Leu Glu His Asp Asp Val
 210 215 220
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln
 225 230 235 240
 Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys
 245 250 255
 Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu
 260 265 270
 Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys
 275 280 285
 Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg
 290 295 300
 Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr
 305 310 315 320
 Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg
 325 330 335
 Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly
 340 345 350
 Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Tyr Ile
 355 360 365

<210> 404
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 404
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Pro Val Pro Val
 20

<210> 405
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 405
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
 165 170 175
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
 180 185 190
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
 195 200 205
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
 210 215 220
 Val
 225

<210> 406
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 406
 Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu Tyr Gln
 1 5 10 15
 Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu Glu Trp

<210> 408
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 408

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Trp | Arg | Gly | Trp | Ala | Gln | Arg | Gly | Trp | Gly | Cys | Gly | Gln | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Trp | Gly | Ala | Ser | Val | Gly | Gly | Arg | Ser | Cys | Glu | Glu | Leu | Thr | Ala | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Thr | Pro | Pro | Gln | Leu | Leu | Gly | Arg | Arg | Phe | Asn | Phe | Phe | Ile | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gln | Lys | Cys | Gly | Phe | Arg | Lys | Ala | Pro | Arg | Lys | Val | Glu | Pro | Arg | Arg |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Ser | Asp | Pro | Gly | Thr | Ser | Gly | Glu | Ala | Tyr | Lys | Arg | Ser | Ala | Leu | Ile |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Pro | Pro | Val | Glu | Glu | Thr | Val | Phe | Tyr | Pro | Ser | Pro | Tyr | Pro | Ile | Arg |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Ser | Leu | Ile | Lys | Pro | Leu | Phe | Phe | Thr | Val | Gly | Phe | Thr | Gly | Cys | Ala |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Gly | Ser | Ala | Ala | Ile | Trp | Gln | Tyr | Glu | Ser | Leu | Lys | Ser | Arg | Val |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gln | Ser | Tyr | Phe | Asp | Gly | Ile | Lys | Ala | Asp | Trp | Leu | Asp | Ser | Ile | Arg |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Pro | Gln | Lys | Glu | Gly | Asp | Phe | Arg | Lys | Glu | Ile | Asn | Lys | Trp | Trp | Asn |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Asn | Leu | Ser | Asp | Gly | Gln | Arg | Thr | Val | Thr | Gly | Ile | Ile | Ala | Ala | Asn |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Val | Leu | Val | Phe | Cys | Leu | Trp | Arg | Val | Pro | Ser | Leu | Gln | Arg | Thr | Met |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ile | Arg | Tyr | Phe | Thr | Ser | Asn | Pro | Ala | Ser | Lys | Val | Leu | Cys | Ser | Pro |
| | | 195 | | | | 200 | | | | | | 205 | | | |
| Met | Leu | Leu | Ser | Thr | Phe | Ser | His | Phe | Ser | Leu | Phe | His | Met | Ala | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asn | Met | Tyr | Val | Leu | Trp | Ser | Phe | Ser | Ser | Ser | Ile | Val | Asn | Ile | Leu |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Gly | Gln | Glu | Gln | Phe | Met | Ala | Val | Tyr | Leu | Ser | Ala | Gly | Val | Ile | Ser |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Asn | Phe | Val | Ser | Tyr | Val | Gly | Lys | Val | Ala | Thr | Gly | Arg | Tyr | Gly | Pro |
| | | | 260 | | | | 265 | | | | | | 270 | | |
| Ser | Leu | Gly | Ala | Ala | Leu | Lys | Ala | Ile | Ile | Ala | Met | Asp | Thr | Ala | Gly |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Met | Ile | Leu | Gly | Trp | Lys | Phe | Phe | Asp | His | Ala | Ala | His | Leu | Gly | Gly |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ala | Leu | Phe | Gly | Ile | Trp | Tyr | Val | Thr | Tyr | Gly | His | Glu | Leu | Ile | Trp |
| 305 | | | | 310 | | | | | | 315 | | | | 320 | |
| Lys | Asn | Arg | Glu | Pro | Leu | Val | Lys | Ile | Trp | His | Glu | Ile | Arg | Thr | Asn |
| | | | 325 | | | | | | 330 | | | | | 335 | |
| Gly | Pro | Lys | Lys | Gly | Gly | Gly | Ser | Lys | | | | | | | |
| | | | 340 | | | | | 345 | | | | | | | |

<210> 409
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 409

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Ser | Gly | Asn | Pro | Gly | Ala | Glu | Val | Thr | Asn | Ser | Ser | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Gly | Pro | Asp | Cys | Cys | Gly | Gly | Leu | Gly | Asn | Ile | Asp | Phe | Arg | Gln |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Asp | Phe | Cys | Val | Met | Thr | Arg | Leu | Leu | Gly | Tyr | Val | Asp | Pro | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asp | Pro | Ser | Phe | Val | Ala | Ala | Val | Ile | Thr | Ile | Thr | Phe | Asn | Pro | Leu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Tyr | Trp | Asn | Val | Val | Ala | Arg | Trp | Glu | His | Lys | Thr | Arg | Lys | Leu | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Arg | Ala | Phe | Gly | Ser | Pro | Tyr | Leu | Ala | Cys | Tyr | Ser | Leu | Ser | Ile | Thr |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Ile | Leu | Leu | Leu | Asn | Phe | Leu | Arg | Ser | His | Cys | Phe | Thr | Gln | Ala | Met |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Ser | Gln | Pro | Arg | Met | Glu | Ser | Leu | Asp | Thr | Pro | Ala | Ala | Tyr | Ser |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Val | Leu | Ala | Leu | Leu | Gly | Leu | Gly | Val | Val | Leu | Val | Leu | Ser | Ser |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Phe | Phe | Ala | Leu | Gly | Phe | Ala | Gly | Thr | Phe | Leu | Gly | Asp | Tyr | Phe | Gly |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 |
| Ile | Leu | Lys | Glu | Ala | Arg | Val | Thr | Val | Phe | Pro | Phe | Asn | Ile | Leu | Asp |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Asn | Pro | Met | Tyr | Trp | Gly | Ser | Thr | Ala | Asn | Tyr | Leu | Gly | Trp | Ala | Ile |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Met | His | Ala | Ser | Pro | Thr | Gly | Leu | Leu | Leu | Thr | Val | Leu | Val | Ala | Leu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Tyr | Ile | Val | Ala | Leu | Leu | Tyr | Glu | Glu | Pro | Phe | Thr | Ala | Glu | Ile |
| | 210 | | | | 215 | | | | | | 220 | | | | |
| Tyr | Arg | Gln | Lys | Ala | Ser | Gly | Ser | His | Lys | Arg | Ser | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | |

<210> 410
 <211> 121
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Thr | Glu | Ala | Glu | Gln | Gln | Leu | Leu | His | His | Ala | Arg | Asn | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Ala | Glu | Glu | Val | Arg | Gln | Leu | Leu | Glu | Thr | Met | Ala | Ser | Asn | Glu |
| | | 20 | | | | | 25 | | | | | | 30 | | |
| Val | Ile | Ala | Asp | Ile | Asn | Cys | Lys | Gly | Arg | Ser | Lys | Ser | Asn | Leu | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Trp | Thr | Pro | Leu | His | Leu | Ala | Cys | Tyr | Phe | Gly | His | Arg | Gln | Val | Val |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Gln | Asp | Leu | Leu | Lys | Ala | Gly | Ala | Glu | Val | Asn | Val | Leu | Asn | Asp | Met |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Gly | Asp | Thr | Pro | Leu | His | Arg | Ala | Ala | Phe | Thr | Gly | Arg | Lys | Val | Lys |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Ile | Ile | Leu | Cys | Ser | Met | Phe | Val | Ser | Glu | Val | Phe | Gly | Gly | Val | Val |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Thr | Ile | Val | Phe | Ser | Val | Ile | Thr | Ile | | | | | | | |
| | | 115 | | | | | 120 | | | | | | | | |

<210> 411
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 411

Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1 5 10 15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
20 25 30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35 40 45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50 55 60
Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65 70 75 80
Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85 90 95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100 105 110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115 120 125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130 135 140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145 150 155 160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165 170

<210> 412

<211> 236

<212> PRT

<213> Homo sapiens

<400> 412

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
1 5 10 15
Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala
20 25 30
Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
35 40 45
Ser Val Leu Lys Leu His His Ser Leu Gln Gln Ser Glu Pro Asp Leu
50 55 60
Arg His Leu Val Leu Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser
65 70 75 80
Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala
85 90 95
Pro Ser Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
100 105 110
Ala Ser Met Ala Ser Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
115 120 125
Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
130 135 140
Ile Gly Gly Ala Ala Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro
145 150 155 160
Ala Thr Gly Cys Leu Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp
165 170 175
Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
180 185 190
Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
195 200 205
Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly

| | | |
|-------------------------|-------------------------|-----|
| 210 | 215 | 220 |
| Thr Gln Ala Leu Glu Arg | Pro Pro Gly Pro Gly Arg | |
| 225 | 230 | 235 |

<210> 413
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 413

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Gly | Leu | Tyr | Phe | Gln | Gln | Ser | Ser | Thr | Asp | Glu | Glu | Ile | Thr |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Phe | Val | Phe | Gln | Glu | Lys | Glu | Asp | Leu | Pro | Val | Thr | Glu | Asp | Asn | Phe |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Val | Lys | Leu | Gln | Val | Lys | Ala | Cys | Ala | Leu | Ser | Gln | Ile | Asn | Thr | Lys |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Leu | Ala | Glu | Met | Lys | Met | Lys | Lys | Asp | Leu | Phe | Pro | Val | Gly | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Ile | Ala | Gly | Ile | Val | Leu | Asp | Val | Gly | Ser | Lys | Val | Ser | Phe | Phe |
| 65 | | | | 70 | | | | | | 75 | | | | 80 | |
| Gln | Pro | Asp | Asp | Glu | Val | Val | Gly | Ile | Leu | Pro | Leu | Asp | Ser | Glu | Asp |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Pro | Gly | Leu | Cys | Glu | Val | Val | Arg | Val | His | Glu | His | Tyr | Leu | Val | His |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Lys | Pro | Glu | Lys | Val | Thr | Trp | Thr | Glu | Ala | Ala | Gly | Ser | Ile | Arg | Asp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gly | Val | Arg | Ala | Tyr | Thr | Ala | Leu | His | Tyr | Leu | Ser | His | Leu | Ser | Pro |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gly | Lys | Ser | Val | Leu | Ile | Met | Asp | Gly | Ala | Ser | Ala | Phe | Gly | Thr | Ile |
| 145 | | | | 150 | | | | | | 155 | | | | 160 | |
| Ala | Ile | Gln | Leu | Ala | His | His | Arg | Gly | Ala | Lys | Val | Phe | Gln | Gln | His |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Ala | Ala | Leu | Lys | Ile | Ser | Ser | Ala | Leu | Lys | Asp | Ser | Asp | Leu | Pro | |
| | | 180 | | | | | | 185 | | | | | 190 | | |

<210> 414
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 414

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Pro | Asp | Pro | Ser | His | Pro | Leu | Glu | Thr | Gln | Ala | Gly | Lys |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Val | Gln | Glu | Ala | Gln | Asp | Ser | Asp | Ser | Asp | Ser | Glu | Gly | Gly | Ala | Ala |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Gly | Gly | Glu | Ala | Asp | Met | Asp | Phe | Leu | Arg | Asn | Leu | Phe | Ser | Gln | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Ser | Leu | Gly | Ser | Gln | Lys | Glu | Arg | Leu | Leu | Asp | Glu | Leu | Thr | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Gly | Val | Ala | Arg | Tyr | Met | Gln | Ser | Glu | Arg | Cys | Arg | Arg | Val | Ile |
| 65 | | | | 70 | | | | | | 75 | | | | 80 | |
| Cys | Leu | Val | Gly | Ala | Gly | Ile | Ser | Thr | Ser | Ala | Gly | Ile | Pro | Asp | Phe |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Arg | Ser | Pro | Ser | Thr | Gly | Leu | Tyr | Asp | Asn | Leu | Glu | Lys | Tyr | His | Leu |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Pro | Tyr | Pro | Glu | Ala | Ile | Phe | Glu | Ile | Ser | Tyr | Phe | Lys | Lys | His | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Glu | Pro | Phe | Phe | Ala | Leu | Ala | Lys | Glu | Leu | Tyr | Pro | Gly | Gln | Phe | Lys |

130 135 140
 Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu
 145 150 155 160
 Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala
 165 170 175
 Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr
 180 185 190
 Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp
 195 200 205
 Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys
 210 215 220
 Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro
 225 230 235 240
 Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu
 245 250 255
 Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu
 260 265 270
 Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu
 275 280 285
 Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly
 290 295 300
 Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp
 305 310 315 320
 Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly
 325 330 335
 Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile
 340 345 350
 Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser
 355 360 365
 Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu
 370 375 380
 Arg Glu Lys Pro Gln
 385

<210> 415
 <211> 481
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu Ser Arg Ala Ser Trp
 1 5 10 15
 Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly His Thr Asp Lys Gln
 20 25 30
 Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg Cys Leu Pro His Leu
 35 40 45
 Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala Phe Arg Ala Met Asp
 50 55 60
 Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln
 65 70 75 80
 Val Gly Gly His Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys
 85 90 95
 Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala
 100 105 110
 Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg
 115 120 125
 Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu
 130 135 140

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616
 617
 618
 619
 620
 621
 622
 623
 624
 625
 626
 627
 628
 629
 630
 631
 632
 633
 634
 635
 636
 637
 638
 639
 640
 641
 642
 643
 644
 645
 646
 647
 648
 649
 650
 651
 652
 653
 654
 655
 656
 657
 658
 659
 660
 661
 662
 663
 664
 665
 666
 667
 668
 669
 670
 671
 672
 673
 674
 675
 676
 677
 678
 679
 680
 681
 682
 683
 684
 685
 686
 687
 688
 689
 690
 691
 692
 693
 694
 695
 696
 697
 698
 699
 700
 701
 702
 703
 704
 705
 706
 707
 708
 709
 710
 711
 712
 713
 714
 715
 716
 717
 718
 719
 720
 721
 722
 723
 724
 725
 726
 727
 728
 729
 730
 731
 732
 733
 734
 735
 736
 737
 738
 739
 740
 741
 742
 743
 744
 745
 746
 747
 748
 749
 750
 751
 752
 753
 754
 755
 756
 757
 758
 759
 760
 761
 762
 763
 764
 765
 766
 767
 768
 769
 770
 771
 772
 773
 774
 775
 776
 777
 778
 779
 780
 781
 782
 783
 784
 785
 786
 787
 788
 789
 790
 791
 792
 793
 794
 795
 796
 797
 798
 799
 800
 801
 802
 803
 804
 805
 806
 807
 808
 809
 810
 811
 812
 813
 814
 815
 816
 817
 818
 819
 820
 821
 822
 823
 824
 825
 826
 827
 828
 829
 830
 831
 832
 833
 834
 835
 836
 837
 838
 839
 840
 841
 842
 843
 844
 845
 846
 847
 848
 849
 850
 851
 852
 853
 854
 855
 856
 857
 858
 859
 860
 861
 862
 863
 864
 865
 866
 867
 868
 869
 870
 871
 872
 873
 874
 875
 876
 877
 878
 879
 880
 881
 882
 883
 884
 885
 886
 887
 888
 889
 890
 891
 892
 893
 894
 895
 896
 897
 898
 899
 900
 901
 902
 903
 904
 905
 906
 907
 908
 909
 910
 911
 912
 913
 914
 915
 916
 917
 918
 919
 920
 921
 922
 923
 924
 925
 926
 927
 928
 929
 930
 931
 932
 933
 934
 935
 936
 937
 938
 939
 940
 941
 942
 943
 944
 945
 946
 947
 948
 949
 950
 951
 952
 953
 954
 955
 956
 957
 958
 959
 960
 961
 962
 963
 964
 965
 966
 967
 968
 969
 970
 971
 972
 973
 974
 975
 976
 977
 978
 979
 980
 981
 982
 983
 984
 985
 986
 987
 988
 989
 990
 991
 992
 993
 994
 995
 996
 997
 998
 999
 1000

Lys Gly Asp His Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu
 145 150 155 160
 Pro Lys Ser Lys Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val
 165 170 175
 Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys
 180 185 190
 Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu
 195 200 205
 Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile
 210 215 220
 Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln
 225 230 235 240
 Gln Gln Leu Gln Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr
 245 250 255
 Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys
 260 265 270
 Val Leu Asp Leu Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser
 275 280 285
 Glu Glu Lys Ala Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser
 290 295 300
 Ala Val Ile Gly Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly
 305 310 315 320
 Ser Gly Gln Leu Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser
 325 330 335
 Val Gln Gly Phe Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg
 340 345 350
 Tyr Leu Arg Arg Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu
 355 360 365
 Leu Lys Ala Val Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser
 370 375 380
 Ser Leu Leu Val Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu
 385 390 395 400
 Asp Ser Asp Ala Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp
 405 410 415
 Glu Ser Ala Gly Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val
 420 425 430
 Asp Val Arg Met Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly
 435 440 445
 Glu Asp Thr Val Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly
 450 455 460
 Leu Gln Ser Leu Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly
 465 470 475 480
 Glu

<210> 416
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 416
 Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
 1 5 10 15
 Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His
 20 25 30
 Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr
 35 40 45
 Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro
 50 55 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Thr | Ala | Arg | Ala | Gly | Ala | Ala | Ala | Val | Val | Leu | Gly | Lys | Gln |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Val | Leu | Val | Val | Gly | Gly | Val | Asp | Glu | Val | Gln | Ser | Pro | Val | Ala | Ala |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Val | Glu | Ala | Phe | Leu | Met | Asp | Glu | Gly | Arg | Trp | Glu | Arg | Arg | Ala | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Pro | Gln | Ala | Ala | Met | Gly | Val | Ala | Thr | Val | Glu | Arg | Asp | Gly | Met |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Val | Tyr | Ala | Leu | Gly | Gly | Met | Gly | Pro | Asp | Thr | Ala | Pro | Gln | Ala | Gln |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Arg | Val | Tyr | Glu | Pro | Arg | Arg | Asp | Cys | Trp | Leu | Ser | Leu | Pro | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Met | Pro | Thr | Pro | Cys | Tyr | Gly | Ala | Ser | Thr | Phe | Leu | His | Gly | Asn | Lys |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Ile | Tyr | Val | Leu | Gly | Gly | Arg | Gln | Gly | Lys | Leu | Pro | Val | Thr | Ala | Phe |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Glu | Ala | Phe | Asp | Leu | Glu | Ala | Arg | Thr | Trp | Thr | Arg | His | Pro | Ser | Leu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Pro | Ser | Arg | Arg | Ala | Phe | Ala | Gly | Cys | Ala | Met | Ala | Glu | Gly | Ser | Val |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Phe | Ser | Leu | Gly | Gly | Leu | Gln | Gln | Pro | Gly | Pro | His | Asn | Phe | Tyr | Ser |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Arg | Pro | His | Phe | Val | Asn | Thr | Val | Glu | Met | Phe | Asp | Leu | Glu | His | Gly |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Ser | Trp | Thr | Lys | Leu | Pro | Arg | Ser | Leu | Arg | Met | Arg | Asp | Lys | Arg | Ala |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Asp | Phe | Val | Val | Gly | Ser | Leu | Gly | Gly | His | Ile | Val | Ala | Ile | Gly | Gly |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Leu | Gly | Asn | Gln | Pro | Cys | Pro | Leu | Gly | Ser | Val | Glu | Ser | Phe | Ser | Leu |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ala | Arg | Arg | Arg | Trp | Glu | Ala | Leu | Pro | Ala | Met | Pro | Thr | Ala | Arg | Cys |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | |
| Ser | Cys | Ser | Ser | Leu | Gln | Ala | Gly | Pro | Arg | Leu | Phe | Val | Ile | Gly | Gly |
| | | | 325 | | | | | 330 | | | | | | 335 | |
| Val | Ala | Gln | Gly | Pro | Ser | Gln | Ala | Val | Glu | Ala | Leu | Cys | Leu | Arg | Asp |
| | | 340 | | | | | | 345 | | | | | 350 | | |
| Gly | Val | | | | | | | | | | | | | | |

<210> 417
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 417
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln
 20

<210> 418
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 418
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ala | Ala | Leu | Trp | Trp | His | Lys | Lys | Gly | Leu | Ala | Val | Leu | Phe | Cys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ile | Leu | Gln | Phe | Leu | Ser | Met | Thr | Trp | Tyr | Ser | Leu | Ser | Tyr | Ile | Pro |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Tyr | Ala | Arg | Asp | Ala | Val | Ile | Lys | Cys | Cys | Ser | Ser | Leu | Leu | Ser | |
| 145 | | | | | 150 | | | | | 155 | | | | | |

<210> 420
 <211> 183
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 420 | | | | | | | | | | | | | | | |
| Met | Glu | Gln | Arg | Leu | Ala | Glu | Phe | Arg | Ala | Ala | Arg | Lys | Arg | Ala | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Ala | Ala | Gln | Pro | Pro | Ala | Ala | Ser | Gln | Gly | Ala | Gln | Thr | Pro | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Lys | Ala | Glu | Ala | Ala | Ala | Thr | Leu | Lys | Ala | Ala | Pro | Gly | Trp | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Arg | Phe | Leu | Val | Trp | Lys | Pro | Arg | Pro | Ala | Ser | Ala | Arg | Ala | Gln |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Gly | Leu | Val | Gln | Glu | Ala | Ala | Gln | Pro | Gln | Gly | Ser | Thr | Ser | Glu |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Thr | Pro | Trp | Asn | Thr | Ala | Ile | Pro | Leu | Pro | Ser | Cys | Trp | Asp | Gln | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Phe | Leu | Thr | Asn | Ile | Thr | Phe | Leu | Lys | Val | Leu | Leu | Trp | Leu | Val | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Gly | Leu | Phe | Val | Glu | Leu | Glu | Phe | Gly | Leu | Ala | Tyr | Phe | Val | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Leu | Phe | Tyr | Trp | Met | Tyr | Val | Gly | Thr | Arg | Gly | Pro | Glu | Glu | Lys |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | Glu | Gly | Glu | Lys | Ser | Ala | Tyr | Ser | Val | Phe | Asn | Pro | Gly | Cys | Glu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ala | Ile | Gln | Gly | Thr | Leu | Thr | Ala | Glu | Gln | Leu | Glu | Arg | Glu | Leu | Gln |
| | | | | 165 | | | | 170 | | | | | | 175 | |
| Leu | Arg | Pro | Leu | Ala | Gly | Arg | | | | | | | | | |
| | | | 180 | | | | | | | | | | | | |

<210> 421
 <211> 143
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 421 | | | | | | | | | | | | | | | |
| Met | Ala | Ala | Pro | Arg | Arg | Gly | Arg | Gly | Ser | Ser | Thr | Val | Leu | Ser | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Pro | Leu | Gln | Met | Leu | Phe | Tyr | Leu | Ser | Gly | Thr | Tyr | Tyr | Ala | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Phe | Leu | Ala | Thr | Leu | Leu | Met | Ile | Thr | Tyr | Lys | Ser | Gln | Val | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Tyr | Pro | His | Arg | Tyr | Leu | Val | Leu | Asp | Leu | Ala | Leu | Leu | Phe | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Met | Gly | Ile | Leu | Glu | Ala | Val | Arg | Leu | Tyr | Leu | Gly | Thr | Arg | Gly | Asn |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Leu | Thr | Glu | Ala | Glu | Arg | Pro | Leu | Ala | Ala | Ser | Leu | Ala | Leu | Thr | Ala |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Thr | Ala | Leu | Leu | Ser | Ala | His | Phe | Leu | Leu | Trp | Gln | Ala | Leu | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |

Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr Leu Leu Ala Leu His Gly
 115 120 125
 Leu Glu Ala Val Leu Gln Val Val Ala Ile Ala Ala Phe Thr Arg
 130 135 140

<210> 422
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 422
 Met Ser Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu
 1 5 10 15
 Pro Val Val Ser Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val
 20 25 30
 Ala Gly Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala
 35 40 45
 Leu Phe Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu
 50 55 60
 His Lys Phe His Gly Gln Val Gln Phe
 65 70

<210> 423
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Pro Pro Phe Gly Gly His Pro Leu Ser Gln Glu Glu Asp Gly Ser
 1 5 10 15
 Gln Arg Cys Cys Cys Leu Ser Ser Leu Arg Ser Val Asp Asp Ser Asn
 20 25 30
 Gly Glu Thr Val Val Ile Met Ala Leu Phe Leu Ala Val Ser Tyr His
 35 40 45
 His Lys Thr Gln Ser Lys Arg Trp Pro Gly Leu Thr Pro Pro His Ser
 50 55 60
 Ser Leu Leu Cys Arg Pro Leu Gln Leu Ser Phe Leu Val Ile Gln Ser
 65 70 75 80
 Val Arg Met Arg Ala Cys Gly Cys Asp Ser Gly His Cys Arg Ile Leu
 85 90 95
 Gly Arg Tyr Ser Leu Leu Gly Trp Ser Gln Gly His Arg Ala Arg Gly
 100 105 110
 Arg Gly Gly Val Ser Leu Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser
 115 120 125
 Glu Gly Gln Gly Gln Trp Leu Met Pro Val Ile Pro Ala Phe
 130 135 140

<210> 424
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 424
 Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr Ala
 1 5 10 15
 Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser Pro
 20 25 30
 Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His Ala

35 40 45
 Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala Asp
 50 55 60
 Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys Pro
 65 70 75 80
 Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser Leu
 85 90 95
 Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro Glu
 100 105 110
 Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val Gln
 115 120 125
 Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser Arg
 130 135 140
 Asn Asp Glu Thr Leu
 145

<210> 425
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 425
 Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys Asn Phe Ala Leu Ser
 1 5 10 15
 Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu Val Glu Lys His Asn
 20 25 30
 Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly Pro Ser Leu Ser Ser
 35 40 45
 Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu Ile Leu Val Ala Thr
 50 55 60
 Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
 65 70 75

<210> 426
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 426
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn
 1 5 10 15
 Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln Gln Ser
 20 25 30
 Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln
 35 40 45
 Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser
 50 55 60
 Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp
 65 70 75 80
 Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu
 85 90 95
 Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu
 100 105 110
 Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe
 115 120 125
 Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu
 130 135 140
 Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Phe Ile

[illegible][illegible][illegible][illegible][illegible][illegible][illegible]

Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala Pro
 20 25 30
 Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu Cys
 35 40 45
 Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser His
 50 55 60
 Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr Asp
 65 70 75 80
 Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
 85 90 95

<210> 430
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 430
 Met Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu
 1 5 10 15
 Pro Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His
 20 25 30
 Cys Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu
 35 40 45
 Leu Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val
 50 55 60
 Val Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn
 65 70 75 80
 Ala Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu
 85 90 95
 Leu Ser Leu

<210> 431
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 431
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu
 1 5 10 15
 Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln
 20 25 30
 Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala
 35 40 45
 Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val Cys
 50 55 60
 Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile
 65 70 75 80
 Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val Met
 85 90 95
 Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu
 100 105 110
 Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
 115 120

<210> 432
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 432

Met Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser
1 5 10 15
Leu Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys
20 25 30
Ser Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr
35 40 45
Gln Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln
50 55 60
Glu Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp
65 70 75 80
Arg Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile
85 90 95
Gly Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln
100 105 110
Glu Arg Thr Ser Ser Leu
115

<210> 433

<211> 49

<212> PRT

<213> Homo sapiens

<400> 433

Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro
1 5 10 15
Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
20 25 30
Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln
35 40 45
His

<210> 434

<211> 89

<212> PRT

<213> Homo sapiens

<400> 434

Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp Ala Val
1 5 10 15
Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe Pro Asp
20 25 30
Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro Gly Glu
35 40 45
Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala Asn Gly
50 55 60
Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val Trp His
65 70 75 80
Glu Asn Ser Gln Glu Glu Arg Lys Tyr
85

<210> 435

<211> 87

<212> PRT

<213> Homo sapiens

<400> 435

Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys Ser
 1 5 10 15
 Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val Phe
 20 25 30
 Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val Glu
 35 40 45
 Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu Val
 50 55 60
 Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly Asp
 65 70 75 80
 Leu Leu Pro Val Asn Arg Ile
 85

<210> 436
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 436
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Gly Pro Gln Ser Gln Thr Pro Glu Asp Cys Pro Ala Arg Pro Glu
 20 25 30
 His Gln Gln Asp Gly Arg Gly His Leu Pro Lys His Glu
 35 40 45

<210> 437
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 437
 Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile His Ser His
 1 5 10 15
 Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln Trp Leu Pro
 20 25 30
 Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys Ser Cys Arg
 35 40 45
 Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser Phe Leu Ile
 50 55 60
 Ser
 65

<210> 438
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 438
 Met Arg Lys Lys Cys Lys Cys Phe Thr Ile Lys Lys Thr Asn Thr Tyr
 1 5 10 15
 Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln Lys Glu Ala Ile Ser Ile
 20 25 30
 Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro Leu Trp Val Thr Arg Leu
 35 40 45
 Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu
 50 55 60
 Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | | | 70 | | | | 75 | | | | 80 | | | |
| Ser | Arg | Asn | Leu | Arg | Tyr | Phe | Ile | Val | Cys | Arg | Asp | Ala | Ser | Ser | Tyr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Pro | Gln | Ser | Leu | Ile | Ser | Gly | Tyr | Ile | Gly | Pro | Cys | Gln | His | Gln |
| | | | | 100 | | | | 105 | | | | | | 110 | |

<210> 439
 <211> 110
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 439 | | | | | | | | | | | | | | | |
| Met | Val | Phe | Gly | Ala | Met | Val | Leu | Leu | Val | Gly | Leu | Glu | Glu | Leu | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Ile | Arg | Asn | Val | Glu | Arg | Leu | Lys | Lys | Asp | Leu | Arg | Ala | Ser | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Cys | Leu | Ile | Asp | Ser | Phe | Leu | Gly | Asp | Ser | Glu | Leu | Ile | Gly | Asp | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Gln | Cys | Val | Asp | Cys | Val | Ile | Pro | Pro | Glu | Gly | Ser | Leu | Leu | Gln |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Ile | Ser | Ser | Tyr | Leu | Tyr | Leu | Asn | Thr | Ala | Leu | Val | Asp | Leu | Pro | Gly |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Val | Ala | Ala | Ser | Gln | Ala | Cys | Asp | Ser | Gln | Gln | Val | Thr | Trp | Leu | Leu |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Tyr | Val | Ala | Asn | Gly | Ala | Tyr | Ser | Ala | Cys | Asn | Arg | Pro | Gly | | |
| | | | 100 | | | | | 105 | | | | | 110 | | |

<210> 440
 <211> 121
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 440 | | | | | | | | | | | | | | | |
| Thr | Ser | Ser | Ser | Gly | Ala | Glu | Val | Thr | Met | Ala | Ala | Ala | Leu | Ala | Arg |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Leu | Gly | Leu | Arg | Pro | Val | Lys | Gln | Val | Arg | Val | Gln | Phe | Cys | Pro | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Lys | Asn | Val | Glu | Ser | Thr | Arg | Thr | Phe | Leu | Gln | Thr | Val | Ser | Ser |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Glu | Lys | Val | Arg | Ser | Thr | Asn | Leu | Asn | Cys | Ser | Val | Ile | Ala | Asp | Val |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Arg | His | Asp | Gly | Ser | Glu | Pro | Cys | Val | Asp | Val | Leu | Phe | Gly | Asp | Gly |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| His | Arg | Leu | Ile | Met | Arg | Gly | Ala | His | Leu | Thr | Ala | Leu | Glu | Met | Leu |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Thr | Ala | Phe | Ala | Ser | His | Ile | Arg | Ala | Arg | Asp | Ala | Ala | Gly | Ser | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asp | Lys | Pro | Gly | Ala | Asp | Thr | Gly | Arg | | | | | | | |
| | | 115 | | | | | 120 | | | | | | | | |

<210> 441
 <211> 99
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 441 | | | | | | | | | | | | | | | |
| Met | Leu | Ala | Arg | Ala | Thr | Phe | Arg | Ala | Ala | Ser | Ala | Pro | Thr | Leu | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Ala Arg Arg Gly Phe Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr
 20 25 30
 His Tyr Pro Glu Gly Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys
 35 40 45
 Lys Gly Phe Ala Phe Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala
 50 55 60
 Leu Pro Phe Leu Leu Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala
 65 70 75 80
 Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala
 85 90 95
 Phe Val Asp

<210> 442
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 442
 Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
 1 5 10 15
 Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
 20 25 30
 Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
 35 40 45
 Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
 50 55 60
 His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
 65 70 75 80
 Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
 85 90 95
 Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu
 100 105 110
 Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val
 115 120 125
 Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp
 130 135 140
 Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser
 145 150 155 160
 Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu
 165 170 175
 Leu Pro Lys Lys Lys Lys Lys
 180

<210> 443
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 443
 Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr
 1 5 10 15
 Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr
 20 25 30
 Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys
 35 40 45
 Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr
 50 55 60
 Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | 70 | | 75 | | 80 | | | | | | | |
| Gly | Ser | Glu | Glu | Leu | Phe | Ser | Ser | Val | Cys | Trp | Arg | Ser | Arg |
| | | | | 85 | | | | | 90 | | | | |

<210> 444
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 444
 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105

<210> 445
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 445
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Cys Lys Leu
 85 90 95
 Leu Cys Gln Lys Leu Met Glu Lys Thr Gly Ile Leu Leu Leu Cys Ala
 100 105 110
 Phe Gly Val Ser Gln Gly Pro Ala Gln Ser Gln Val Glu Val Ser Leu
 115 120 125
 Gly Pro Gly Thr Asp Tyr Arg Thr Leu Gly Lys Thr Leu His Cys His
 130 135 140
 Val Thr Gln Phe Pro His Leu Pro Asp Gly Cys Cys Cys Glu Asn Tyr
 145 150 155 160
 Glu Met Lys

<210> 446
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 446

```
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1          5          10          15
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
          20          25          30
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
          35          40          45
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
          50          55          60
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
65          70          75          80
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
          85          90          95
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
          100          105          110
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
          115          120          125
```

<210> 447

<211> 96

<212> PRT

<213> Homo sapiens

<400> 447

```
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg
1          5          10          15
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys
          20          25          30
Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met
          35          40          45
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala
          50          55          60
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro
65          70          75          80
Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu
          85          90          95
```

<210> 448

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 114

<223> Xaa = Glu,Val

<220>

<221> UNSURE

<222> 113

<223> Xaa = His,Gln

<220>

<221> UNSURE

<222> 115

<223> Xaa = Ile,Val

<400> 448

Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile Thr
1 5 10 15
Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met Lys
20 25 30
Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg Leu
35 40 45
Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met Val
50 55 60
Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu Ser
65 70 75 80
Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys Thr
85 90 95
Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln Pro
100 105 110
Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser Val
115 120 125
Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys Ala
130 135 140
Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys Cys
145 150 155 160

<210> 449
<211> 117
<212> PRT
<213> Homo sapiens

<400> 449
Met Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp
1 5 10 15
Val Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu
20 25 30
Cys Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr
35 40 45
Trp Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu
50 55 60
Leu Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser
65 70 75 80
Val Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys
85 90 95
Lys Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu
100 105 110
Leu Gly Gly Ile Ser
115

<210> 450
<211> 335
<212> PRT
<213> Homo sapiens

<400> 450
Met Cys Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val
1 5 10 15
Leu Ala Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln
20 25 30
Asp Pro Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala
35 40 45
Ser Lys Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala
50 55 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Ile | Gly | Ser | His | His | Ile | Ser | Leu | Asn | Ile | Asp | Pro | Ala | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Lys | Ala | Val | Met | Gly | Ile | Phe | Ser | Leu | Val | Thr | Gly | Lys | Ser | Pro | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Phe | Ala | Ala | His | Gly | Gly | Ser | Ser | Arg | Glu | Asn | Leu | Ala | Leu | Gln | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Gln | Ala | Arg | Ile | Arg | Met | Val | Leu | Ala | Tyr | Leu | Phe | Ala | Gln | Leu |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Ser | Leu | Trp | Ser | Arg | Gly | Val | His | Gly | Gly | Leu | Leu | Val | Leu | Gly | Ser |
| | 130 | | | | 135 | | | | | | 140 | | | | |
| Ala | Asn | Val | Asp | Glu | Ser | Leu | Leu | Gly | Tyr | Leu | Thr | Lys | Tyr | Asp | Cys |
| 145 | | | | 150 | | | | | 155 | | | | | | 160 |
| Ser | Ser | Ala | Asp | Ile | Asn | Pro | Ile | Gly | Gly | Ile | Ser | Lys | Thr | Asp | Leu |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Arg | Ala | Phe | Val | Gln | Phe | Cys | Ile | Gln | Arg | Phe | Gln | Leu | Pro | Ala | Leu |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Gln | Ser | Ile | Leu | Leu | Ala | Pro | Ala | Thr | Ala | Glu | Leu | Glu | Pro | Leu | Ala |
| | 195 | | | | | 200 | | | | | | 205 | | | |
| Asp | Gly | Gln | Val | Ser | Gln | Thr | Asp | Glu | Glu | Asp | Met | Gly | Met | Thr | Tyr |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ala | Glu | Leu | Ser | Val | Tyr | Gly | Lys | Leu | Arg | Lys | Val | Ala | Lys | Met | Gly |
| 225 | | | | 230 | | | | | 235 | | | | | | 240 |
| Pro | Tyr | Ser | Met | Phe | Cys | Lys | Leu | Leu | Gly | Met | Trp | Arg | His | Ile | Cys |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Thr | Pro | Arg | Gln | Val | Ala | Asp | Lys | Val | Lys | Arg | Phe | Phe | Ser | Lys | Tyr |
| | | 260 | | | | | 265 | | | | | | 270 | | |
| Ser | Met | Asn | Arg | His | Lys | Met | Thr | Thr | Leu | Thr | Pro | Ala | Tyr | His | Ala |
| | 275 | | | | | 280 | | | | | | 285 | | | |
| Glu | Asn | Tyr | Ser | Pro | Glu | Asp | Asn | Arg | Phe | Asp | Leu | Arg | Pro | Phe | Leu |
| | 290 | | | | 295 | | | | | 300 | | | | | |
| Tyr | Asn | Thr | Ser | Trp | Pro | Trp | Gln | Phe | Arg | Cys | Ile | Glu | Asn | Gln | Val |
| 305 | | | | 310 | | | | | 315 | | | | | | 320 |
| Leu | Gln | Leu | Glu | Arg | Ala | Glu | Pro | Gln | Ser | Leu | Asp | Gly | Val | Asp | |
| | | | 325 | | | | | 330 | | | | | | 335 | |

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys,Asn

<400> 451

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Trp | Val | Ile | Asn | His | Ala | Ile | Leu | Pro | Arg | Met | Arg | Met | His |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Lys | Arg | Gln | Thr | Ile | Thr | Arg | His | Ser | Ala | Ser | Leu | Ser | Phe | His |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Ala | Leu | Pro | Arg | Ser | Ala | Phe | Leu | Gln | Leu | Cys | Leu | Leu | Arg | Gln | Ile |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| His | Gln | Ile | Pro | Cys | Leu | Ser | Ile | Phe | Ser | Ser | Thr | Leu | Arg | Ala | Gln |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Thr | His | Asp | Ser | Gly | Ile | Gly | Cys | Thr | Thr | Ala | Xaa | Pro | Gly | Gly | Arg |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 |
| Arg | Gln | Glu | Gln | Leu | Arg | | | | | | | | | | |
| | | | | 85 | | | | | | | | | | | |

<210> 452
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 452
 Met Lys Ile Ala Leu Cys Gln Arg Glu Leu Pro Ser Pro Arg Ser Cys
 1 5 10 15
 Leu Leu Ser Arg Asp Val Thr Gly Val Ile Cys Thr Arg Met Pro Arg
 20 25 30
 Leu Ala Ile Cys Ser Lys Thr Ala Gln Lys Ala Leu Pro Cys Ile Pro
 35 40 45
 Leu Leu His Thr Ser Pro Leu Cys Leu Gln Leu Leu Ser Ala Gly Leu
 50 55 60
 His Ile Tyr Ala Thr Leu Cys Lys Ser Cys Ala Ser Arg Asn His Lys
 65 70 75 80
 Asn Ile Phe Leu His Leu Leu His Ser Leu Ser Ala Ala
 85 90

<210> 453
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 453
 Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe
 1 5 10 15
 Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu
 20 25 30
 Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val
 35 40 45
 Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val
 50 55 60
 Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu Gln
 65 70 75 80
 Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu Gln
 85 90 95
 Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
 100 105

<210> 454
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 454
 Met Ser Leu Cys Glu Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg
 1 5 10 15
 Ile Lys Leu Ser Gly Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe
 20 25 30
 Cys Asp Gln His Gly Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys
 35 40 45
 Pro Ala Cys Asn Ser Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr
 50 55 60
 Glu Leu Ser Pro Ser Glu Tyr Lys Ala Met Val Leu Ala Gly Leu
 65 70 75 80
 Arg Pro Glu Ile Val Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| Thr | Tyr | Gln | Val | His | Gln | Glu | Arg | Leu | Tyr | Gln | Glu | Tyr | Asn | Phe | Ser | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Lys | Ala | Glu | Gly | His | Leu | Lys | Gln | Met | Glu | Lys | Ile | Tyr | Thr | Gln | Gln | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Ile | Gln | Ser | Lys | Asp | Val | Glu | Leu | Thr | Ser | Met | Lys | Gly | Glu | Val | Thr | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| Ser | Met | Lys | Lys | Val | Leu | Glu | Glu | Tyr | Lys | Lys | Lys | Phe | Ser | Asp | Ile | | |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | | | |
| Ser | Glu | Lys | Leu | Met | Glu | Arg | Asn | Arg | Gln | Tyr | Gln | Lys | Leu | Gln | Gly | | |
| | | | 165 | | | | | 170 | | | | | | 175 | | | |
| Leu | Tyr | Asp | Ser | Leu | Arg | Leu | Arg | Asn | Ile | Thr | Ile | Ala | Asn | His | Glu | | |
| | | 180 | | | | | | 185 | | | | | 190 | | | | |
| Gly | Thr | Leu | Glu | Pro | Ser | Met | Ile | Ala | Gln | Ser | Gly | Val | Leu | Gly | Phe | | |
| | 195 | | | | | 200 | | | | | 205 | | | | | | |
| Pro | Leu | Gly | Asn | Asn | Ser | Lys | Phe | Pro | Leu | Asp | Asn | Thr | Pro | Val | Arg | | |
| | 210 | | | | | 215 | | | | 220 | | | | | | | |
| Asn | Arg | Gly | Asp | Gly | Asp | Gly | Asp | Phe | Gln | Phe | Arg | Pro | Phe | Phe | Ala | | |
| 225 | | | | 230 | | | | 235 | | | | | | 240 | | | |
| Gly | Ser | Pro | Thr | Ala | Pro | Glu | Pro | Ser | Asn | Ser | Phe | Phe | Ser | Phe | Val | | |
| | | | 245 | | | | | 250 | | | | | | 255 | | | |
| Ser | Pro | Ser | Arg | Glu | Leu | Glu | Gln | Gln | Gln | Val | Ser | Ser | Arg | Ala | Phe | | |
| | | 260 | | | | 265 | | | | | | | 270 | | | | |
| Lys | Val | Lys | Arg | Ile | | | | | | | | | | | | | |
| | | 275 | | | | | | | | | | | | | | | |

<210> 455
 <211> 173
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | | | | | | | | | | | | | | |
| Met | Leu | Val | Met | Tyr | Leu | Leu | Ala | Ala | Leu | Phe | Gly | Tyr | Leu | Thr | Phe | | |
| 1 | | | 5 | | | | | | 10 | | | | 15 | | | | |
| Tyr | Gly | Glu | Val | Glu | Asp | Glu | Leu | Leu | His | Ala | Tyr | Ser | Lys | Val | Tyr | | |
| | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Thr | Leu | Asp | Ile | Pro | Leu | Leu | Met | Val | Arg | Leu | Ala | Val | Leu | Val | Ala | | |
| | 35 | | | | | 40 | | | | | 45 | | | | | | |
| Val | Thr | Leu | Thr | Val | Pro | Ile | Val | Leu | Phe | Pro | Ile | Arg | Thr | Ser | Val | | |
| | 50 | | | | | 55 | | | | 60 | | | | | | | |
| Ile | Thr | Leu | Leu | Phe | Pro | Lys | Arg | Pro | Phe | Ser | Trp | Ile | Arg | His | Phe | | |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | | | |
| Leu | Ile | Ala | Ala | Val | Leu | Ile | Ala | Leu | Asn | Asn | Val | Leu | Val | Ile | Leu | | |
| | | | 85 | | | | | 90 | | | | 95 | | | | | |
| Val | Pro | Thr | Ile | Lys | Tyr | Ile | Phe | Gly | Phe | Ile | Gly | Ala | Ser | Ser | Ala | | |
| | | 100 | | | | | 105 | | | | 110 | | | | | | |
| Thr | Met | Leu | Ile | Phe | Ile | Leu | Pro | Ala | Val | Phe | Tyr | Leu | Lys | Leu | Val | | |
| | 115 | | | | | 120 | | | | | 125 | | | | | | |
| Lys | Lys | Glu | Thr | Phe | Arg | Ser | Pro | Gln | Lys | Val | Gly | Ala | Leu | Ile | Phe | | |
| | 130 | | | | | 135 | | | | 140 | | | | | | | |
| Leu | Val | Val | Gly | Ile | Phe | Phe | Met | Ile | Gly | Ser | Met | Ala | Leu | Ile | Ile | | |
| 145 | | | | 150 | | | | 155 | | | | | | 160 | | | |
| Ile | Asp | Trp | Ile | Tyr | Asp | Pro | Pro | Asn | Ser | Lys | His | His | | | | | |
| | | 165 | | | | | | 170 | | | | | | | | | |

<210> 456
 <211> 370
 <212> PRT

<213> Homo sapiens

<400> 456

```
Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
1      5      10      15
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
      20      25      30
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
      35      40      45
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
      50      55      60
Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
      65      70      75      80
Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
      85      90      95
Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
      100     105     110
Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
      115     120     125
Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
      130     135     140
Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
      145     150     155     160
Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
      165     170     175
Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
      180     185     190
Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
      195     200     205
Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
      210     215     220
Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
      225     230     235     240
Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
      245     250     255
Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
      260     265     270
Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
      275     280     285
Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
      290     295     300
Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
      305     310     315     320
Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
      325     330     335
Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
      340     345     350
Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
      355     360     365
Val Glu
      370
```

<210> 457

<211> 393

<212> PRT

<213> Homo sapiens

<400> 457

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

```

Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu
1      5      10      15
Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly
      20      25      30
Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr
      35      40      45
Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr
      50      55      60
Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu His
65      70      75      80
Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser
      85      90      95
Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr
      100     105     110
Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala
      115     120     125
Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu Asn
130     135     140
Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys
145     150     155     160
Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile Leu
      165     170     175
Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His
      180     185     190
Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp
      195     200     205
Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr
210     215     220
Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr
225     230     235     240
Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val
      245     250     255
Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg
      260     265     270
Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp
275     280     285
Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn Cys
290     295     300
Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu Ser
305     310     315     320
Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu Leu
      325     330     335
Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg His
      340     345     350
Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala Leu
355     360     365
Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu Pro
370     375     380
Met Glu Ser Gly Lys Glu Lys Ala Thr
385     390

```

<210> 458

<211> 116

<212> PRT

<213> Homo sapiens

<400> 458

Met Val Gly Gly Glu Ala Ala Ala Ala Val Glu Glu Leu Val Ser Gly

1 5 10 15
 Val Arg Gln Ala Asp Phe Ala Glu Gln Phe Arg Ser Tyr Ser Glu
 20 25 30
 Ser Glu Lys Gln Trp Lys Ala Arg Met Glu Phe Ile Leu Arg His Leu
 35 40 45
 Pro Asp Tyr Arg Asp Pro Pro Asp Gly Ser Gly Arg Leu Asp Gln Leu
 50 55 60
 Leu Ser Leu Ser Met Val Trp Ala Asn His Leu Phe Leu Gly Cys Ser
 65 70 75 80
 Tyr Asn Lys Asp Leu Leu Asp Lys Val Met Glu Met Ala Asp Gly Ile
 85 90 95
 Glu Val Glu Asp Leu Pro Gln Phe Thr Thr Arg Ser Glu Leu Met Lys
 100 105 110
 Lys His Gln Ser
 115

<210> 459
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 459
 Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
 1 5 10 15
 Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
 20 25 30
 Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
 35 40 45
 Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
 50 55 60
 Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
 65 70 75 80
 Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln Thr Glu Asp Ser Trp
 85 90 95
 Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro Leu Thr Val Arg Arg
 100 105 110
 His Val Pro Ala Val Trp Val Leu Ser Arg Asp Pro Leu Asp Pro
 115 120 125
 Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
 130 135 140
 Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg Arg Arg Ala Arg Asp
 145 150 155 160
 Thr Arg Ser

<210> 460
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 460
 Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
 1 5 10 15
 Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala
 20 25 30
 Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu
 35 40 45
 Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu
 50 55 60

Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr
 65 70 75 80
 Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys
 85 90 95
 Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr
 100 105 110
 Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp
 115 120 125
 Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser
 130 135 140
 Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala
 145 150 155 160
 Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu
 165 170 175
 Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr
 180 185 190
 Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly
 195 200 205
 Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu
 210 215 220
 Lys Thr Ile His Glu Glu
 225 230

<210> 461
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> 95
 <223> Xaa = Cys, Trp

<400> 461
 Met Glu Arg Pro Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu
 1 5 10 15
 Phe Arg Asn Glu Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe
 20 25 30
 Phe Thr Ala Leu Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr
 35 40 45
 Lys Ser Tyr Ile Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser
 50 55 60
 Tyr Phe Tyr Ala Ala Ile Val Ala Val Val Ala Val His Val Val Leu
 65 70 75 80
 Ala Leu Phe Val Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg
 85 90 95
 Glu Gly Lys Gln Asp
 100

<210> 462
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 462
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
 1 5 10 15
 Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu

20 25 30
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 35 40 45
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
 50 55 60
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 65 70 75 80
 Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro
 85 90

<210> 463
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 463
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala
 1 5 10 15
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu
 20 25 30
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Lys Leu Leu Pro Leu Asp
 35 40 45
 Thr Tyr Val Glu Ser Pro Ala Ala Val Met Glu Leu Val Pro Ser Asp
 50 55 60
 Lys Glu Arg Gly Leu Gln Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile
 65 70 75 80
 Leu Arg Arg Ala Gly Cys Val Arg Ala Leu Ala Lys Ile Glu Arg Phe
 85 90 95
 Glu Phe Tyr Glu Arg Ala Lys Lys Ala Phe Ala Val Val Ala Thr Gly
 100 105 110
 Glu Thr Ala Leu Tyr Gly Asn Leu Ile Leu Arg Lys Gly Val Leu Ala
 115 120 125
 Leu Asn Pro Leu Leu
 130

<210> 464
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala
 1 5 10 15
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu
 20 25 30
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Ala Ala Ala Pro Gly His
 35 40 45
 Leu Cys Gly Glu Ser Gly Cys Ser His Gly Ala Gly Ala Gln Arg Gln
 50 55 60
 Gly Glu Gly Pro Ala Asp Pro Ser Val Asp Gly Val Arg Val His Pro
 65 70 75 80
 Thr Gln Gly Arg Leu Cys Glu Ser Pro Gly Lys Asp Arg Glu Val
 85 90 95

<210> 465
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 465

Met Thr Pro Ile Lys Leu Leu Asn Leu Thr Ser Arg Tyr Asn Phe Arg
1 5 10 15
Arg Thr Phe Gly Ile Glu Leu Ser Ser Asn Ser Ser Tyr Cys Lys Arg
20 25 30
Gly Asn Gly Tyr Arg Ser Arg Val Pro Lys Glu Cys Glu Cys Asn Trp
35 40 45
Leu His Leu Glu Ser Asp Thr Leu Lys Lys Leu Pro Ile Ile Ser Pro
50 55 60
Ser Trp Thr Cys Arg Ile Ile Leu Phe Leu Tyr Phe Ser Gly Gln Leu
65 70 75 80
Leu Gln Leu Ser Leu Ser Cys Leu Gln Leu Ile Lys Leu
85 90

<210> 466

<211> 500

<212> PRT

<213> Homo sapiens

<400> 466

Met Glu Val Ser Thr Asn Pro Ser Ser Asn Ile Asp Pro Gly Asn Tyr
1 5 10 15
Val Glu Met Asn Asp Ser Ile Thr His Leu Pro Ser Lys Val Val Ile
20 25 30
Gln Asp Ile Thr Met Glu Leu His Cys Pro Leu Cys Asn Asp Trp Phe
35 40 45
Arg Asp Pro Leu Met Leu Ser Cys Gly His Asn Phe Cys Glu Ala Cys
50 55 60
Ile Gln Asp Phe Trp Arg Leu Gln Ala Lys Glu Thr Phe Cys Pro Glu
65 70 75 80
Cys Lys Met Leu Cys Gln Tyr Asn Asn Cys Thr Phe Asn Pro Val Leu
85 90 95
Asp Lys Leu Val Glu Lys Ile Lys Lys Leu Pro Leu Leu Lys Gly His
100 105 110
Pro Gln Cys Pro Glu His Gly Glu Asn Leu Lys Leu Phe Ser Lys Pro
115 120 125
Asp Gly Lys Leu Ile Cys Phe Gln Cys Lys Asp Ala Arg Leu Ser Val
130 135 140
Gly Gln Ser Lys Glu Phe Leu Gln Ile Ser Asp Ala Val His Phe Phe
145 150 155 160
Met Glu Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys
165 170 175
Glu Leu Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His
180 185 190
Lys Glu Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe Leu
195 200 205
Lys Leu His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr Glu
210 215 220
Leu Arg Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn Leu
225 230 235 240
Ser Gln Leu Gln Glu Gln Cys Leu Leu Ala Lys Asp Met Leu Val Ser
245 250 255
Ile Gln Ala Lys Thr Glu Gln Gln Asn Ser Phe Asp Phe Leu Lys Asp
260 265 270
Ile Thr Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu Ala
275 280 285
Thr Arg Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys Gly

| | | |
|---|-----|-----|
| 290 | 295 | 300 |
| Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro | | |
| 305 | 310 | 315 |
| Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu | | 320 |
| | 325 | 330 |
| Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys | | 335 |
| | 340 | 345 |
| Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu | | 350 |
| | 355 | 360 |
| Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val | | 365 |
| | 370 | 375 |
| Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile | | 380 |
| 385 | 390 | 395 |
| Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu | | 400 |
| | 405 | 410 |
| Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe | | 415 |
| | 420 | 425 |
| Ser Leu Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp | | 430 |
| | 435 | 440 |
| Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His | | 445 |
| | 450 | 455 |
| Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe | | 460 |
| 465 | 470 | 475 |
| Cys Pro Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile | | 480 |
| | 485 | 490 |
| | | 495 |
| Leu His Pro Gln | | |
| 500 | | |

<210> 467
 <211> 140
 <212> PRT
 <213> Homo sapiens

| |
|---|
| <400> 467 |
| Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe |
| 1 5 10 15 |
| Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr |
| 20 25 30 |
| Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln |
| 35 40 45 |
| Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro |
| 50 55 60 |
| Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr |
| 65 70 75 80 |
| Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln His Ile Arg Thr Ser |
| 85 90 95 |
| Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu |
| 100 105 110 |
| Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile |
| 115 120 125 |
| Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile Cys |
| 130 135 140 |

<210> 468
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 468

Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
1 5 10 15
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
20 25 30
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
35 40 45
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
50 55 60
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
65 70 75 80
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
85 90 95
Trp Trp Thr Gln
100

<210> 469

<211> 119

<212> PRT

<213> Homo sapiens

<400> 469

Met Ala Ser Tyr Ser Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly
1 5 10 15
Pro Gly His Arg Ser Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro
20 25 30
Pro Leu Pro Arg Pro Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu
35 40 45
Glu Leu Gly Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp
50 55 60
Leu Phe Cys His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu
65 70 75 80
Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala
85 90 95
Cys Ile Gly Glu Arg Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys
100 105 110
Arg Asn Arg Ala Trp His Lys
115

<210> 470

<211> 140

<212> PRT

<213> Homo sapiens

<400> 470

Met Arg Ser Glu Cys Val Leu Gly Ala Ala Ser Asp Ser Gly Gln Glu
1 5 10 15
Ala Pro Arg Asp Thr Trp Phe Leu Gln Gly Trp Lys Ala Ser Arg Arg
20 25 30
Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr
35 40 45
Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln
50 55 60
Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr
65 70 75 80
Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro
85 90 95
Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
 35 40 45
 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
 50 55 60
 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
 65 70 75 80
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
 85 90 95
 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
 100 105 110
 Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly
 115 120 125
 Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val
 130 135 140

<210> 474
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
 85 90 95
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 475
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 475
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ser Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Cys Arg Ser Phe Ala Val His Thr Arg
 85 90 95

Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 476
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala Gly
 1 5 10 15
 Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro Gln
 20 25 30
 Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr
 35 40 45
 Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu
 50 55 60
 Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala
 65 70 75 80
 Ser Gly Arg Ser Pro
 85

<210> 477
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 477
 Met Gly Arg Pro Trp Met Val Met Ile Leu Glu Ser Lys Ser Glu Glu
 1 5 10 15
 Lys Met Trp Tyr Gly Val Phe Leu Trp Ala Leu Val Ser Ser Leu Phe
 20 25 30
 Phe His Val Pro Ala Gly Leu Leu Ala Leu Phe Thr Leu Arg His His
 35 40 45
 Lys Tyr Gly Arg Phe Met Ser Val Ser Ile Leu Leu Met Gly Ile Val
 50 55 60
 Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser Ala Ala Ile Ala Gly Val
 65 70 75 80
 Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro Phe Glu Ala Leu Thr Leu
 85 90 95
 Gly Thr Gly Gln Thr Phe Cys Val Leu Val Val Ser Phe Leu Arg Ile
 100 105 110
 Leu Ala Thr Leu
 115

<210> 478
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 478
 Met Asn Arg Tyr Cys Gly Lys Ile Phe Val Ser Val Met Val Lys Leu
 1 5 10 15
 Gln Lys Asn Lys Leu Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe

20 25 30
 Phe Glu Tyr Leu Glu Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser
 35 40 45
 Ala Lys Ser His His Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala
 50 55 60
 Ala Pro Leu Leu Ser Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn
 65 70 75 80
 Gly Leu Gly Lys Cys His Asp Pro His Phe Thr Gly Glu Glu Thr Glu
 85 90 95
 Ala Gln Arg Gly Lys Leu Thr Thr
 100

<210> 479
 <211> 439
 <212> PRT
 <213> Homo sapiens

<400> 479
 Leu Gly Asp His Gly Trp Glu Leu Ser Leu Glu Glu Asp Ala Gln Leu
 1 5 10 15
 Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln Arg
 20 25 30
 Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr Asn
 35 40 45
 Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln Lys
 50 55 60
 Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn Gln
 65 70 75 80
 Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro Glu
 85 90 95
 Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser Ala
 100 105 110
 His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly Ala
 115 120 125
 Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile Leu
 130 135 140
 Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile Tyr
 145 150 155 160
 Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr Ile
 165 170 175
 Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys Tyr
 180 185 190
 Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn Cys
 195 200 205
 Leu Glu Gly Thr His Glu Phe Glu Ala Ile Gly Phe Gln Lys Val
 210 215 220
 Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val Leu
 225 230 235 240
 Ser Glu Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys Glu
 250 255
 Gln Leu Leu Ala Ala Pro Val Arg Ala Lys Leu Asp Arg Gln Arg
 260 265 270
 Arg Val Phe Gln Pro Ser Ala Ser Gln Phe Glu Leu Pro Gly
 275 285
 Asp Phe Phe Asn Leu Thr Ala Glu Lys Arg Glu Gln Arg Leu
 290 295 300
 Arg Ser Glu Ala Val Glu Arg Leu Ser Val Thr Lys Ala Met
 305 310 315 320

Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr Leu
 325 330 335
 Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe Tyr
 340 345 350
 Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala Leu
 355 360 365
 Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys
 370 375 380
 Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val Pro
 385 390 395 400
 Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp Ile
 405 410 415
 Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu Leu
 420 425 430
 Ser Ala Ile Glu Lys Leu Leu
 435

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu
 1 5 10 15
 Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala
 20 25 30
 Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys
 35 40 45
 Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly
 50 55 60
 Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg
 65 70 75 80
 Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val
 85 90 95
 Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Ser Asp Lys Asn Asn
 100 105 110
 Tyr Thr Ser Gly
 115

<210> 481
 <211> 171
 <212> PRT
 <213> Homo sapiens

<400> 481
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly
 1 5 10 15
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe
 20 25 30
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg
 35 40 45
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr
 50 55 60
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val
 65 70 75 80
 Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His
 85 90 95

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Leu | Leu | Gln | Gly | Glu | Arg | Asn | Pro | Arg | Leu | Glu | Asp | Ala | Ile | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Thr | Asp | Leu | Asn | Arg | Thr | Phe | Pro | Asp | Asn | Val | Lys | Phe | Arg | Lys | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Thr | Asp | Pro | Cys | Leu | Gln | Arg | Thr | Leu | Tyr | Asn | Val | Leu | Leu | Ala | Tyr |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Gly | His | His | Asn | Gln | Gly | Val | Gly | Tyr | Cys | Gln | Gly | Met | Asn | Phe | Ile |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ala | Gly | Tyr | Leu | Ile | Leu | Ile | Thr | Asn | Asn | Glu | | | | | |
| | | | | 165 | | | | | | 170 | | | | | |

<210> 482

<211> 177

<212> PRT

<213> Homo sapiens

<400> 482

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Pro | Ala | Glu | Arg | Ser | Arg | Val | Pro | Arg | Ile | Asp | Pro | Tyr | Gly |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
| Phe | Glu | Arg | Pro | Glu | Asp | Phe | Asp | Asp | Ala | Ala | Tyr | Glu | Lys | Phe | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Ser | Tyr | Leu | Val | Thr | Leu | Thr | Arg | Arg | Ala | Ile | Lys | Trp | Ser | Arg |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Leu | Gln | Gly | Gly | Gly | Val | Pro | Arg | Ser | Arg | Thr | Val | Lys | Arg | Tyr |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Val | Arg | Lys | Gly | Val | Pro | Leu | Glu | His | Arg | Ala | Arg | Val | Trp | Met | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Ser | Gly | Ala | Gln | Ala | Gln | Met | Asp | Gln | Asn | Pro | Gly | Tyr | Tyr | His |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gln | Leu | Leu | Gln | Gly | Glu | Arg | Asn | Pro | Arg | Leu | Glu | Asp | Ala | Ile | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Thr | Asp | Leu | Asn | Arg | Thr | Phe | Pro | Asp | Asn | Val | Lys | Phe | Arg | Lys | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Thr | Asp | Pro | Cys | Leu | Gln | Arg | Thr | Leu | Tyr | Asn | Val | Leu | Leu | Ala | Tyr |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Gly | His | His | Asn | Gln | Gly | Val | Gly | Tyr | Cys | Gln | Gly | Met | Asn | Phe | Ile |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ala | Gly | Tyr | Leu | Ile | Leu | Ile | Thr | Asn | Asn | Asp | Lys | Asn | Leu | Phe | Gly |
| | | | | 165 | | | | | | 170 | | | | | 175 |

Cys